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(21) International Application Number: PCT/US95/02118 (22) International Filing Date: 14 February 1995 (14.02.95) (30) Priority Data: <table border="0"><tr><td>08/196,030</td><td>14 February 1994 (14.02.94)</td><td>US</td></tr><tr><td>08/242,654</td><td>13 May 1994 (13.05.94)</td><td>US</td></tr><tr><td>08/283,314</td><td>29 July 1994 (29.07.94)</td><td>US</td></tr><tr><td>08/344,185</td><td>23 November 1994 (23.11.94)</td><td>US</td></tr><tr><td>08/344,190</td><td>23 November 1994 (23.11.94)</td><td>US</td></tr><tr><td>08/344,557</td><td>27 January 1995 (27.01.95)</td><td>US</td></tr></table> (71) Applicant (for all designated States except US): ABBOTT LABORATORIES [US/US]; Chad 0377/AP6D-2, 100 Abbott Park Road, Abbott Park, IL 60064-3500 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): SIMONS, John, N. [US/US]; 738 N. Allegheny Road, Grayslake, IL 60030 (US). PILOT-MATIAS, Tami, J. [US/US]; 2100 Cranbrook Road, Green Oaks, IL 60048 (US). DAWSON, George, J. [US/US]; 914 South Dymond Road, Libertyville, IL 60048 (US). SCHLAUDER, George, G. [US/US]; 7640 Karlove, Skokie, IL 60076 (US). DESAI, Suresh, M. [US/US]; 1408 Amy Lane, Libertyville, IL 60048 (US). LEARY,			08/196,030	14 February 1994 (14.02.94)	US	08/242,654	13 May 1994 (13.05.94)	US	08/283,314	29 July 1994 (29.07.94)	US	08/344,185	23 November 1994 (23.11.94)	US	08/344,190	23 November 1994 (23.11.94)	US	08/344,557	27 January 1995 (27.01.95)	US	Thomas, P. [US/US]; 6820 107th Avenue, Kenosha, WI 53143 (US). MUERHOFF, Anthony, Scott [US/US]; 611 68th Place, Kenosha, WI 53143 (US). ERKER, James, Carl [US/US]; 359 N. White Tail Drive, Hainesville, IL 60030 (US). BUIK, Sheri, L. [US/US]; 660 East Princeton Court, Round Lake, IL 60073 (US). MUSHAHWAR, Isa, K. [US/US]; 18790 Arbor Boulevard, Grayslake, IL 60030 (US). (74) Agents: POREMBSKI, Priscilla, E. et al.; Abbott Laboratories, Chad 0377/AP6D-2, 100 Abbott Park Road, Abbott Park, IL 60064-3500 (US). (81) Designated States: CA, JP, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
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(54) Title: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE (57) Abstract <p>Hepatitis GB Virus (HGBV) nucleic acid and amino acid sequences useful for a variety of diagnostic and therapeutic applications, kits for using the HGBV nucleic acid or amino acid sequences, HGBV immunogenic particles, and antibodies which specifically bind to HGBV. Also provided are methods for producing antibodies, polyclonal or monoclonal, from the HGBV nucleic acid or amino acid sequences.</p>																					

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NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS
AND METHODS FOR THEIR USE

This application is a continuation-in-part application of U.S. Serial No.
5 08/377,557 filed January 27, 1995, which is a continuation-in-part of U.S. Serial
No. 08/344,185 filed November 23, 1994 and U.S. Serial No. 08/344,190 filed
November 23, 1994, which are each continuation-in-part applications of
08/283,314 filed July 29, 1994, which is a continuation-in-part application of
U.S. Serial No. 08/242,654, filed May 13, 1994, which is a continuation-in-part
10 application of U.S. Serial No. 08/196,030 filed February 14, 1994, all of which
enjoy common ownership and each of which is incorporated herein by reference.

Background of the Invention

This invention relates generally to a group of infectious viral agents causing
15 hepatitis in man, and more particularly, relates to materials such as polynucleotides
derived from this group of viruses, polypeptides encoded therein, antibodies
which specifically bind to these polypeptides, and diagnostics and vaccines that
employ these materials.

Hepatitis is one of the most important diseases transmitted from a donor to
20 a recipient by transfusion of blood products, organ transplantation and
hemodialysis; it also can be transmitted via ingestion of contaminated food stuffs
and water, and by person to person contact. Viral hepatitis is known to include a
group of viral agents with distinctive viral genes and modes of replication, causing
hepatitis with differing degrees of severity of hepatic damage through different
25 routes of transmission. In some cases, acute viral hepatitis is clinically diagnosed
by well-defined patient symptoms including jaundice, hepatic tenderness and an
elevated level of liver transaminases such as aspartate transaminase (AST), alanine
transaminase (ALT) and isocitrate dehydrogenase (ISD). In other cases, acute
viral hepatitis may be clinically inapparent. The viral agents of hepatitis include
30 hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV),
hepatitis delta virus (HDV), hepatitis E virus (HEV), Epstein-Barr virus (EBV)
and cytomegalovirus (CMV).

Although specific serologic assays available by the late 1960's to screen
blood donations for the presence of HBV surface antigen (HBsAg) were
35 successful in reducing the incidence of post-transfusion hepatitis (PTH) in blood
recipients, PTH continued to occur at a significant rate. H. J. Alter et al., Ann.
Int. Med. 77:691-699 (1972); H. J. Alter et al., Lancet ii:838-841 (1975).

Investigators began to search for a new agent, termed "non-A, non-B hepatitis" (NANBH), that caused viral hepatitis not associated with exposure to viruses previously known to cause hepatitis in man (HAV, HBV, CMV and EBV). See, for example, S. M. Feinstone et al., New Engl. J. Med. 292:767-770 (1975);
5 Anonymous editorial, Lancet ii:64-65 (1975); F. B. Hollinger in B. N. Fields and D. M. Knipe et al., Virology, Raven Press, New York, pp. 2239-2273 (1990).

Several lines of epidemiological and laboratory evidence have suggested the existence of more than one parenterally transmitted NANB agent, including multiple attacks of acute NANBH in intravenous drug users; distinct incubation
10 periods of patients acquiring NANBH post-transfusion; the outcome of cross-challenge chimpanzee experiments; the ultrastructural liver pathology of infected chimpanzees; and the differential resistance of the putative agents to chloroform. J. L. Dienstag, Gastroenterology 85:439-462 (1983); J. L. Dienstag, Gastroenterology 85:743-768 (1983); F. B. Hollinger et al., J. Infect. Dis.
15 142:400-407 (1980); D. W. Bradley in F. Chisari, ed., Advances in Hepatitis Research, Masson, New York, pp. 268-280 (1984); and D. W. Bradley et al., J. Infect. Dis. 148:254-265 (1983).

A serum sample obtained from a surgeon who had developed acute hepatitis was shown to induce hepatitis when inoculated into tamarins (*Saguinus species*). Four of four tamarins developed elevated liver enzymes within a few
20 weeks following their inoculation, suggesting that an agent in the surgeon's serum could produce hepatitis in tamarins. Serial passage in various non-human primates demonstrated that this hepatitis was caused by a transmissible agent; filtration studies suggested the agent to be viral in nature. The transmissible agent
25 responsible for these cases of hepatitis in the surgeon and tamarins was termed the "GB agent." F. Deinhardt et al., J. Exper. Med. 125:673-688 (1967). F. Deinhardt et al., J. Exper. Med., supra; E. Tabor et al., J. Med. Virol. 5:103-108 (1980); R. O. Whittington et al., Viral and Immunological Diseases in Nonhuman Primates, Alan R. Liss, Inc., New York, pp. 221-224 (1983)

30 Although it was suggested that the GB agent may be an agent causing NANBH in humans and that the GB agent was not related to the known NANBH agents studied in various laboratories, no definitive or conclusive studies on the GB agent are known, and no viral agent has been discovered or molecularly characterized. F. Deinhardt et al., Am. J. Med. Sci. 270:73-80 (1975); and J. L.
35 Dienstag et al., Nature 264:260-261 (1976). See also E. Tabor et al., J. Med. Virol., supra; E. Tabor et al., J. Infect. Dis. 140:794-797 (1979); R. O. Whittington et al., supra; and P. Karayiannis et al., Hepatology 9:186-192 (1989).

Early studies indicated that the GB agent was unrelated to any known human hepatitis virus. S. M. Feinstone et al., Science 182:1026-1028 (1973); P. J. Provost et al., Proc. Soc. Exp. Biol. Med. 148:532-539 (1975); J. L. Melnick, Intervirology 18:105-106 (1982); A. W. Holmes et al., Nature 243:419-420 (1973); and F. Deinhardt et al., Am. J. Med. Sci., supra. However, questions were raised regarding whether the GB agent was a virus which induced hepatitis infection in humans, or a latent tamarin virus activated by the GB serum and once activated, easily passaged to other tamarins, inducing hepatitis in them. Also, a small percentage of marmosets inoculated with GB-positive serum did not develop clinical hepatitis (4 of 52, or 7.6%), suggesting that these animals may have been naturally immune and thus, that the GB agent may be a marmoset virus. W. P. Parks et al., J. Infect. Dis. 120:539-547 (1969); W. P. Parks et al., J. Infect. Dis. 120:548-559 (1969). Morphological studies have been equivocal, with immune electron microscopy studies in one report indicating that the GB agent formed immune complexes with a size distribution of 20-22 nm and resembling the spherical structure of a parvovirus, while another study reported that immune electron microscopy data obtained from liver homogenates of GB-positive tamarins indicated that aggregates of 34-36 nm with icosahedral symmetry were detected, suggesting that the GB agent was a calici-like virus. See, for example, J. D. Almeida et al., Nature 261:608-609 (1976); J. L. Dienstag et al., Nature, supra.

Two hepatitis-causing viruses recently have been discovered and reported: HCV, which occurs primarily through parenteral transmission, and HEV, which is transmitted enterically. See, for example, Q. L. Choo et al., Science 244:359-362 (1989), G. Kuo et al., Science 244:362-364 (1989), E. P. Publication No. 0 318 216 (published May 31, 1989), G. R. Reyes et al., Science 247:1335-1339 (1990). HCV is responsible for a majority of PTH ascribed to the NANBH agent(s) and many cases of acute NANBH not acquired by transfusion. Anonymous editorial, Lancet 335:1431-1432 (1990); J. L. Dienstag, Gastroenterology 99:1177-1180 (1990); and M. J. Alter et al., JAMA 264:2231-2235 (1990).

While the detection of HCV antibody in donor samples eliminates 70 to 80% of NANBH infected blood in the blood supply system, the discovery and detection of HCV has not totally prevented the transmission of hepatitis. H. Alter et al., New Eng. J. Med. 321:1494-1500 (1989). Recent publications have questioned whether additional hepatitis agents may be responsible for PTH and for community acquired acute and/or chronic hepatitis that is not associated with PTH. For example, of 181 patients monitored in a prospective clinical survey conducted

in France from 1988 to 1990, investigators noted a total of 18 cases of PTH. Thirteen of these 18 patients tested negative for anti-HCV antibodies, HBsAg, HBV and HCV nucleic acids. The authors speculated as to the potential importance of a non-A, non-B, non-C agent causing PTH. V. Thiers et al., J. Hepatology 18:34-39 (1993). Also, of 1,476 patients monitored in another study conducted in Germany from 1985 to 1988, 22 cases of documented cases of PTH were not related to infection with HBV or HCV. T. Peters et al., J. Med. Virol. 39:139-145 (1993).

It would be advantageous to identify and provide materials derived from a group of novel and unique viruses causing hepatitis, such as, polynucleotides, recombinant and synthetic polypeptides encoded therein, antibodies which specifically bind to these polypeptides, and diagnostics and vaccines that employ these materials. Such materials could greatly enhance the ability of the medical community to more accurately diagnose acute and/or chronic viral hepatitis and could provide a safer blood and organ supply by detecting non-A, non-B and non-C hepatitis in these blood and organ donations.

Summary of the Invention

The present invention provides a purified polynucleotide or fragment thereof derived from hepatitis GB virus (HGBV) capable of selectively hybridizing to the genome of HGBV or the complement thereof, wherein said polynucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity, more preferably, 40% identity, even more preferably, 60% identity, and yet more preferably, 80% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C. Also provided is a recombinant polynucleotide or fragment thereof derived from hepatitis GB virus (HGBV) capable of selectively hybridizing to the genome of HGBV or the complement thereof, wherein said nucleotide comprises a sequence that encodes at least one epitope of HGBV, and wherein said recombinant nucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C. Such a recombinant polynucleotide is contained within a recombinant vector and further comprises a host cell transformed with said vector.

The present invention also provides a hepatitis GB virus (HGBV) recombinant polynucleotide or fragment thereof comprising a nucleotide sequence derived from an HGBV genome, wherein said polynucleotide is contained within a recombinant vector and further comprises a host cell transformed with said vector. and further wherein said sequence encodes an epitope of HGBV. The HGBV recombinant polynucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C. The present invention provides a recombinant expression system comprising an open reading frame of DNA or RNA derived from hepatitis GB virus (HGBV) wherein said open reading frame comprises a sequence of HGBV genome or cDNA and wherein said open reading frame is operably linked to a control sequence compatible with a desired host, and further comprises a cell transformed with said recombinant expression system and a polypeptide of at least about eight amino acids in length produced by said cell.

The present invention additionally provides a purified hepatitis GB virus (HGBV) comprising a preparation of HGBV polypeptide or fragment thereof, a recombinant polypeptide comprising an amino acid sequence or fragment thereof wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity, more preferably 40% identity and yet more preferably 60% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C. Antibodies, both polyclonal and monoclonal, are provided by the present invention, as well as, a fusion polypeptide comprising at least one hepatitis GB virus (HGBV) polypeptide or fragment thereof, a particle that is immunogenic against hepatitis GB virus (HGBV) infection, comprising a non-HGBV polypeptide having an amino acid sequence capable of forming a particle when said sequence is produced in a eukaryotic or prokaryotic host, and at least one HGBV epitope, and a polynucleotide probe for hepatitis GB virus (HGBV) wherein said polynucleotide probe is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

Assay kits also are provided, as well as methods for producing a polypeptide containing at least one hepatitis GB virus (HGBV) epitope comprising incubating host cells transformed with an expression vector comprising a sequence encoding a polypeptide characterized by a positive stranded RNA genome wherein
5 said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C. Also provided are methods of detecting HGBV nucleic acids, antigens and antibodies in test samples, including methods which utilize
10 solid phases, recombinant or synthetic peptides, or probes. Vaccines also are provided by the present invention, as are tissue culture grown cell infected with hepatitis GB virus (HGBV), a method for producing antibodies to hepatitis GB virus (HGBV) comprising administering to an individual an isolated immunogenic polypeptide or fragment thereof comprising at least one HGBV epitope in an
15 amount sufficient to produce an immune response. Diagnostic reagents also are provided herein which comprises polynucleotides or polypeptides or fragments thereof.

Brief Description of the Drawings

20 FIGURES 1-12 are graphs of individual tamarins which plot the amount of liver enzyme (ALT or ICD) as measured in mU/ml against time (weeks post inoculation), where ALT CO indicates the cutoff value for ALT, and ICD CO indicates the cutoff value of ICD, wherein
25 FIGURE 1 shows the graph of tamarin T-1053;
FIGURE 2 shows the graph of tamarin T-1048;
FIGURE 3 shows the graph of tamarin T-1057;
FIGURE 4 shows the graph of tamarin T-1061;
FIGURE 5 shows the graph of tamarin T-1047;
FIGURE 6 shows the graph of tamarin T-1042;
30 FIGURE 7 shows the graph of tamarin T-1044;
FIGURE 8 shows the graph of tamarin T-1034;
FIGURE 9 shows the graph of tamarin T-1055;
FIGURE 10 shows the graph of tamarin T-1051;
FIGURE 11 shows the graph of tamarin T-1038; and
35 FIGURE 12 shows the graph of tamarin T-1049.

FIGURE 13 presents a flow diagram of the steps involved in representational difference analysis (RDA), the procedure used for identifying clones.

FIGURE 14 shows an ethidium bromide stained 2.0% agarose gel of the products from the representational difference analysis (RDA) performed on pre-inoculation and acute phase HGBV-infected tamarin plasma.

FIGURE 15 shows an autoradiogram from a Southern blot of genomic DNA, amplicon DNA and products from the first three rounds of subtraction/hybridization.

FIGURE 16 shows the same autoradiogram as described in FIGURE 15, except that an alternative radiolabeled probe is used.

FIGURE 17 shows an ethidium bromide stained 1.5% agarose gel of polymerase chain reaction (PCR) amplified product from genomic DNA.

FIGURE 18 shows an autoradiogram from a Southern blot of the 1.5% agarose gel in FIGURE 17.

FIGURE 19 shows an ethidium bromide stained 1.5% agarose gel of RT-PCR product obtained from normal human serum and pre-inoculation and acute phase tamarin plasmas.

FIGURE 20 shows an autoradiogram from a Southern blot of the same gel described in FIGURE 19.

FIGURES 21 A and B show autoradiograms from Northern blots of total cellular RNA extracted from the liver of an uninfected tamarin and an HGBV-infected tamarin.

FIGURE 22 shows a diagram that demonstrates each of the recombinant polynucleotide isolates are present on contiguous RNA species.

FIGURES 23 A-C show dot plot analyses of the nucleic acid sequences wherein:

FIGURE 23A shows a dot blot comparison of HGBV-A;

FIGURE 23B shows a dot blot comparison of HGBV-B;

FIGURE 23C shows a dot blot comparison of HGBV-A v. HGBV-B.

FIGURES 24 A-B show the conserved residues as follows:

FIGURE 24A shows the conserved residues in the putative NTP-binding helicase domain of predicted translation products of HGBV-A, HGBV-B and HCV-1 NS3,

FIGURE 24B shows the conserved residues of the RNA-dependent RNA polymerase domain of predicted translation products of HGBV-A, HGBV-B and HCV-1 NS5b.

FIGURES 25 A-B show Coomassie-stained 10% SDS-polyacrylamide gels of CKS fusion protein whole cell lysates; three CKS fusion proteins demonstrate immunoreactivity with HGBV-infected tamarin sera.

FIGURES 26 to 30 are graphs of individual tamarins which plot 1) the amount of liver enzyme (ALT) as measured in mU/ml against time (weeks post inoculation) as shown by a solid line; 2) ELISA absorbance values for the CKS-1.7 recombinant protein as shown by filled circles connected by dotted lines; 3) ELISA absorbance values for the CKS-1.4 recombinant protein as shown by open circles connected by dotted lines; 4) ELISA absorbance values for the CKS-4.1 recombinant protein as shown by crosses connected by dotted lines; 5) negative PCR results using SEQ ID #21 primers as shown by empty squares; 6) positive PCR results using SEQ ID #21 primers as shown by filled squares; 7) negative PCR results using SEQ ID #26 primers as shown by empty diamonds; 8) positive PCR results using SEQ ID #26 primers as shown by filled diamonds; 9) inoculation dates are indicated by the arrowheads, wherein

FIGURE 26 shows the graph of tamarin T-1048;
FIGURE 27 shows the graph of tamarin T-1057;
FIGURE 28 shows the graph of tamarin T-1061;
FIGURE 29 shows the graph of tamarin T-1051; and
FIGURE 30 shows the graph of tamarin T-1034.

FIGURES 31-34 are graphs of a human test specimens which plots 1) the amount of liver enzyme (ALT) as measured in mU/ml against time (weeks post inoculation) as shown by a solid line; 2) ELISA absorbance values for the CKS-1.7 recombinant protein as shown by dotted lines, filled circles; 3) ELISA absorbance values for the CKS-1.4 recombinant protein as shown by dotted lines, open circles, wherein

FIGURE 31 shows a graph of patient 101;
FIGURE 32 shows a graph of patient 257;
FIGURE 33 shows a graph of patient 260; and
FIGURE 34 shows a graph of patient 340.
FIGURE 35 shows conserved residues, wherein

FIGURE 35A shows the conserved residues in the putative NTP-binding helicase domain of predicted translation products of Contig. A, Contig. B and HCV-1 NS3, and

FIGURE 35B shows the conserved residues of the RNA-dependent RNA polymerase domain of predicted translation products of Contig. A, Contig. B and HCV-1 NS5b.

FIGURE 36 shows a nucleotide alignment of HGBV-A, HGBV-B,
5 HGBV-C and HCV-1.

FIGURE 37 shows a PhosphoImage (Molecular Dynamics, Sunnyvale, CA) from a Southern blot of the PCR products after hybridization with the radiolabeled probe from GB-C

FIGURE 38 shows a nucleotide alignment of HGBV-C with two variant
10 clones .

FIGURE 39 presents a schematic of the assembled contig of HGBV-C.

FIGURE 40 shows a nucleotide alignment of HGBV-C with four variant clones.

FIGURE 41 shows a PhosphoImage (Molecular Dynamics, Sunnyvale,
15 CA) of a Southern blot of PCR products generated from a Canadian hepatitis patient after hybridization with radiolabeled from Canadian patient GB-C.5.

FIGURE 42 depicts a phylogenetic tree produced from alignment of the helicase domains of the viruses indicated.

FIGURE 43 SCOTT depicts a phylogenetic tree produced from alignment
20 of the RNA-dependent RNA polymerase domains of the viruses indicated.

FIGURE 44 presents a phylogenetic tree produced from alignment of the large open reading frames (putative precursor polypeptides) of the viruses indicated.

Detailed Description of the Invention

25 The present invention provides characterization of a newly ascertained etiological agents of non-A, non-B, non-C, non-D and non-E hepatitis-causing agents, collectively so-termed "Hepatitis GB Virus," or "HGBV." The present invention provides a method for determining the presence of the HGBV etiological agents, methods for obtaining the nucleic acid of this etiological agents created
30 from infected serum, plasma or liver homogenates from individuals, either humans or tamarins, with HGBV to detect newly synthesized antigens derived from the genome of heretofore unisolated viral agents, and of selecting clones which produced products which are only found in infectious individuals as compared to non-infected individuals.

35 Portions of the nucleic acid sequences derived from HGBV are useful as probes to determine the presence of HGBV in test samples, and to isolate naturally occurring variants. These sequences also make available polypeptide sequences of

HGBV antigens encoded within the HGBV genome(s) and permit the production of polypeptides which are useful as standards or reagents in diagnostic tests and/or as components of vaccines. Monoclonal and polyclonal antibodies directed against at least one epitope contained within these polypeptide sequences also are useful
5 for diagnostic tests as well as therapeutic agents, for screening of antiviral agents, and for the isolation of the HGBV agent from which these nucleic acid sequences are derived. Isolation and sequencing of other portions of the HGBV genome also can be accomplished by utilizing probes or PCR primers derived from these nucleic acid sequences, thus allowing additional probes and polypeptides of the
10 HGBV to be established, which will be useful in the diagnosis and/or treatment of HGBV, both as a prophylactic and therapeutic agent.

According to one aspect of the invention, there will be provided a purified HGBV polynucleotide, a recombinant HGBV polynucleotide, a recombinant polynucleotide comprising a sequence derived from an HGBV genome; a
15 recombinant polypeptide encoding an epitope of HGBV; a synthetic peptide encoding an epitope of HGBV; a recombinant vector containing any of the above described recombinant polypeptides, and a host cell transformed with any of these vectors. These recombinant polypeptides and synthetic peptides may be used alone or in combination, or in conjunction with other substances representing
20 epitopes of HGBV.

In another aspect of the invention there will be provided purified HGBV; a preparation of polypeptides from the purified HGBV; a purified HGBV polypeptide; a purified polypeptide comprising an epitope which is immunologically identical with an epitope contained in HGBV.

25 In yet another aspect of the invention there will be provided a recombinant expression system comprising an open reading frame (ORF) of DNA derived from an HGBV genome or from HGBV cDNA, wherein the ORF is operably linked to a control sequence compatible with a desired host, a cell transformed with the recombinant expression system, and a polypeptide produced by the transformed
30 cell.

Additional aspects of the present invention include at least one recombinant HGBV polypeptide, at least one recombinant polypeptide comprised of a sequence derived from an HGBV genome or from HGBV cDNA; at least one recombinant polypeptide comprised of an HGBV epitope and at least one fusion polypeptide
35 comprised of an HGBV polypeptide.

The present invention also provides methods for producing a monoclonal antibody which specifically binds to at least one epitope of HGBV; a purified

preparation of polyclonal antibodies which specifically bind to at least one HGBV epitope; and methods for using these antibodies, which include diagnostic, prognostic and therapeutic uses.

In still another aspect of the invention there will be provided a particle
5 which immunizes against HGBV infection comprising a non-HGBV polypeptide having an amino acid sequence capable of forming a particle when said sequence is produced in an eukaryotic host, and an HGBV epitope.

A polynucleotide probe for HGBV also will be provided.

The present invention provides kits containing reagents which can be used
10 for the detection of the presence and/or amount of polynucleotides derived from HGBV, such reagents comprising a polynucleotide probe containing a nucleotide sequence from HGBV of about 8 or more nucleotides in a suitable container; a reagent for detecting the presence and/or amount of an HGBV antigen comprising an antibody directed against the HGBV antigen to be detected in a suitable
15 container; a reagent for detecting the presence and/or amount of antibodies directed against an HGBV antigen comprising a polypeptide containing an HGBV epitope present in the HGBV antigen, provided in a suitable container. Other kits for various assay formats also are provided by the present invention as described herein.

Other aspects of the present invention include a polypeptide comprising at
20 least one HGBV epitope attached to a solid phase and an antibody to an HGBV epitope attached to a solid phase. Also included are methods for producing a polypeptide containing an HGBV epitope comprising incubating host cells transformed with an expression vector containing a sequence encoding a
25 polypeptide containing an HGBV epitope under conditions which allow expression of the polypeptide, and a polypeptide containing an HGBV epitope produced by this method.

The present invention also provides assays which utilize the recombinant or synthetic polypeptides provided by the invention, as well as the antibodies
30 described herein in various formats, any of which may employ a signal generating compound in the assay. Assays which do not utilize signal generating compounds to provide a means of detection also are provided. All of the assays described generally detect either antigen or antibody, or both, and include contacting a test sample with at least one reagent provided herein to form at least one
35 antigen/antibody complex and detecting the presence of the complex. These assays are described in detail herein.

Vaccines for treatment of HGBV infection comprising an immunogenic peptide containing an HGBV epitope, or an inactivated preparation of HGBV, or an attenuated preparation of HGBV, or the use of recombinant vaccines that express HGBV epitope(s) and/or the use of synthetic peptides, also are included in
5 the present invention. An effective vaccine may make use of combinations of these immunogenic peptides (such as, a cocktail of recombinant antigens, synthetic peptides and native viral antigens administered simultaneously or at different times); some of these may be utilized alone and be supplemented with other representations of immunogenic epitopes at later times. Also included in the
10 present invention is a method for producing antibodies to HGBV comprising administering to an individual an isolated immunogenic polypeptide containing an HGBV epitope in an amount sufficient to produce an immune response in the inoculated individual.

Also provided by the present invention is a tissue culture grown cell
15 infected with HGBV.

In yet another aspect of the present invention is provided a method for isolating DNA or cDNA derived from the genome of an unidentified infectious agent, which is a unique modification of representational difference analysis (RDA), and which is described in detail hereinbelow.

20 Definitions

The term "Hepatitis GB Virus" or "HGBV", as used herein, collectively denotes a viral species which causes non-A, non-B, non-C, non-D, non-E hepatitis in man, and attenuated strains or defective interfering particles derived therefrom. This may include acute viral hepatitis transmitted by contaminated
25 foodstuffs, drinking water, and the like; hepatitis due to HGBV transmitted via person to person contact (including sexual transmission, respiratory and parenteral routes) or via intravenous drug use. The methods as described herein will allow the identification of individuals who have acquired HGBV. Individually, the HGBV isolates are specifically referred to as "HGBV-A", "HGBV-B" and
30 "HGBV-C." As described herein, the HGBV genome is comprised of RNA. Analysis of the nucleotide sequence and deduced amino acid sequence of the HGBV reveals that viruses of this group have a genome organization similar to that of the Flaviridae family. Based primarily, but not exclusively, upon similarities in genome organization, the International Committee on the Taxonomy
35 of Viruses has recommended that this family be composed of three genera: Flavivirus, Pestivirus, and the hepatitis C group. Similarity searches at the amino acid level reveal that the hepatitis GB virus subclones have some, albeit low,

sequence resemblance to hepatitis C virus. The information provided herein is sufficient to allow classification of other strains of HGBV.

Several lines of evidence demonstrate that HGBV-C is not a genotype of HCV. First, sera containing HGB-C sequences were tested for the presence of HCV antibody. Routine detection of individuals exposed to or infected with HCV relies upon antibody tests which utilize antigens derived from three or more regions from HCV-1. These tests allow detection of antibodies to the known genotypes of HCV (See, for example, Sakamoto et al., *J. Gen. Virol.* 75:1761-1768 (1994) and Stuyver et al., *J. Gen. Virol.* 74:1093-1102 (1993). HCV-specific ELISAs failed to detect sera containing GB-C sequences in six of eight cases (TABLE A). Second, several human sera that were seronegative for HCV antibodies have been shown to be positive for HCV genomic RNA by a highly sensitive RT-PCR assay (Sugitani, *Lancet* 339:1018-1019 (1992). This assay failed to detect HCV RNA in seven of eight sera containing HGB-C sequences (TABLE A). Thus, HGBV-C is not a genotype of HCV based on both serologic and molecular assays.

The alignment of a portion of the predicted translation product of HGB-C within the helicase region with the homologous region of HGBV-A, HGBV-B, HCV-1 and additional members of the *Flaviviridae*, followed by phylogenetic analysis of the aligned sequences suggests that HGBV-C is more closely related to HGBV-A than to any member of the HCV group. The sequences of HGBV-C and HGBV-A, while exhibiting an evolutionary distance of 0.42, are not as divergent as HGBV-C is from HGBV-B, which shows an evolutionary distance of 0.92 (TABLE 33, *infra*). Thus, HGBV-A and HGBV-C may be considered to be members of one subgroup of the GB viruses and GBV-B a member of its own subgroup. The phylogenetic analysis of the helicase sequences from various HCV isolates show that they form a much less diverged group, exhibiting a maximum evolutionary distance of 0.20 (TABLE 32, *infra*). A comparison of the HCV group and the HGBV group shows a minimum evolutionary distance between any two sequences from each group of 0.69. The distance values reported hereinabove were used to generate a phylogenetic tree presented in FIGURE 42. The relatively high degree of divergence among these viruses suggests that the GB viruses are not merely types or subtypes within the hepatitis C group; rather, they constitute their own phyletic group (or groups). Phylogenetic analysis using sequence information derived from a small portion of HCV viral genomes has been shown to be an acceptable method for the assignment of new isolates into genotypic groups (Simmonds et al., *Hepatology* 19:1321-1324 (1994). In the current

analysis, the use of a 110 amino acid sequence within the helicase gene from representative HCV isolates has properly grouped them into their respective genotypes (Simmonds et al., *J. Gen. Virol.* 75:1053-1061 (1994). Therefore, the evolutionary distances shown, in all likelihood, accurately reflect the high degree of divergence between the GB viruses and the hepatitis C virus.

In previous applications, it was stated that "HGBV strains are identifiable on the polypeptide level and that HGBV strains are more than 40% homologous, preferably more than about 60% homologous, and even more preferably more than about 80% homologous at the polypeptide level." As it is used, the term "homologous," when referring to the degree of relatedness of two polynucleotide or polypeptide sequences, can be ambiguous and actually implies an evolutionary relationship. As is now the current convention in the art, the term "homologous" is no longer used; instead the terms "similarity" and/or "identity" are used to describe the degree of relatedness between two polynucleotides or polypeptide sequences. The techniques for determining amino acid sequence "similarity" and/or "identity" are well-known in the art and include, for example, directly determining the amino acid sequence and comparing it to the sequences provided herein; determining the nucleotide sequence of the genomic material of the putative HGBV (usually via a cDNA intermediate), and determining the amino acid sequence encoded therein, and comparing the corresponding regions. In general, by "identity" is meant the exact match-up of either the nucleotide sequence of HGBV and that of another strain(s) or the amino acid sequence of HGBV and that of another strain(s) at the appropriate place on each genome. Also, in general, by "similarity" is meant the exact match-up of amino acid sequence of HGBV and that of another strain(s) at the appropriate place, where the amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. The programs available in the Wisconsin Sequence Analysis Package, Version 8 (available from the Genetics Computer Group, Madison, Wisconsin, 53711), for example, the GAP program, are capable of calculating both the identity and similarity between two polynucleotide or two polypeptide sequences. Other programs for calculating identity and similarity between two sequences are known in the art.

Additionally, the following parameters are applicable, either alone or in combination, in identifying a strain of HGBV-A, HGBV-B or HGBV-C. It is expected that the overall nucleotide sequence identity of the genomes between HGBV-A, HGBV-B or HGBV-C and a strain of one of these hepatitis GB viruses will be about 45% or greater, since it is now believed that the HGBV strains may

be genetically related, preferably about 60% or greater, and more preferably, about 80% or greater.

Also, it is expected thjat the overall sequence identity of the genomes between HGBV-A and a strain of HGBV-A at the amino acid level will be about
5 35% or greater since it is now believed that the HGBV strains may be genetically related, preferably about 40% or greater, more preferably, about 60% or greater, and even more preferably, about 80% or greater. In addition, there will be corresponding contiguous sequences of at least about 13 nucleotides, which may be provided in combination of more than one contiguous sequence. Also, it is
10 expected that the overall sequence identity of the genomes between HGBV-B and a strain of HGBV-B at the amino acid level will be about 35% or greater since it is now believed that the HGBV strains may be genetically related, preferably about 40% or greater, more preferably, about 60% or greater, and even more preferably, about 80% or greater. In addition, there will be corresponding contiguous
15 sequences of at least about 13 nucleotides, which may be provided in combination of more than one contiguous sequence. Also, it is expected that the overall sequence identity of the genomes between HGBV-C and a strain of HGBV-C at the amino acid level will be about 35% or greater since it is now believed that the HGBV strains may be genetically related, preferably about 40% or greater, more
20 preferably, about 60% or greater, and even more preferably, about 80% or greater. In addition, there will be corresponding contiguous sequences of at least about 13 nucleotides, which may be provided in combination of more than one contiguous sequence.

The compositions and methods described herein will enable the
25 propagation, identification, detection and isolation of HGBV and its possible strains. Moreover, they also will allow the preparation of diagnostics and vaccines for the possible different strains of HGBV, and will have utility in screening procedures for anti-viral agents. The information will be sufficient to allow a viral taxonomist to identify other strains which fall within the species. We believe that
30 HGBV encodes the sequences that are included herein. Methods for assaying for the presence of these sequences are known in the art and include, for example, amplification methods such as ligase chain reaction (LCR), polymerase chain reaction (PCR) and hybridization. In addition, these sequences contain open reading frames from which an immunogenic viral epitope may be found. This
35 epitope is unique to HGBV when compared to other known hepatitis-causing viruses. The uniqueness of the epitope may be determined by its immunological reactivity with HGBV and lack of immunological reactivity with Hepatitis A, B, C,

D and E viruses. Methods for determining immunological reactivity are known in the art and include, for example, radioimmunoassay (RIA), enzyme-linked immunosorbant assay (ELISA), hemagglutination (HA), fluorescence polarization immunoassay (FPIA) and several examples of suitable techniques are described
5 herein.

A polynucleotide "derived from" a designated sequence for example, the HGBV cDNA, or from the HGBV genome, refers to a polynucleotide sequence which is comprised of a sequence of approximately at least about 6 nucleotides, is preferably at least about 8 nucleotides, is more preferably at least about 10-12
10 nucleotides, and even more preferably is at least about 15-20 nucleotides corresponding, i.e., similar to or complementary to, a region of the designated nucleotide sequence. Preferably, the sequence of the region from which the polynucleotide is derived is similar to or complementary to a sequence which is unique to the HGBV genome. Whether or not a sequence is complementary to or
15 similar to a sequence which is unique to an HGBV genome can be determined by techniques known to those skilled in the art. Comparisons to sequences in databanks, for example, can be used as a method to determine the uniqueness of a designated sequence. Regions from which sequences may be derived include but are not limited to regions encoding specific epitopes, as well as non-translated
20 and/or non-transcribed regions.

The derived polynucleotide will not necessarily be derived physically from the nucleotide sequence of HGBV, but may be generated in any manner, including but not limited to chemical synthesis, replication or reverse transcription or transcription, which are based on the information provided by the sequence of
25 bases in the region(s) from which the polynucleotide is derived. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be consistent with an intended use.

A "polypeptide" or "amino acid sequence derived from a designated nucleic acid sequence or from the HGBV genome refers to a polypeptide having an amino acid sequence identical to that of a polypeptide encoded in the sequence or a
30 portion thereof wherein the portion consists of at least 3 to 5 amino acids, and more preferably at least 8 to 10 amino acids, and even more preferably 15 to 20 amino acids, or which is immunologically identifiable with a polypeptide encoded in the sequence.

35 A "recombinant polypeptide" as used herein means at least a polypeptide of genomic, semisynthetic or synthetic origin which by virtue of its origin or manipulation is not associated with all or a portion of the polypeptide with which it

is associated in nature or in the form of a library and/or is linked to a polynucleotide other than that to which it is linked in nature. A recombinant or derived polypeptide is not necessarily translated from a designated nucleic acid sequence of HGBV or from an HGBV genome. It also may be generated in any
5 manner, including chemical synthesis or expression of a recombinant expression system, or isolation from mutated HGBV.

The term "synthetic peptide" as used herein means a polymeric form of amino acids of any length, which may be chemically synthesized by methods well-known to the routineer. These synthetic peptides are useful in various
10 applications.

The term "polynucleotide" as used herein means a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes double- and single-stranded DNA, as well as double- and single-stranded RNA. It
15 also includes modifications, either by methylation and/or by capping, and unmodified forms of the polynucleotide.

"HGBV containing a sequence corresponding to a cDNA" means that the HGBV contains a polynucleotide sequence which is similar to or complementary to a sequence in the designated DNA. The degree of similarity or complementarity to
20 the cDNA will be approximately 50% or greater, will preferably be at least about 70%, and even more preferably will be at least about 90%. The sequence which corresponds will be at least about 70 nucleotides, preferably at least about 80 nucleotides, and even more preferably at least about 90 nucleotides in length. The correspondence between the HGBV and the cDNA can be determined by methods
25 known in the art, and include, for example, a direct comparison of the sequenced material with the cDNAs described, or hybridization and digestion with single strand nucleases, followed by size determination of the digested fragments.

"Purified viral polynucleotide" refers to an HGBV genome or fragment thereof which is essentially free, i.e., contains less than about 50%, preferably less
30 than about 70%, and even more preferably, less than about 90% of polypeptides with which the viral polynucleotide is naturally associated. Techniques for purifying viral polynucleotides are well known in the art and include, for example, disruption of the particle with a chaotropic agent, and separation of the polynucleotide(s) and polypeptides by ion-exchange chromatography, affinity
35 chromatography, and sedimentation according to density. Thus, "purified viral polypeptide" means an HGBV polypeptide or fragment thereof which is essentially free, that is, contains less than about 50%, preferably less than about 70%, and

even more preferably, less than about 90% of of cellular components with which the viral polypeptide is naturally associated. Methods for purifying are known to the routineer.

5 "Polypeptide" as used herein indicates a molecular chain of amino acids and does not refer to a specific length of the product. Thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term, however, is not intended to refer to post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like.

10 "Recombinant host cells," "host cells," "cells," "cell lines," "cell cultures," and other such terms denoting microorganisms or higher eucaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transfer DNA, and include the original progeny of the original cell which has been transfected.

15 As used herein "replicon" means any genetic element, such as a plasmid, a chromosome or a virus, that behaves as an autonomous unit of polynucleotide replication within a cell. That is, it is capable of replication under its own control.

A "vector" is a replicon in which another polynucleotide segment is attached, such as to bring about the replication and/or expression of the attached
20 segment.

The term "control sequence" refers to polynucleotide sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, such control sequences generally include promoter, ribosomal
25 binding site and terminators; in eukaryotes, such control sequences generally include promoters, terminators and, in some instances, enhancers. The term "control sequence" thus is intended to include at a minimum all components whose presence is necessary for expression, and also may include additional components whose presence is advantageous, for example, leader sequences.

30 "Operably linked" refers to a situation wherein the components described are in a relationship permitting them to function in their intended manner. Thus, for example, a control sequence "operably linked" to a coding sequence is ligated in such a manner that expression of the coding sequence is achieved under conditions compatible with the control sequences.

35 The term "open reading frame" or "ORF" refers to a region of a polynucleotide sequence which encodes a polypeptide; this region may represent a portion of a coding sequence or a total coding sequence.

A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5' -terminus and a translation stop
5 codon at the 3' -terminus. A coding sequence can include, but is not limited to, mRNA, cDNA, and recombinant polynucleotide sequences.

The term "immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptide(s) which also are present in and are unique to the designated polypeptide(s), usually HGBV proteins. Immunological identity may
10 be determined by antibody binding and/or competition in binding. These techniques are known to the routineer and also are described herein. The uniqueness of an epitope also can be determined by computer searches of known data banks, such as GenBank, for the polynucleotide sequences which encode the epitope, and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" means an antigenic determinant of a polypeptide.
15 Conceivably, an epitope can comprise three amino acids in a spatial conformation which is unique to the epitope. Generally, an epitope consists of at least five such amino acids, and more usually, it consists of at least eight to ten amino acids. Methods of examining spatial conformation are known in the art and include, for
20 example, x-ray crystallography and two-dimensional nuclear magnetic resonance.

A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly by the kinetics of antibody binding, and/or by
25 competition in binding using as competitor(s) a known polypeptide(s) containing an epitope against which the antibody is directed. The methods for determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

As used herein, the term "immunogenic polypeptide containing an HGBV
30 epitope" means naturally occurring HGBV polypeptides or fragments thereof, as well as polypeptides prepared by other means, for example, chemical synthesis or the expression of the polypeptide in a recombinant organism.

The term "transformation" refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion.
35 For example, direct uptake, transduction, or f-mating are included. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host genome.

"Treatment" refers to prophylaxis and/or therapy.

The term "individual" as used herein refers to vertebrates, particularly members of the mammalian species and includes but is not limited to domestic animals, sports animals, primates and humans; more particularly the term refers to tamarins and humans.

The term "plus strand" (or "+") as used herein denotes a nucleic acid that contains the sequence that encodes the polypeptide. The term "minus strand" (or "-") denotes a nucleic acid that contains a sequence that is complementary to that of the "plus" strand.

"Positive stranded genome" of a virus denotes that the genome, whether RNA or DNA, is single-stranded and which encodes a viral polypeptide(s).

The term "test sample" refers to a component of an individual's body which is the source of the analyte (such as, antibodies of interest or antigens of interest). These components are well known in the art. These test samples include biological samples which can be tested by the methods of the present invention described herein and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitorurinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; fixed tissue specimens; and fixed cell specimens.

"Purified HGBV" refers to a preparation of HGBV which has been isolated from the cellular constituents with which the virus is normally associated, and from other types of viruses which may be present in the infected tissue. The techniques for isolating viruses are known to those skilled in the art and include, for example, centrifugation and affinity chromatography.

"PNA" denotes a "peptide nucleic analog" which may be utilized in a procedure such as an assay to determine the presence of a target. PNAs are neutrally charged moieties which can be directed against RNA targets or DNA. PNA probes used in assays in place of, for example, DNA probes, offer advantages not achievable when DNA probes are used. These advantages include manufacturability, large scale labeling, reproducibility, stability, insensitivity to changes in ionic strength and resistance to enzymatic degradation which is present in methods utilizing DNA or RNA. These PNAs can be labeled with such signal generating compounds as fluorescein, radionucleotides, chemiluminescent compounds, and the like. PNAs thus can be used in methods in place of DNA or RNA. Although assays are described herein utilizing DNA, it is within the scope

of the routineer that PNAs can be substituted for RNA or DNA with appropriate changes if and as needed in assay reagents.

General Uses

After preparing recombinant proteins, synthetic peptides, or purified viral
5 polypeptides of choice as described by the present invention, the recombinant or
synthetic peptides can be used to develop unique assays as described herein to
detect either the presence of antigen or antibody to HGBV. These compositions
also can be used to develop monoclonal and/or polyclonal antibodies with a
specific recombinant protein or synthetic peptide which specifically bind to the
10 immunological epitope of HGBV which is desired by the routineer. Also, it is
contemplated that at least one polynucleotide of the invention can be used to
develop vaccines by following methods known in the art.

It is contemplated that the reagent employed for the assay can be provided
in the form of a test kit with one or more containers such as vials or bottles, with
15 each container containing a separate reagent such as a monoclonal antibody, or a
cocktail of monoclonal antibodies, or a polypeptide (either recombinant or
synthetic) employed in the assay. Other components such as buffers, controls,
and the like, known to those of ordinary skill in art, may be included in such test
kits.

20 "Solid phases" ("solid supports") are known to those in the art and include
the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads,
nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or
other animal) red blood cells, duracytes and others. The "solid phase" is not
critical and can be selected by one skilled in the art. Thus, latex particles,
25 microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls
of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red
blood cells and duracytes are all suitable examples. Suitable methods for
immobilizing peptides on solid phases include ionic, hydrophobic, covalent
interactions and the like. A "solid phase", as used herein, refers to any material
30 which is insoluble, or can be made insoluble by a subsequent reaction. The solid
phase can be chosen for its intrinsic ability to attract and immobilize the capture
reagent. Alternatively, the solid phase can retain an additional receptor which has
the ability to attract and immobilize the capture reagent. The additional receptor can
include a charged substance that is oppositely charged with respect to the capture
35 reagent itself or to a charged substance conjugated to the capture reagent. As yet
another alternative, the receptor molecule can be any specific binding member
which is immobilized upon (attached to) the solid phase and which has the ability

to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid phase material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, 5 microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes and other configurations known to those of ordinary skill in the art.

It is contemplated and within the scope of the invention that the solid phase also can comprise any suitable porous material with sufficient porosity to allow 10 access by detection antibodies and a suitable surface affinity to bind antigens. Microporous structures are generally preferred, but materials with gel structure in the hydrated state may be used as well. Such useful solid supports include: natural polymeric carbohydrates and their synthetically modified, cross-linked or substituted derivatives, such as agar, agarose, cross-linked alginic acid, substituted 15 and cross-linked guar gums, cellulose esters, especially with nitric acid and carboxylic acids, mixed cellulose esters, and cellulose ethers; natural polymers containing nitrogen, such as proteins and derivatives, including cross-linked or modified gelatins; natural hydrocarbon polymers, such as latex and rubber; synthetic polymers which may be prepared with suitably porous structures, such 20 as vinyl polymers, including polyethylene, polypropylene, polystyrene, polyvinylchloride, polyvinylacetate and its partially hydrolyzed derivatives, polyacrylamides, polymethacrylates, copolymers and terpolymers of the above polycondensates, such as polyesters, polyamides, and other polymers, such as polyurethanes or polyepoxides; porous inorganic materials such as sulfates or 25 carbonates of alkaline earth metals and magnesium, including barium sulfate, calcium sulfate, calcium carbonate, silicates of alkali and alkaline earth metals, aluminum and magnesium; and aluminum or silicon oxides or hydrates, such as clays, alumina, talc, kaolin, zeolite, silica gel, or glass (these materials may be used as filters with the above polymeric materials); and mixtures or copolymers of 30 the above classes, such as graft copolymers obtained by initializing polymerization of synthetic polymers on a pre-existing natural polymer. All of these materials may be used in suitable shapes, such as films, sheets, or plates, or they may be coated onto or bonded or laminated to appropriate inert carriers, such as paper, glass, plastic films, or fabrics.

35 The porous structure of nitrocellulose has excellent absorption and adsorption qualities for a wide variety of reagents including monoclonal antibodies. Nylon also possesses similar characteristics and also is suitable. It is

contemplated that such porous solid supports described hereinabove are preferably in the form of sheets of thickness from about 0.01 to 0.5 mm, preferably about 0.1 mm. The pore size may vary within wide limits, and is preferably from about 0.025 to 15 microns, especially from about 0.15 to 15 microns. The surfaces of such supports may be activated by chemical processes which cause covalent linkage of the antigen or antibody to the support. The irreversible binding of the antigen or antibody is obtained, however, in general, by adsorption on the porous material by poorly understood hydrophobic forces. Suitable solid supports also are described in U.S. Patent Application Serial No. 227,272.

The "indicator reagent" comprises a "signal generating compound" (label) which is capable of generating and generates a measurable signal detectable by external means conjugated (attached) to a specific binding member for HGBV. "Specific binding member" as used herein means a member of a specific binding pair. That is, two different molecules where one of the molecules through chemical or physical means specifically binds to the second molecule. In addition to being an antibody member of a specific binding pair for HGBV, the indicator reagent also can be a member of any specific binding pair, including either hapten-anti-hapten systems such as biotin or anti-biotin, avidin or biotin, a carbohydrate or a lectin, a complementary nucleotide sequence, an effector or a receptor molecule, an enzyme cofactor and an enzyme, an enzyme inhibitor or an enzyme, and the like. An immunoreactive specific binding member can be an antibody, an antigen, or an antibody/antigen complex that is capable of binding either to HGBV as in a sandwich assay, to the capture reagent as in a competitive assay, or to the ancillary specific binding member as in an indirect assay.

The various "signal generating compounds" (labels) contemplated include chromogens, catalysts such as enzymes, luminescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums and luminol, radioactive elements, and direct visual labels. Examples of enzymes include alkaline phosphatase, horseradish peroxidase, beta-galactosidase, and the like. The selection of a particular label is not critical, but it will be capable of producing a signal either by itself or in conjunction with one or more additional substances.

The present invention provides assays which utilize specific binding members. A "specific binding member," as used herein, is a member of a specific binding pair. That is, two different molecules where one of the molecules through chemical or physical means specifically binds to the second molecule. Therefore, in addition to antigen and antibody specific binding pairs of common

immunoassays, other specific binding pairs can include biotin and avidin, carbohydrates and lectins, complementary nucleotide sequences, effector and receptor molecules, cofactors and enzymes, enzyme inhibitors and enzymes, and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. Immunoreactive specific binding members include antigens, antigen fragments, antibodies and antibody fragments, both monoclonal and polyclonal, and complexes thereof, including those formed by recombinant DNA molecules. The term "hapten", as used herein, refers to a partial antigen or non-protein binding member which is capable of binding to an antibody, but which is not capable of eliciting antibody formation unless coupled to a carrier protein.

"Analyte," as used herein, is the substance to be detected which may be present in the test sample. The analyte can be any substance for which there exists a naturally occurring specific binding member (such as, an antibody), or for which a specific binding member can be prepared. Thus, an analyte is a substance that can bind to one or more specific binding members in an assay. "Analyte" also includes any antigenic substances, haptens, antibodies, and combinations thereof. As a member of a specific binding pair, the analyte can be detected by means of naturally occurring specific binding partners (pairs) such as the use of intrinsic factor protein as a member of a specific binding pair for the determination of Vitamin B12, the use of folate-binding protein to determine folic acid, or the use of a lectin as a member of a specific binding pair for the determination of a carbohydrate. The analyte can include a protein, a peptide, an amino acid, a nucleotide target, and the like.

Other embodiments which utilize various other solid phases also are contemplated and are within the scope of this invention. For example, ion capture procedures for immobilizing an immobilizable reaction complex with a negatively charged polymer, described in co-pending U. S. Patent Application Serial No. 150,278 corresponding to EP publication 0326100 and U. S. Patent Application Serial No. 375,029 (EP publication no. 0406473), can be employed according to the present invention to effect a fast solution-phase immunochemical reaction. An immobilizable immune complex is separated from the rest of the reaction mixture by ionic interactions between the negatively charged poly-anion/immune complex and the previously treated, positively charged porous matrix and detected by using various signal generating systems previously described, including those described in chemiluminescent signal measurements as described in co-pending U.S. Patent Application Serial No. 921,979 corresponding to EPO Publication No. 0 273,115.

Also, the methods of the present invention can be adapted for use in systems which utilize microparticle technology including in automated and semi-automated systems wherein the solid phase comprises a microparticle (magnetic or non-magnetic). Such systems include those described in pending U. S. Patent
5 Applications 425,651 and 425,643, which correspond to published EPO applications Nos. EP 0 425 633 and EP 0 424 634, respectively.

The use of scanning probe microscopy (SPM) for immunoassays also is a technology to which the monoclonal antibodies of the present invention are easily adaptable. In scanning probe microscopy, in particular in atomic force
10 microscopy, the capture phase, for example, at least one of the monoclonal antibodies of the invention, is adhered to a solid phase and a scanning probe microscope is utilized to detect antigen/antibody complexes which may be present on the surface of the solid phase. The use of scanning tunnelling microscopy eliminates the need for labels which normally must be utilized in many
15 immunoassay systems to detect antigen/antibody complexes. Such a system is described in pending U. S. patent application Serial No. 662,147. The use of SPM to monitor specific binding reactions can occur in many ways. In one embodiment, one member of a specific binding partner (analyte specific substance which is the monoclonal antibody of the invention) is attached to a surface suitable
20 for scanning. The attachment of the analyte specific substance may be by adsorption to a test piece which comprises a solid phase of a plastic or metal surface, following methods known to those of ordinary skill in the art. Or, covalent attachment of a specific binding partner (analyte specific substance) to a test piece which test piece comprises a solid phase of derivatized plastic, metal,
25 silicon, or glass may be utilized. Covalent attachment methods are known to those skilled in the art and include a variety of means to irreversibly link specific binding partners to the test piece. If the test piece is silicon or glass, the surface must be activated prior to attaching the specific binding partner. Activated silane compounds such as triethoxy amino propyl silane (available from Sigma Chemical
30 Co., St. Louis, MO), triethoxy vinyl silane (Aldrich Chemical Co., Milwaukee, WI), and (3-mercapto-propyl)-trimethoxy silane (Sigma Chemical Co., St. Louis, MO) can be used to introduce reactive groups such as amino-, vinyl, and thiol, respectively. Such activated surfaces can be used to link the binding partner directly (in the cases of amino or thiol) or the activated surface can be further
35 reacted with linkers such as glutaraldehyde, bis (succinimidyl) suberate, SPPD 9 succinimidyl 3-[2-pyridyldithio] propionate), SMCC (succinimidyl-4-[N-maleimidomethyl] cyclohexane-1-carboxylate), SIAB (succinimidyl [4-iodoacetyl]

aminobenzoate), and SMPB (succinimidyl 4-[1-maleimidophenyl] butyrate) to separate the binding partner from the surface. The vinyl group can be oxidized to provide a means for covalent attachment. It also can be used as an anchor for the polymerization of various polymers such as poly acrylic acid, which can provide multiple attachment points for specific binding partners. The amino surface can be reacted with oxidized dextrans of various molecular weights to provide hydrophilic linkers of different size and capacity. Examples of oxidizable dextrans include Dextran T-40 (molecular weight 40,000 daltons), Dextran T-110 (molecular weight 110,000 daltons), Dextran T-500 (molecular weight 500,000 daltons), Dextran T-2M (molecular weight 2,000,000 daltons) (all of which are available from Pharmacia), or Ficoll (molecular weight 70,000 daltons (available from Sigma Chemical Co., St. Louis, MO). Also, polyelectrolyte interactions may be used to immobilize a specific binding partner on a surface of a test piece by using techniques and chemistries described by pending U. S. Patent applications Serial No. 150,278, filed January 29, 1988, and Serial No. 375,029, filed July 7, 1989. The preferred method of attachment is by covalent means. Following attachment of a specific binding member, the surface may be further treated with materials such as serum, proteins, or other blocking agents to minimize non-specific binding. The surface also may be scanned either at the site of manufacture or point of use to verify its suitability for assay purposes. The scanning process is not anticipated to alter the specific binding properties of the test piece.

Various other assay formats may be used, including "sandwich" immunoassays and probe assays. For example, the monoclonal antibodies of the present invention can be employed in various assay systems to determine the presence, if any, of HGBV proteins in a test sample. Fragments of these monoclonal antibodies provided also may be used. For example, in a first assay format, a polyclonal or monoclonal anti-HGBV antibody or fragment thereof, or a combination of these antibodies, which has been coated on a solid phase, is contacted with a test sample which may contain HGBV proteins, to form a mixture. This mixture is incubated for a time and under conditions sufficient to form antigen/antibody complexes. Then, an indicator reagent comprising a monoclonal or a polyclonal antibody or a fragment thereof, which specifically binds to an HGBV region, or a combination of these antibodies, to which a signal generating compound has been attached, is contacted with the antigen/antibody complexes to form a second mixture. This second mixture then is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence of HGBV antigen present in the test sample and captured on the solid

phase, if any, is determined by detecting the measurable signal generated by the signal generating compound. The amount of HGBV antigen present in the test sample is proportional to the signal generated.

Alternatively, a polyclonal or monoclonal anti-HGBV antibody or fragment thereof, or a combination of these antibodies which is bound to a solid support, the test sample and an indicator reagent comprising a monoclonal or polyclonal antibody or fragments thereof, which specifically binds to HGBV antigen, or a combination of these antibodies to which a signal generating compound is attached, are contacted to form a mixture. This mixture is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence, if any, of HGBV proteins present in the test sample and captured on the solid phase is determined by detecting the measurable signal generated by the signal generating compound. The amount of HGBV proteins present in the test sample is proportional to the signal generated.

In another alternate assay format, one or a combination of at least two monoclonal antibodies of the invention can be employed as a competitive probe for the detection of antibodies to HGBV protein. For example, HGBV proteins, either alone or in combination, can be coated on a solid phase. A test sample suspected of containing antibody to HGBV antigen then is incubated with an indicator reagent comprising a signal generating compound and at least one monoclonal antibody of the invention for a time and under conditions sufficient to form antigen/antibody complexes of either the test sample and indicator reagent to the solid phase or the indicator reagent to the solid phase. The reduction in binding of the monoclonal antibody to the solid phase can be quantitatively measured. A measurable reduction in the signal compared to the signal generated from a confirmed negative NANB, non-C, non-D, non-E hepatitis test sample indicates the presence of anti-HGBV antibody in the test sample.

In yet another detection method, each of the monoclonal or polyclonal antibodies of the present invention can be employed in the detection of HGBV antigens in fixed tissue sections, as well as fixed cells by immunohistochemical analysis. Cytochemical analysis wherein these antibodies are labelled directly (fluorescein, colloidal gold, horseradish peroxidase, alkaline phosphatase, etc.) or are labelled by using secondary labelled anti-species antibodies (with various labels as exemplified herein) to track the histopathology of disease also are within the scope of the present invention.

In addition, these monoclonal antibodies can be bound to matrices similar to CNBr-activated Sepharose and used for the affinity purification of specific

HGBV proteins from cell cultures, or biological tissues such as blood and liver such as to purify recombinant and native viral HGBV antigens and proteins.

The monoclonal antibodies of the invention can also be used for the generation of chimeric antibodies for therapeutic use, or other similar applications.

5 The monoclonal antibodies or fragments thereof can be provided individually to detect HGBV antigens. Combinations of the monoclonal antibodies (and fragments thereof) provided herein also may be used together as components in a mixture or "cocktail" of at least one anti-HGBV antibody of the invention with antibodies to other HGBV regions, each having different binding specificities.

10 Thus, this cocktail can include the monoclonal antibodies of the invention which are directed to HGBV proteins and other monoclonal antibodies to other antigenic determinants of the HGBV genome.

 The polyclonal antibody or fragment thereof which can be used in the assay formats should specifically bind to a specific HGBV region or other HGBV
15 proteins used in the assay. The polyclonal antibody used preferably is of mammalian origin; human, goat, rabbit or sheep anti-HGBV polyclonal antibody can be used. Most preferably, the polyclonal antibody is rabbit polyclonal anti-HGBV antibody. The polyclonal antibodies used in the assays can be used either alone or as a cocktail of polyclonal antibodies. Since the cocktails used in the
20 assay formats are comprised of either monoclonal antibodies or polyclonal antibodies having different HGBV specificity, they would be useful for diagnosis, evaluation and prognosis of HGBV infection, as well as for studying HGBV protein differentiation and specificity.

 It is contemplated and within the scope of the present invention that the
25 HGBV group of viruses may be detectable in assays by use of a synthetic, recombinant or native peptide that is common to all HGBV viruses. It also is within the scope of the present invention that different synthetic, recombinant or native peptides identifying different epitopes from HGBV-A, HGBV-B, HGBV-C, or yet other HGBV viruses, can be used in assay formats. In the later case,
30 these can be coated onto one solid phase, or each separate peptide may be coated on separate solid phases, such as microparticles, and then combined to form a mixture of peptides which can be later used in assays. Such variations of assay formats are known to those of ordinary skill in the art and are discussed hereinbelow.

35 In another assay format, the presence of antibody and/or antigen to HGBV can be detected in a simultaneous assay, as follows. A test sample is .. simultaneously contacted with a capture reagent of a first analyte, wherein said

capture reagent comprises a first binding member specific for a first analyte attached to a solid phase and a capture reagent for a second analyte, wherein said capture reagent comprises a first binding member for a second analyte attached to a second solid phase, to thereby form a mixture. This mixture is incubated for a time and under conditions sufficient to form capture reagent/first analyte and capture reagent/second analyte complexes. These so-formed complexes then are contacted with an indicator reagent comprising a member of a binding pair specific for the first analyte labelled with a signal generating compound and an indicator reagent comprising a member of a binding pair specific for the second analyte labelled with a signal generating compound to form a second mixture. This second mixture is incubated for a time and under conditions sufficient to form capture reagent/first analyte/indicator reagent complexes and capture reagent/second analyte/indicator reagent complexes. The presence of one or more analytes is determined by detecting a signal generated in connection with the complexes formed on either or both solid phases as an indication of the presence of one or more analytes in the test sample. In this assay format, proteins derived from human expression systems may be utilized as well as monoclonal antibodies produced from the proteins derived from the mammalian expression systems as disclosed herein. Such assay systems are described in greater detail in pending U.S. Patent Application Serial No. 07/574,821 entitled Simultaneous Assay for Detecting One Or More Analytes, which corresponds to EP Publication No. 0473065.

In yet other assay formats, recombinant proteins and/or synthetic peptides may be utilized to detect the presence of anti-HGBV in test samples. For example, a test sample is incubated with a solid phase to which at least one recombinant protein or synthetic peptide has been attached. These are reacted for a time and under conditions sufficient to form antigen/antibody complexes. Following incubation, the antigen/antibody complex is detected. Indicator reagents may be used to facilitate detection, depending upon the assay system chosen. In another assay format, a test sample is contacted with a solid phase to which a recombinant protein or synthetic peptide produced as described herein is attached and also is contacted with a monoclonal or polyclonal antibody specific for the protein, which preferably has been labelled with an indicator reagent. After incubation for a time and under conditions sufficient for antibody/antigen complexes to form, the solid phase is separated from the free phase, and the label is detected in either the solid or free phase as an indication of the presence of HGBV antibody. Other assay formats utilizing the proteins of the present invention are contemplated. These

include contacting a test sample with a solid phase to which at least one antigen from a first source has been attached, incubating the solid phase and test sample for a time and under conditions sufficient to form antigen/antibody complexes, and then contacting the solid phase with a labelled antigen, which antigen is derived
5 from a second source different from the first source. For example, a recombinant protein derived from a first source such as E. coli is used as a capture antigen on a solid phase, a test sample is added to the so-prepared solid phase, and a recombinant protein derived from a different source (i.e., non-E. coli) is utilized as a part of an indicator reagent. Likewise, combinations of a recombinant antigen on
10 a solid phase and synthetic peptide in the indicator phase also are possible. Any assay format which utilizes an antigen specific for HGBV from a first source as the capture antigen and an antigen specific for HGBV from a different second source are contemplated. Thus, various combinations of recombinant antigens, as well as the use of synthetic peptides, purified viral proteins, and the like, are within the
15 scope of this invention. Assays such as this and others are described in U.S. Patent No. 5,254,458, which enjoys common ownership and is incorporated herein by reference.

Other assay systems which utilize an antibody (polyclonal, monoclonal or naturally-occurring) which specifically binds HGBV viral particles or sub-viral
20 particles housing the viral genome (or fragments thereof) by virtue of a contact between the specific antibody and the viral protein (peptide, etc.). This captured particle then can be analyzed by methods such as LCR or PCR to determine whether the viral genome is present in the test sample. Test samples which can be assayed according to this method include blood, liver, sputum, urine, fecal
25 material, saliva, and the like. The advantage of utilizing such an antigen capture amplification method is that it can separate the viral genome from other molecules in the test specimen by use of a specific antibody. Such a method has been described in pending U.S. patent application Serial No. 08/141,429.

While the present invention discloses the preference for the use of solid
30 phases, it is contemplated that the reagents such as antibodies, proteins and peptides of the present invention can be utilized in non-solid phase assay systems. These assay systems are known to those skilled in the art, and are considered to be within the scope of the present invention.

Materials and Methods

35 General Techniques

Conventional and well-known techniques and methods in the fields of molecular biology, microbiology, recombinant DNA and immunology are

- employed in the practice of the invention unless otherwise noted. Such techniques are explained and detailed in the literature. See, for example, J. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd edition, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1989); D. N. Glover, ed., DNA Cloning, Volumes I and II (1985); M.J. Gait ed., Oligonucleotide Synthesis, (1984); B.D. Hames et al., eds., Nucleic Acid Hybridization, (1984); B.D. Hames et al., eds., Transcription and Translation, (1984); R. I. Freshney ed., Animal Cell Culture, (1986); Immobilized Cells and Enzymes, IRL Press (1986); B. Perbal, A Practical Guide to Molecular Cloning, (1984); the series, Methods in Enzymology, Academic Press, Inc., Orlando, Florida; J. H. Miller et al., eds., Gene Transfer Vectors For Mammalian Cells, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1987); Wu et al., eds., Methods in Enzymology, Vol. 154 and 155; Mayer et al., eds., Immunological Methods In Cell and Molecular Biology, Academic Press, London (1987); Scopes, Protein Purification: Principles and Practice, 2nd ed., Springer-Verlag, N.Y.; and D. Weir et al., eds., Handbook Of Experimental Immunology, Volumes I-IV (1986); N. Lisitisyn et al., Science 259:946-951 (1993).

The reagents and methods of the present invention are made possible by the provision of a family of closely related nucleotide sequences, isolated by representational difference analysis modified as described herein, present in the plasma, serum or liver homogenate of an HGBV infected individual, either tamarin or human. This family of nucleotide sequences is not of human or tamarin origin, since it will be shown that it hybridizes to neither human nor tamarin genomic DNA from uninfected individuals, since nucleotides of this family of sequences are present only in liver (or liver homogenates), plasma or serum of individuals infected with HGBV, and since the sequence is not present in GenBank. In addition, the family of sequences will show no significant identity at the nucleic acid level to sequences contained within the HAV, HBV, HCV, HDV and HEV genome, and low level identity, considered not significant, as translation products. Infectious sera, plasma or liver homogenates from HGBV infected humans contain these polynucleotide sequences, whereas sera, plasma or liver homogenates from non-infected humans do not contain these sequences. Northern blot analysis of infected liver with some of these polynucleotide sequences demonstrate that they are derived from a large RNA transcript similar in size to a viral genome. Sera, plasma or liver homogenates from HGBV-infected humans contain antibodies which bind to this polypeptide, whereas sera, plasma or liver homogenates from non-infected humans do not contain antibodies to this polypeptide; these antibodies

are induced in individuals following acute non-A, non-B, non-C, non-D and non-E infection. By these criteria, it is believed that the sequence is a viral sequence, wherein the virus causes or is associated with non-A, non-B, non-C, non-D and non-E hepatitis.

5 The availability of this family of nucleic acid sequences permits the construction of DNA probes and polypeptides useful in diagnosing non-A, non-B, non-C, non-D, non-E hepatitis due to HGBV infections, and in screening blood donors, donated blood, blood products and individuals for infection. For example, from the sequence it is possible to synthesize DNA oligomers of about
10 eight to ten nucleotides, or larger, which are useful as hybridization probes or PCR primers to detect the presence of the viral genome in, for example, sera of subjects suspected of harboring the virus, or for screening donated blood for the presence of the virus. The family of nucleic acid sequences also allows the design and production of HGBV specific polypeptides which are useful as diagnostic reagents
15 for the presence of antibodies raised during infection with HGBV. Antibodies to purified polypeptides derived from the nucleic acid sequences may also be used to detect viral antigens in infected individuals and in blood. These nucleic acid sequences also enable the design and production of polypeptides which may be used as vaccines against HGBV, and also for the production of antibodies, which
20 then may be used for protection of the disease, and/or for therapy of HGBV infected individuals.

 The family of nucleic acid sequences also enables further characterization of the HGBV genome. Polynucleotide probes derived from these sequences may be used to screen genomic or cDNA libraries for additional overlapping nucleic
25 acid sequences which then may be used to obtain more overlapping sequences. Unless the genome is segmented and the segments lack common sequences, this technique may be used to gain the sequence of the entire genome. However, if the genome is segmented, other segments of the genome can be obtained by either repeating the RDA cloning procedure as described and modified hereinbelow or by
30 repeating the lambda-gt11 serological screening procedure discussed hereinbelow to isolate the clones which will be described herein, or alternatively by isolating the genome from purified HGBV particles.

 The family of cDNA sequences and the polypeptides derived from these sequences, as well as antibodies directed against these polypeptides, also are
35 useful in the isolation and identification of the HGBV etiological agent(s). For example, antibodies directed against HGBV epitopes contained in polypeptides derived from the nucleic acid sequences may be used in methods based upon

affinity chromatography to isolate the virus. Alternatively, the antibodies can be used to identify viral particles isolated by other techniques. The viral antigens and the genomic material within the isolated viral particles then may be further characterized.

5 The information obtained from further sequencing of the HGBV genome(s), as well as from further characterization of the HGBV antigens and characterization of the genome enables the design and synthesis of additional probes and polypeptides and antibodies which may be used for diagnosis, prevention and therapy of HGBV induced non-A, non-B, non-C non-D, non-E
10 hepatitis, and for screening of infected blood and blood-related products.

 The availability of probes for HGBV, including antigens, antibodies and polynucleotides derived from the genome from which the family of nucleic acid sequences is derived also allows for the development of tissue culture systems which will be of major use in elucidating the biology of HGBV. Once this is
15 known, it is contemplated that new treatment regimens may be developed based upon antiviral compounds which preferentially inhibit the replication of or infection by HGBV.

 In one method used to identify and isolate the etiological agent of HGBV, the cloning/isolation of the GB agent was achieved by modifying the published
20 procedure known as representational difference analysis (RDA), as reported by N. Lisitsyn et al., Science 259: 946-951 (1993). This method is based upon the principles of subtractive hybridization for cloning DNA differences between two complex mammalian genomes. Briefly, in this procedure, the two genomes under evaluation are identified generically as the "tester" (containing the target sequence
25 of interest) and the "driver" (representing normal DNA). Lisitsyn et al.'s description of RDA is limited to identifying and cloning DNA differences between complex, but similar DNA backgrounds. These differences may include any large DNA viruses (eg. $\geq 25,000$ base pairs of DNA) that is present in a cell line, blood, plasma or tissue sample and absent in an uninfected cell line, blood, plasma or
30 tissue sample. Because previous literature suggested that HGBV may be a small virus containing either a DNA or RNA genome of $\leq 10,000$ bases, the RDA protocol was modified such as to allow the detection of small viruses. The major steps of the procedure are described hereinbelow and are diagramed in FIGURE 13.

35 Briefly, in step 1, total nucleic acid (DNA and RNA) is isolated using commercially available kits. RDA requires that the sample be highly matched. Ideally, tester and driver nucleic acid samples should be obtained from the same

source (animal, human or other). It may be possible to use highly related, but non-identical, material for the source of the tester and driver nucleic acids. Double stranded DNA is generated from the total nucleic acid by random primed reverse transcription of the RNA followed by random primed DNA synthesis. This treatment converts single strand RNA viruses and single strand DNA viruses to double strand DNA molecules which are amenable to RDA. If one chooses to assume that an unknown virus has a DNA or an RNA genome, a DNA-only or RNA-only extraction procedure can be employed and double-stranded DNA can be generated as described in the art.

10 In step 2, the tester and driver nucleic acids are amplified to generate an abundant amount of material which represents the total nucleic acid extracted from the pre-inoculation and infectious plasma sources (ie. the tester amplicon and the driver amplicon). This is achieved by cleaving double-stranded DNA prepared as described above with a restriction endonuclease which has a 4 bp recognition site (such as Sau3A I). The DNA fragments are ligated to oligonucleotide adaptors (set #1). The DNA fragments are end-filled and PCR amplified. Following PCR amplification, the oligonucleotide adaptor (set #1) is then removed by restriction endonuclease digestion (for example, with Sau3A I), liberating a large amount of tester and driver nucleic acid to be used in subsequent subtractive hybridization techniques.

20 In step 3, the experimental design is to enrich for DNA unique to the tester genome. This is achieved by combining subtractive hybridization and kinetic enrichment into a single step. Briefly, an oligonucleotide adaptor set (#2 or #3) is ligated to the 5' ends of the tester amplicon. The tester amplicon and an excess of driver amplicon are mixed, denatured and allowed to hybridized for 20 hours. A large amount of the sequences that are held in common between the tester and driver DNA will anneal during this time. In addition, sequences that are unique to the tester amplicon will reanneal. However, because of the limited time of hybridization, some single-standed tester and driver DNA will remain.

30 In step 4, the 3' ends of the reannealed tester and driver DNA are filled in using a thermostable DNA polymerase at elevated temperature as described in the art. The reannealed sequences that are unique to the tester contain the ligated adaptor on both strands of the annealed sequence. Thus, 3' end-filling of these molecules creates sequences complementary to PCR primers on both DNA strands. As such, these DNA species will be amplified exponentially when subjected to PCR. In contrast, the relatively large amount of hybrid molecules containing sequences held in common between tester and driver amplicons (ie. one

strand was derived from the tester amplicon and one strand was derived from the driver amplicon) will be amplified linearly when subjected to PCR. This is because only one strand (derived from the tester amplicon) contains the ligated adaptor sequence, and 3' end filling will only generate sequences complementary to the PCR primer on the strand derived from the driver amplicon.

In step 5, the double-strand DNA of interest is enriched quantitatively using PCR for 10 cycles of amplification. As stated above in step 4, reannealed tester sequences will be amplified exponentially whereas sequences held in common between tester and driver amplicons will be amplified linearly.

In step 6, single-strand DNA which remains is removed by a single strand DNA nuclease digestion using mung bean nuclease as described in the art.

In step 7, double-stranded DNA which remains after nuclease digestion is PCR amplified an additional 15 to 25 cycles.

Finally in step 8, these DNA products are cleaved with restriction endonuclease to remove the oligonucleotide adaptors. These DNA products can then be subjected to subsequent rounds of amplification (beginning at step #3 using the oligonucleotide adaptor set that was not used in the previous cycle of RDA) or cloned into a suitable plasmid vector for further analysis.

The RDA procedure as described supra is a modification of the representational difference analysis known in the art. The method was modified to isolate viral clones from pre-inoculation and infectious sera sources. These modifications are discussed further below and relate to the preparation of amplicons for both tester and driver DNA. First, the starting material was not double-stranded DNA obtained from the genomic DNA of mammalian cells as reported previously, but total nucleic acid extracted from infectious and pre-inoculation biological blood samples obtained from tamarins. It is possible that other biological samples (for example, organs, tissue, bile, feces or urine) could be used as sources of nucleic acid from which tester and driver amplicons are generated. Second, the amount of starting nucleic acid is substantially less than that described in the art. Third, a restriction endonuclease with a 4 bp instead of a 6 bp recognition site was used. This is substantially different from the prior art. Lisitsyn et al. teach that RDA works because the generation of amplicons (ie. representations) decreases the complexity of the DNA that is being hybridized (ie. subtracted).

In the prior art, restriction enzymes that have 6 bp recognition sites were used to fragment the genome. These restriction endonucleases cleave approximately every 4000 bp. However, the PCR conditions described in the

prior art amplify sequences ≤ 1500 bp in size. Therefore, subsequent PCR amplification of a complex species of DNA (such as a genome) that has been fragmented with a restriction enzyme that recognizes a 6 bp sequence results in the generation of amplicons that contain the fraction of the DNA that was ≤ 1500 bp in size after restriction endonuclease digestion. This reduction in DNA complexity (estimated to be a 10- to 50-fold reduction) is reported to be necessary for the hybridization step of RDA to work. If the complexity is not reduced, unique sequences in the tester will not be able to efficiently hybridize during the subtraction step, and therefore, these unique sequences will not be amplified exponentially during the subsequent PCR steps of RDA.

The reduction of complexity of the nucleic acid sequences being subjected to RDA undermines using RDA effectively to isolate relatively small viruses. The odds of two 6 bp-recognition sites occurring within 1.5 kb of each other is sufficiently rare that one might miss a small (≤ 10 kb) virus (TABLE 1).

TABLE 1

	<u>Virus</u>	<u>Enzyme</u>	<u># of Fragments < 1.5kb</u>
20	λ (~50 kb)	BamH I	0
		Bgl II	3
		Hind III	1
25	Parvo B19 (~5 kb)	BamH I	0
		Bgl II	0
		Hind III	2
		Sau3A I (4 bp site)	5-7
30	HBV (~3.2 kb)	BamH I	1-2
		Bgl II	1-2
		HindIII	0
		Sau3A I (4 bp site)	12

However, we have discovered that RDA may be useful in cloning small viruses if a more frequently cutting restriction endonuclease is used to fragment the DNA being subjected to RDA. As shown in TABLE 1, amplicons based on 4 bp recognition site enzymes will almost certainly contain several fragments from any small virus, as restriction endonucleases which have 4 bp recognition sites fragment DNA approximately every 250 base pairs. However, it is likely that amplicons will be as complex as the source of the nucleic acid from which they were generated because nearly all of the DNA species will be ≤ 1500 bp after digestion with a 4 bp recognizing restriction endonuclease and thus, subject to PCR amplification. Since the relative viral sequence copy number is predicted to

be higher than any specific or endogenous sequence copy number, the unique viral sequences that are present in the tester amplicon should be able to form double stranded molecules during the hybridization step (step 3, above). Therefore, these sequences will be amplified exponentially as described above. It is reasoned that
5 as the relative viral sequence copy number becomes closer to that of the background or endogenous nucleic acid sequence copy number, a restriction endonuclease which recognizes a redundant 6 bp sequence (for example BstYI or HincII) and cleaves approximately every 1000 bp, or the simultaneous use of several restriction endonuclease which recognizes 6 bp sequences, may be used to
10 fragment the DNA prior to amplification by PCR. In this way, one can moderately reduce the complexity of the amplicons being subjected to RDA while minimizing the risk of excluding viral sequences from the tester amplicon. The utility of this procedure is demonstrated by the cloning of HGBV sequences from infectious tamarin plasma described herein.

15 Immunoscreening to identify HGBV immunoreactive epitopes

Immunoscreening as described herein as follows also provided an additional means of identifying HGBV sequences. Pooled or individual serum, plasma or liver homogenates from an individual meeting the criteria and within the parameters set forth below with acute or chronic HGBV infection is used to isolate
20 viral particles. Nucleic acids isolated from these particles are used as the template in the construction of a genomic and/or cDNA library to the viral genome. The procedures used for isolation of putative HGBV particles and for constructing the genomic and/or cDNA library in lambda-gt11 or similar systems known in the art is discussed hereinbelow. Lambda-gt11 is a vector that has been developed
25 specifically to express inserted cDNAs as fusion polypeptides with beta-galactosidase and to screen large numbers of recombinant phage with specific antisera raised against a defined antigen. The lambda-gt11 cDNA library generated from a cDNA pool containing cDNA is screened for encoded epitopes that can bind specifically with sera derived from individuals who previously had experienced
30 non-A, non-B, non-C, non-D and non-E hepatitis. See V. Hunyh et al., in D. Glover, ed, DNA Cloning Techniques: A Practical Approach, IRL Press, Oxford, England, pp. 49-78 (1985). Approximately 10^6 - 10^7 phage are screened, from which positive phage are identified, purified, and then tested for specificity of binding to sera from different individuals previously infected with the HGBV
35 agent. Phage which selectively bind sera or plasma from patients meeting the criteria described hereinbelow and not in patients who did not meet these described criteria, are preferred for further study. By utilizing the technique of isolating

overlapping nucleic acid sequences, clones containing additional upstream and downstream HGBV sequences are obtained. Analysis of the nucleotide sequences of the HGBV nucleic acid sequences encoded within the isolated clones is performed to determine whether the composite sequence contains one long
5 continuous ORF.

The sequences (and their complements) retrieved from the HGBV sequence as provided herein, and the sequences or any portion thereof, can be prepared using synthetic methods or by a combination of synthetic methods with retrieval of partial sequences using methods similar to those described herein. This
10 description thus provides one method by which genomic or cDNA sequences corresponding to the entire HGBV genome may be isolated. Other methods for isolating these sequences, however, will be obvious to those skilled in the art and are considered to be within the scope of the present invention.

Deposit of Strains.

15 Strains replicated (clones 2, 4, 10, 16, 18, 23 and 50) from the HGBV nucleic acid sequence library have been deposited at the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, as of February 10, 1994, under the terms of the Budapest Treaty and will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the
20 last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. The deposits and any other deposited material described herein are provided for convenience only, and are not required to practice the present invention in view of the teachings provided herein. The HGBV cDNA sequences in all of the deposited materials are incorporated herein by reference.
25 The plasmids were accorded the following A.T.C.C. deposit numbers: Clone 2 was accorded A.T.C.C. Deposit No. 69556; Clone 4 was accorded A.T.C.C. Deposit No. 69557; Clone 10 was accorded A.T.C.C. Deposit No. 69558; Clone 16 was accorded A.T.C.C. Deposit No. 69559; Clone 18 was accorded A.T.C.C. Deposit No. 69560; Clone 23 was accorded A.T.C.C. Deposit No. 69561; and
30 Clone 50 was accorded A.T.C.C. Deposit No. 69562.

Strains replicated (clones 11, 13, 48 and 119) from the HGBV nucleic acid sequence library have been deposited at the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, as of April 29, 1994, under the terms of the Budapest Treaty and will be maintained for a period of thirty (30)
35 years from the date of deposit, or for five (5) years after the last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. The deposits and any other deposited material described herein are provided for

convenience only, and are not required to practice the present invention in view of the teachings provided herein. The HGBV cDNA sequences in all of the deposited materials are incorporated herein by reference. The plasmids were accorded the following A.T.C.C. deposit numbers: Clone 11 was accorded A.T.C.C. Deposit
5 No. No. 69613; Clone 13 was accorded A.T.C.C. Deposit No. 69611; Clone 48 was accorded A.T.C.C. Deposit No. 69610; and Clone 119 was accorded A.T.C.C. Deposit No. 69612.

Additional strains (clones 4-B1.1, 66-3A1.49, 70-3A1.37 and 78-1C1.17) from the HGBV nucleic acid sequence library have been deposited at the American
10 Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, as of July 28, 1994, under the terms of the Budapest Treaty and will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. The deposits and any other deposited material described
15 herein are provided for convenience only, and are not required to practice the present invention in view of the teachings provided herein. The HGBV cDNA sequences in all of the deposited materials are incorporated herein by reference. The plasmids were accorded the following A.T.C.C. deposit numbers: Clone 4-B1.1 was accorded A.T.C.C. Deposit No. No. 69666; Clone 66-3A1.49 was
20 accorded A.T.C.C. Deposit No. 69665; Clone 70-3A1.37 was accorded A.T.C.C. Deposit No. 69664; and Clone 78-1C1.17 was accorded A.T.C.C. Deposit No. 69663.

Clone pHGBV-C clone #1 was deposited at the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852 as of November 8,
25 1994, under the terms of the Budapest Treaty and will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. The deposits and any other deposited material described herein are provided for convenience only, and are not required to practice the present
30 invention in view of the teachings provided herein. pHGBV-C clone #1 was accorded A.T.C.C. Deposit No. 69711. The HGBV cDNA sequences in all of the deposited materials are incorporated herein by reference.

Preparation of Viral Polypeptides and Fragments

The availability of nucleic acid sequences permits the construction of
35 expression vectors encoding antigenically active regions of the polypeptide encoded in either strand. These antigenically active regions may be derived from structural regions of the virus, including, for example, envelope (coat) or core

antigens, in addition to nonstructural regions of the virus, including, for example, polynucleotide binding proteins, polynucleotide polymerase(s), and other viral proteins necessary for replication and/or assembly of the viral particle. Fragments encoding the desired polypeptides are derived from the genomic or cDNA clones
5 using conventional restriction digestion or by synthetic methods, and are ligated into vectors which may, for example, contain portions of fusion sequences such as beta-galactosidase (β -gal) or superoxide dismutase (SOD) or CMP-KDO synthetase (CKS). Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in EPO
10 0196056, published October 1, 1986, and those of CKS are described in EPO Publication No. 0331961, published September 13, 1989. Any desired portion of the nucleic acid sequence containing an open reading frame, in either sense strand, can be obtained as a recombinant protein, such as a mature or fusion protein; alternatively, a polypeptide encoded in the HGBV genome or cDNA can be
15 provided by chemical synthesis.

The nucleic acid sequence encoding the desired polypeptide, whether in fused or mature form, and whether or not containing a signal sequence to permit secretion, may be ligated into expression vectors suitable for any convenient host. Both eucaryotic and prokaryotic host systems are used in the art to form
20 recombinant proteins, and some of these are listed herein. The polypeptide then is isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification can be performed by techniques known in the art, and include salt fractionation, chromatography on ion exchange resins, affinity chromatography, centrifugation, among others. Such polypeptides may be
25 used as diagnostic reagents, or for passive immunotherapy. In addition, antibodies to these polypeptides are useful for isolating and identifying HGBV particles. The HGBV antigens also may be isolated from HGBV virions. These virions can be grown in HGBV infected cells in tissue culture, or in an infected individual.

30 Preparation of Antigenic Polypeptides and Conjugation With Solid Phase

An antigenic region or fragment of a polypeptide generally is relatively small, usually about 8 to 10 amino acids or less in length. Fragments of as few as 5 amino acids may characterize an antigenic region. These segments may correspond to regions of HGBV antigen. By using the HGBV genomic or cDNA
35 sequences as a basis, nucleic acid sequences encoding short segments of HGBV polypeptides can be expressed recombinantly either as fusion proteins or as isolated polypeptides. These short amino acid sequences also can be obtained by

chemical synthesis. The small chemically synthesized polypeptides may be linked to a suitable carrier molecule when the synthesized polypeptide provided is correctly configured to provide the correct epitope but too small to be antigenic. Linking methods are known in the art and include but are not limited to using N-succinimidyl-3-(2-pyridylthio)propionate (SPDP) and succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (SMCC). Polypeptides lacking sulfhydryl groups can be modified by adding a cysteine residue. These reagents create a disulfide linkage between themselves and peptide cysteine residues on one protein and an amide linkage through the epsilon-amino on a lysine, or other free amino group in the other. A variety of such disulfide/amide-forming agents are known. Other bifunctional coupling agents form a thioester rather than a disulfide linkage. Many of these thio-ether-forming agents are commercially available and are known to those of ordinary skill in the art. The carboxyl groups can be activated by combining them with succinimide or 1-hydroxyl-2-nitro-4-sulfonic acid, sodium salt. Any carrier which does not itself induce the production of antibodies harmful to the host can be used. Suitable carriers include proteins, polysaccharides such as latex functionalized sepharose, agarose, cellulose, cellulose beads, polymeric amino acids such as polyglutamic acid, polylysine, amino acid copolymers and inactive virus particles, among others. Examples of protein substrates include serum albumins, keyhole limpet hemocyanin, immunoglobulin molecules, thyroglobulin, ovalbumin, tetanus toxoid, and yet other proteins known to those skilled in the art.

Preparation of Hybrid Particle Immunogens Containing HGBV Epitopes

The immunogenicity of HGBV epitopes also may be enhanced by preparing them in mammalian or yeast systems fused with or assembled with particle-forming proteins such as those associated with HBV surface antigen. Constructs wherein the HGBV epitope is linked directly to the particle-forming protein coding sequences produce hybrids which are immunogenic with respect to the HGBV epitope. In addition, all of the vectors prepared include epitopes specific for HGBV, having varying degrees of immunogenicity. Particles constructed from particle forming protein which include HGBV sequences are immunogenic with respect to HGBV and HBV.

Hepatitis B surface antigen has been determined to be formed and assembled into particles in *S. cerevisiae* and mammalian cells; the formation of these particles has been reported to enhance the immunogenicity of the monomer subunit. P. Valenzuela et al., *Nature* 298:334 (1982); P. Valenzuela et al., in I. Millman et al., eds., *Hepatitis B*, Plenum Press, pp. 225-236 (1984). The

constructs may include immunodominant epitopes of HBsAg. Such constructs have been reported expressible in yeast, and hybrids including heterologous viral sequences for yeast expression have been disclosed. See, for example, EPO 174, 444 and EPO 174,261. These constructs also have been reported capable of being
5 expressed in mammalian cells such as Chinese hamster ovary (CHO) cells.

Michelle et al., International Symposium on Viral Hepatitis, 1984. In HGBV, portions of the particle-forming protein coding sequence may be replaced with codons encoding an HGBV epitope. In this replacement, regions that are not required to mediate the aggregation of the units to form immunogenic particles in
10 yeast or mammals can be deleted, thus eliminating additional HGBV antigenic sites from competition with the HGBV epitope.

Vaccine Preparation

Vaccines may be prepared from one or more immunogenic polypeptides or nucleic acids derived from HGBV nucleic acid sequences or from the HGBV
15 genome to which they correspond. Vaccines may comprise recombinant polypeptides containing epitope(s) of HGBV. These polypeptides may be expressed in bacteria, yeast or mammalian cells, or alternatively may be isolated from viral preparations. It also is anticipated that various structural proteins may contain epitopes of HGBV which give rise to protective anti-HGBV antibodies.
20 Synthetic peptides therefore also can be utilized when preparing these vaccines. Thus, polypeptides containing at least one epitope of HGBV may be used, either singly or in combinations, in HGBV vaccines. It also is contemplated that nonstructural proteins as well as structural proteins may provide protection against viral pathogenicity, even if they do not cause the production of neutralizing
25 antibodies.

Considering the above, multivalent vaccines against HGBV may comprise one or more structural proteins, and/or one or more nonstructural proteins. These vaccines may be comprised of, for example, recombinant HGBV polypeptides and/or polypeptides isolated from the virions and/or synthetic peptides. These
30 immunogenic epitopes can be used in combinations, i.e., as a mixture of recombinant proteins, synthetic peptides and/or polypeptides isolated from the virion; these may be administered at the same or different time. Additionally, it may be possible to use inactivated HGBV in vaccines. Such inactivation may be by preparation of viral lysates, or by other means known in the art to cause
35 inactivation of hepatitis-like viruses, for example, treatment with organic solvents or detergents, or treatment with formalin. Attenuated HGBV strain preparation also is disclosed in the present invention. It is contemplated that some of the

proteins in HGBV may cross-react with other known viruses, and thus that shared epitopes may exist between HGBV and other viruses which would then give rise to protective antibodies against one or more of the disorders caused by these pathogenic agents. It is contemplated that it may be possible to design multiple
5 purpose vaccines based upon this belief.

The preparation of vaccines which contain at least one immunogenic peptide as an active ingredient is known to one skilled in the art. Typically, such vaccines are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in or suspension in liquid prior to injection also may be
10 prepared. The preparation may be emulsified or the protein may be encapsulated in liposomes. The active immunogenic ingredients often are mixed with pharmacologically acceptable excipients which are compatible with the active ingredient. Suitable excipients include but are not limited to water, saline, dextrose, glycerol, ethanol and the like; combinations of these excipients in various
15 amounts also may be used. The vaccine also may contain small amounts of auxiliary substances such as wetting or emulsifying reagents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the vaccine. For example, such adjuvants can include aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-DMP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (CGP
20 11687, also referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, also referred to as MTP-PE), and RIBI (MPL + TDM+ CWS) in a 2% squalene/Tween-80® emulsion. The effectiveness of an adjuvant may be determined by measuring the amount of antibodies directed against an
25 immunogenic polypeptide containing an HGBV antigenic sequence resulting from administration of this polypeptide in vaccines which also are comprised of the various adjuvants.

The vaccines usually are administered by intravenous or intramuscular injection. Additional formulations which are suitable for other modes of
30 administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include but are not limited to polyalkylene glycols or triglycerides. Such suppositories may be formed from mixtures containing the active ingredient in the range of about 0.5% to about 10%, preferably, about 1% to about 2%. Oral formulation include such normally
35 employed excipients as, for example pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. These compositions may take the form of solutions, suspensions,

tablets, pills, capsules, sustained release formulations or powders and contain about 10% to about 95% of active ingredient, preferably about 25% to about 70%.

The proteins used in the vaccine may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts such as acid addition salts (formed with free amino groups of the peptide) and which are formed with inorganic acids such as hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and others known to those skilled in the art. Salts formed with the free carboxyl groups also may be derived from inorganic bases such as sodium, potassium, ammonium, calcium or ferric hydroxides and the like, and such organic bases such as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine procaine, and others known to those skilled in the art.

Vaccines are administered in a way compatible with the dosage formulation, and in such amounts as will be prophylactically and/or therapeutically effective. The quantity to be administered generally is in the range of about 5 micrograms to about 250 micrograms of antigen per dose, and depends upon the subject to be dosed, the capacity of the subject's immune system to synthesize antibodies, and the degree of protection sought. Precise amounts of active ingredient required to be administered also may depend upon the judgment of the practitioner and may be unique to each subject. The vaccine may be given in a single or multiple dose schedule. A multiple dose is one in which a primary course of vaccination may be with one to ten separate doses, followed by other doses given at subsequent time intervals required to maintain and/or to reinforce the immune response, for example, at one to four months for a second dose, and if required by the individual, a subsequent dose(s) after several months. The dosage regimen also will be determined, at least in part, by the need of the individual, and be dependent upon the practitioner's judgment. It is contemplated that the vaccine containing the immunogenic HGBV antigen(s) may be administered in conjunction with other immunoregulatory agents, for example, with immune globulins.

Preparation of Antibodies Against HGBV Epitopes

The immunogenic peptides prepared as described herein are used to produce antibodies, either polyclonal or monoclonal. When preparing polyclonal antibodies, a selected mammal (for example, a mouse, rabbit, goat, horse or the like) is immunized with an immunogenic polypeptide bearing at least one HGBV epitope. Serum from the immunized animal is collected after an appropriate incubation period and treated according to known procedures. If serum containing polyclonal antibodies to an HGBV epitope contains antibodies to other antigens,

the polyclonal antibodies can be purified by, for example, immunoaffinity chromatography. Techniques for producing and processing polyclonal antibodies are known in the art and are described in, among others, Mayer and Walker, eds., Immunochemical Methods In Cell and Molecular Biology, Academic Press,

- 5 London (1987). Polyclonal antibodies also may be obtained from a mammal previously infected with HGBV. An example of a method for purifying antibodies to HGBV epitopes from serum of an individual infected with HGBV using affinity chromatography is provided herein.

- Monoclonal antibodies directed against HGBV epitopes also can be
10 produced by one skilled in the art. The general methodology for producing such antibodies is well-known and has been described in, for example, Kohler and Milstein, Nature 256:494 (1975) and reviewed in J.G.R. Hurrel, ed., Monoclonal Hybridoma Antibodies: Techniques and Applications, CRC Press Inc., Boca
Raton, FL (1982), as well as that taught by L. T. Mimms et al., Virology 176:604-
15 619 (1990). Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See also, M. Schreier et al., Hybridoma Techniques, Scopes (1980) Protein Purification, Principles and Practice, 2nd Edition, Springer-Verlag, New York (1984); Hammerling et al.,
20 Monoclonal Antibodies and T-Cell Hybridomas (1981); Kennet et al., Monoclonal Antibodies (1980). Examples of uses and techniques of monoclonal antibodies are disclosed in U.S. patent applications Serial Nos. 748,292; 748,563; 610,175, 648,473; 648,477; and 648,475.

- Monoclonal and polyclonal antibodies thus developed, directed against
25 HGBV epitopes, are useful in diagnostic and prognostic applications, and also, those which are neutralizing are useful in passive immunotherapy. Monoclonal antibodies especially can be used to produce anti-idiotypic antibodies. These anti-idiotypic antibodies are immunoglobulins which carry an "internal image" of the antigen of the infectious agent against which protection is desired. See, for
30 example, A. Nisonoff et al., Clin. Immunol. Immunopath. 21:397-406 (1981), and Dreesman et al., J. Infect. Dis. 151:761 (1985). Techniques for raising such idiotypic antibodies are known in the art and exemplified, for example, in Grych et al., Nature 316:74 (1985); MacNamara et al., Science 226:1325 (1984); and Uytdehaag et al., J. Immunol. 134:1225 (1985). These anti-idiotypic antibodies
35 also may be useful for treatment of HGBV infection, as well as for elucidation of the immunogenic regions of HGBV antigens.

Diagnostic Oligonucleotide Probes and Kits

Using determined portions of the isolated HGBV nucleic acid sequences as a basis, oligomers of approximately eight nucleotides or more can be prepared, either by excision or synthetically, which hybridize with the HGBV genome and are useful in identification of the viral agent(s), further characterization of the viral genome, as well as in detection of the virus(es) in diseased individuals. The natural or derived probes for HGBV polynucleotides are a length which allows the detection of unique viral sequences by hybridization. While six to eight nucleotides may be a workable length, sequences of ten to twelve nucleotides are preferred, and those of about 20 nucleotides may be most preferred. These sequences preferably will derive from regions which lack heterogeneity. These probes can be prepared using routine, standard methods including automated oligonucleotide synthetic methods. A complement of any unique portion of the HGBV genome will be satisfactory. Complete complementarity is desirable for use as probes, although it may be unnecessary as the length of the fragment is increased.

When used as diagnostic reagents, the test sample to be analyzed, such as blood or serum, may be treated such as to extract the nucleic acids contained therein. The resulting nucleic acid from the sample may be subjected to gel electrophoresis or other size separation techniques; or, the nucleic acid sample may be dot-blotted without size separation. The probes then are labelled. Suitable labels and methods for attaching labels to probes are known in the art, and include but are not limited to radioactive labels incorporated by nick translation or kinasing, biotin, fluorescent and chemiluminescent probes. Examples of many of these labels are disclosed herein. The nucleic acids extracted from the sample then are treated with the labelled probe under hybridization conditions of suitable stringencies.

The probes can be made completely complementary to the HGBV genome. Therefore, usually high stringency conditions are desirable in order to prevent false positives. However, conditions of high stringency should be used only if the probes are complementary to regions of the HGBV genome which lack heterogeneity. The stringency of hybridization is determined by a number of factors during the washing procedure, including temperature, ionic strength, length of time and concentration of formamide. See, for example, J. Sambrook (*supra*). Hybridization can be carried out by a number of various techniques. Amplification can be performed, for example, by Ligase Chain Reaction (LCR), Polymerase Chain Reaction (PCR), Q-beta replicase, NASBA, etc.

It is contemplated that the HGBV genome sequences may be present in serum of infected individuals at relatively low levels, for example, approximately 10^2 - 10^3 sequences per ml. This level may require that amplification techniques be used in hybridization assays, such as the Ligase Chain Reaction or the Polymerase Chain Reaction. Such techniques are known in the art. For example, the "Bio-Bridge" system uses terminal deoxynucleotide transferase to add unmodified 3'-poly-dT-tails to a nucleic acid probe (Enzo Biochem. Corp.). The poly dt-tailed probe is hybridized to the target nucleotide sequence, and then to a biotin-modified poly-A. Also, in EP 124221 there is described a DNA hybridization assay wherein the analyte is annealed to a single-stranded DNA probe that is complementary to an enzyme-labelled oligonucleotide, and the resulting tailed duplex is hybridized to an enzyme-labelled oligonucleotide. EP 204510 describes a DNA hybridization assay in which analyte DNA is contacted with a probe that has a tail, such as a poly-dT-tail, an amplifier strand that has a sequence that hybridizes to the tail of the probe, such as a poly-A sequence, and which is capable of binding a plurality of labelled strands. The technique first may involve amplification of the target HGBV sequences in sera to approximately 10^6 sequences/ml. This may be accomplished by following the methods described by Saiki et al., Nature 324:163 (1986). The amplified sequence(s) then may be detected using a hybridization assay such as those known in the art. The probes can be packaged in diagnostic kits which include the probe nucleic acid sequence which sequence may be labelled; alternatively, the probe may be unlabelled and the ingredients for labelling could be included with the kit. The kit also may contain other suitably packaged reagents and materials needed or desirable for the particular hybridization protocol, for example, standards as well as instructions for performing the assay.

Other known amplification methods which can be utilized herein include but are not limited to the so-called "NASBA" or "3SR" technique taught in PNAS USA 87:1874-1878 (1990) and also discussed in Nature:350 (No. 6313):91-92 (1991) and Q-beta replicase.

Flourescence *in situ* hybridization ("FISH") also can be performed utilizing the reagents described herein. *In situ* hybridization involves taking morphologically intact tissues, cells or chromosomes through the nucleic acid hybridization process to demonstrate the presence of a particular piece of genetic information and its specific location within individual cells. Since it does not require homogenization of cells and extraction of the target sequence, it provides precise localization and distribution of a sequence in cell populations. *In situ*

hybridization can identify the sequence of interest concentrated in the cells containing it. It also can identify the type and fraction of the cells in a heterogeneous cell population containing the sequence of interest. DNA and RNA can be detected with the same assay reagents. PNAs can be utilized in FISH methods to detect targets without the need for amplification. If increased signal is desired, multiple fluorophores can be used to increase signal and thus, sensitivity of the method. Various methods of FISH are known, including a one-step method using multiple oligonucleotides or the conventional multi-step method. It is within the scope of the present invention that these types of methods can be automated by various means including flow cytometry and image analysis.

Immunoassay and Diagnostic Kits

Both the polypeptides which react immunologically with serum containing HGBV antibodies and composites thereof, and the antibodies raised against the HGBV specific epitopes in these polypeptides are useful in immunoassays to detect the presence of HGBV antibodies, or the presence of the virus and/or viral antigens in biological test samples. The design of these immunoassays is subject to variation, and a variety of these are known in the art; a variety of these have been described herein. The immunoassay may utilize one viral antigen, such as a polypeptide derived from any clone-containing HGBV nucleic acid sequence, or from the composite nucleic acid sequences derived from the HGBV nucleic acid sequences in these clones, or from the HGBV genome from which the nucleic acid sequences in these clones is derived. Or, the immunoassay may use a combination of viral antigens derived from these sources. It may use, for example, a monoclonal antibody directed against the same viral antigen, or polyclonal antibodies directed against different viral antigens. Assays can include but are not limited to those based on competition, direct reaction or sandwich-type assays. Assays may use solid phases or may be performed by immunoprecipitation or any other methods which do not utilize solid phases. Examples of assays which utilize labels as the signal generating compound and those labels are described herein. Signals also may be amplified by using biotin and avidin, enzyme labels or biotin anti-biotin systems, such as that described in pending U.S. patent application Serial Nos. 608,849; 070,647; 418,981; and 687,785. Recombinant polypeptides which include epitopes from immunodominant regions of HGBV may be useful for the detection of viral antibodies in biological test samples of infected individuals. It also is contemplated that antibodies may be useful in discriminating acute from non-acute infections. Kits suitable for immunodiagnosis and containing the appropriate reagents are constructed by packaging the appropriate

materials, including the polypeptides of the invention containing HGBV epitopes or antibodies directed against HGBV epitopes in suitable containers, along with the remaining reagents and materials required for the conduct of the assay, as well as suitable assay instructions.

5 Assay formats can be designed which utilize the recombinant proteins detailed herein, and although we describe and detail CKS proteins, it also is contemplated that other expression systems, such as superoxide dismutase (SOD), and others, can be used in the present invention to generate fusion proteins capable of use in a variety of ways, including as antigens in immunoassays, immunogens
10 for antibody production, and the like. In an assay format to detect the presence of antibody against a specific analyte (for example, an infectious agent such as a virus) in a human test sample, the human test sample is contacted and incubated with a solid phase coated with at least one recombinant protein (polypeptide). If antibodies are present in the test sample, they will form a complex with the
15 antigenic polypeptide and become affixed to the solid phase. After the complex has formed, unbound materials and reagents are removed by washing the solid phase. The complex is reacted with an indicator reagent and allowed to incubate for a time and under conditions for second complexes to form. The presence of antibody in the test sample to the CKS recombinant polypeptide(s) is determined
20 by detecting the signal generated. Signal generated above a cut-off value is indicative of antibody to the analyte present in the test sample. With many indicator reagents, such as enzymes, the amount of antibody present is proportional to the signal generated. Depending upon the type of test sample, it may be diluted with a suitable buffer reagent, concentrated, or contacted with the
25 solid phase without any manipulation ("neat"). For example, it usually is preferred to test serum or plasma samples which previously have been diluted, or concentrate specimens such as urine, in order to determine the presence and/or amount of antibody present.

 In addition, more than one recombinant protein can be used in the assay
30 format just described to test for the presence of antibody against a specific infectious agent by utilizing CKS fusion proteins against various antigenic epitopes of the viral genome of the infectious agent under study. Thus, it may be preferred to use recombinant polypeptides which contain epitopes within a specific viral antigenic region as well as epitopes from other antigenic regions from the viral
35 genome to provide assays which have increased sensitivity and perhaps greater specificity than using a polypeptide from one epitope. Such an assay can be utilized as a confirmatory assay. In this particular assay format, a known amount

of test sample is contacted with (a) known amount(s) of at least one solid support coated with at least one recombinant protein for a time and under conditions sufficient to form recombinant protein/antibody complexes. The complexes are contacted with known amount(s) of appropriate indicator reagent(s) for a time and under suitable conditions for a reaction to occur, wherein the resultant signal generated is compared to a negative test sample in order to determine the presence of antibody to the analyte in the test sample. It further is contemplated that, when using certain solid phases such as microparticles, each recombinant protein utilized in the assay can be attached to a separate microparticle, and a mixture of these microparticles made by combining the various coated microparticles, which can be optimized for each assay.

Variations to the above-described assay formats include the incorporation of CKS-recombinant proteins of different analytes attached to the same or to different solid phases for the detection of the presence of antibody to either analyte (for example, CKS-recombinant proteins specific for certain antigenic regions of one infective agent coated on the same or different solid phase with CKS-recombinant proteins specific for certain antigenic region(s) of a different infective agent, to detect the presence of either (or both) infective agents.

In yet another assay format, CKS recombinant proteins containing antigenic epitopes are useful in competitive assays such as neutralization assays. To perform a neutralization assay, a recombinant polypeptide representing epitopes of an antigenic region of an infectious agent such as a virus, is solubilized and mixed with a sample diluent to a final concentration of between 0.5 to 50.0 $\mu\text{g/ml}$. A known amount of test sample (preferably 10 μl), either diluted or non-diluted, is added to a reaction well, followed by 400 μl of the sample diluent containing the recombinant polypeptide. If desired, the mixture may be preincubated for approximately 15 minutes to two hours. A solid phase coated with the CKS recombinant protein described herein then is added to the reaction well, and incubated for one hour at approximately 40°C. After washing, a known amount of an indicator reagent, for example, 200 μl of a peroxidase labelled goat anti-human IgG in a conjugate diluent is added and incubated for one hour at 40°C. After washing and when using an enzyme conjugate such as described, an enzyme substrate, for example, OPD substrate, is added and incubated at room temperature for thirty minutes. The reaction is terminated by adding a stopping reagent such as 1N sulfuric acid to the reaction well. Absorbance is read at 492 nm. Test samples which contain antibody to the specific polypeptide generate a reduced signal caused by the competitive binding of the peptides to these antibodies in solution. The

percentage of competitive binding may be calculated by comparing absorbance value of the sample in the presence of recombinant polypeptide to the absorbance value of the sample assayed in the absence of a recombinant polypeptide at the same dilution. Thus, the difference in the signals generated between the sample in the presence of recombinant protein and the sample in the absence of recombinant protein is the measurement used to determine the presence or absence of antibody.

In another assay format, the recombinant proteins can be used in immunodot blot assay systems. The immunodot blot assay system uses a panel of purified recombinant polypeptides placed in an array on a nitrocellulose solid support. The prepared solid support is contacted with a sample and captures specific antibodies (specific binding member) to the recombinant protein (other specific binding member) to form specific binding member pairs. The captured antibodies are detected by reaction with an indicator reagent. Preferably, the conjugate specific reaction is quantified using a reflectance optics assembly within an instrument which has been described in U. S. Patent Application Serial No. 07/227,408 filed August 2, 1988. The related U. S. Patent Application Serial No. 07/227,586 and 07/227,590 (both of which were filed on August 2, 1988) further described specific methods and apparatus useful to perform an immunodot assay, as well as U. S. Patent No. 5,075,077 (U.S. Serial No. 07/227,272 filed August 2, 1988), which enjoys common ownership and is incorporated herein by reference. Briefly, a nitrocellulose-base test cartridge is treated with multiple antigenic polypeptides. Each polypeptide is contained within a specific reaction zone on the test cartridge. After all the antigenic polypeptides have been placed on the nitrocellulose, excess binding sites on the nitrocellulose are blocked. The test cartridge then is contacted with a test sample such that each antigenic polypeptide in each reaction zone will react if the test sample contains the appropriate antibody. After reaction, the test cartridge is washed and any antigen-antibody reactions are identified using suitable well-known reagents. As described in the patents and patent applications listed herein, the entire process is amenable to automation. The specifications of these applications related to the method and apparatus for performing an immunodot blot assay are incorporated herein by reference.

CKS fusion proteins can be used in assays which employ a first and second solid support, as follow, for detecting antibody to a specific antigen of an analyte in a test sample. In this assay format, a first aliquot of a test sample is contacted with a first solid support coated with CKS recombinant protein specific for an analyte for a time and under conditions sufficient to form recombinant protein/analyte antibody complexes. Then, the complexes are contacted with an

indicator reagent specific for the recombinant antigen. The indicator reagent is detected to determine the presence of antibody to the recombinant protein in the test sample. Following this, the presence of a different antigenic determinant of the same analyte is determined by contacting a second aliquot of a test sample with
5 a second solid support coated with CKS recombinant protein specific for the second antibody for a time and under conditions sufficient to form recombinant protein/ second antibody complexes. The complexes are contacted with a second indicator reagent specific for the antibody of the complex. The signal is detected in order to determine the presence of antibody in the test sample, wherein the
10 presence of antibody to either analyte recombinant protein, or both, indicates the presence of anti-analyte in the test sample. It also is contemplated that the solid supports can be tested simultaneously.

The use of haptens is known in the art. It is contemplated that haptens also can be used in assays employing CKS fusion proteins in order to enhance
15 performance of the assay.

Further Characterization of the HGBV Genome, Virions, and Viral Antigens Using Probes

The HGBV nucleic acid sequences may be used to gain further information on the sequence of the HGBV genome, and for identification and isolation of the
20 HGBV agent. Thus, it is contemplated that this knowledge will aid in the characterization of HGBV including the nature of the HGBV genome, the structure of the viral particle, and the nature of the antigens of which it is composed. This information, in turn, can lead to additional polynucleotide probes, polypeptides derived from the HGBV genome, and antibodies directed against HGBV epitopes
25 which would be useful for the diagnosis and/or treatment of HGBV caused non-A, non-B, non-C, non-D and non-E hepatitis.

The nucleic acid sequence information is useful for the design of probes or PCR primers for the isolation of additional nucleic acid sequences which are derived from yet undefined regions of the HGBV genome. For example, PCR
30 primers or labelled probes containing a sequence of 8 or more nucleotides, and preferably 20 or more nucleotides, which are derived from regions close to the 5'-termini or 3'-termini of the family of HGBV nucleic acid sequences may be used to isolate overlapping nucleic acid sequences from HGBV genomic or cDNA libraries or directly from viral nucleic acid. These sequences which overlap the HGBV
35 nucleic acid sequences, but which also contain sequences derived from regions of the genome from which the above-mentioned HGBV nucleic acid sequence are not derived, may then be used to synthesize probes for identification of other

overlapping fragments which do not necessarily overlap the nucleic acid sequences in the clones. Unless the HGBV genome is segmented and the segments lack common sequences, it is possible to sequence the entire viral genome(s) utilizing the technique of isolation of overlapping nucleic acid sequences derived from the viral genome(s). Characterization of the genomic segments alternatively could be from the viral genome(s) isolated from purified HGBV particles. Methods for purifying HGBV particles and for detecting them during the purification procedure are described herein. Procedures for isolating polynucleotide genomes from viral particles are well-known in the art. The isolated genomic segments then could be cloned and sequenced. Thus, it is possible to clone and sequence the HGBV genome(s) irrespective of their nature.

Methods for constructing HGBV genomic or cDNA libraries are known in the art, and vectors useful for this purpose are known in the art. These vectors include lambda-gt11, lambda-gt10, and others. The HGBV derived nucleic acid sequence detected by the probes derived from the HGBV genomic or cDNAs, may be isolated from the clone by digestion of the isolated polynucleotide with the appropriate restriction enzyme(s), and sequenced.

The sequence information derived from these overlapping HGBV nucleic acid sequences is useful for determining areas of homology and heterogeneity within the viral genome(s), which could indicate the presence of different strains of the genome and or of populations of defective particles. It is also useful for the design of hybridization probes to detect HGBV or HGBV antigens or HGBV nucleic acids in biological samples, and during the isolation of HGBV, utilizing the techniques described herein. The overlapping nucleic acid sequences may be used to create expression vectors for polypeptides derived from the HGBV genome(s). Encoded within the family of nucleic acid sequences are antigen(s) containing epitopes which are contemplated to be unique to HGBV, i.e., antibodies directed against these antigens are absent from individuals infected with HAV, HBV, HCV, and HEV, and with the genomic sequences in GenBank are contemplated to indicate that minimal homology exists between these nucleic acid sequences and the polynucleotide sequences of those sources. Thus, antibodies directed against the antigens encoded with the HGBV nucleic acid sequences may be used to identify the non-A, non-B, non-C, non-D and non-E particle isolated from infected individuals. In addition, they also are useful for the isolation of the HGBV agent(s).

HGBV particles may be isolated from the sera of infected individuals or from cell cultures by any of the methods known in the art, including, for example,

techniques based on size discrimination such as sedimentation or exclusion methods, or techniques based on density such as ultracentrifugation in density gradients, or precipitation with agents such as polyethylene glycol (PEG), or chromatography on a variety of materials such as anionic or cationic exchange materials, and materials which bind due to hydrophobic interactions, as well as affinity columns. During the isolation procedure the presence of HGBV may be detected by hybridization analysis of the extracted genome, using probes derived from HGBV nucleic acid sequences or by immunoassay which utilize as probes antibodies directed against HGBV antigens encoded within the family of HGBV nucleic acid sequences. The antibodies may be polyclonal or monoclonal, and it may be desirable to purify the antibodies before their use in the immunoassay. Such antibodies directed against HGBV antigens which are affixed to solid phases are useful for the isolation of HGBV by immunoaffinity chromatography. Methods for immunoaffinity chromatography are known in the art, and include methods for affixing antibodies to solid phases so that they retain their immunoselective activity. These methods include adsorption, and covalent binding. Spacer groups may be included in the bifunctional coupling agents such that the antigen binding site of the antibody remains accessible.

During the purification procedure the presence of HGBV may be detected and/or verified by nucleic acid hybridization or PCR, utilizing as probes or primers polynucleotides derived from a family of HGBV genomic or cDNA sequences, as well as from overlapping HGBV nucleic acid sequences. Fractions are treated under conditions which would cause the disruption of viral particles, such as by use of detergents in the presence of chelating agents, and the presence of viral nucleic acid determined by hybridization techniques or PCR. Further confirmation that the isolated particles are the agents which induce HGBV infection may be obtained by infecting an individual which is preferably a tamarin with the isolated virus particles, followed by a determination of whether the symptoms of non-A, non-B, non-C, non-D and non-E hepatitis, as described herein, result from the infection.

Such viral particles obtained from the purified preparations then may be further characterized. The genomic nucleic acid, once purified, can be tested to determine its sensitivity to RNase or DNase I; based on these tests, the determination of HGBV as a RNA genome or DNA genome may be made. The strandedness and circularity or non-circularity can be determined by methods known in the art including its visualization by electron microscopy, its migration in density gradients and its sedimentation characteristics. From hybridization of the

HGBV genome, the negative or positive strandedness of the purified nucleic acid can be determined. In addition, the purified nucleic acid can be cloned and sequenced by known techniques, including reverse transcriptase, if the genomic material is RNA. Utilizing the nucleic acid derived from the viral particles, it then
5 is possible to sequence the entire genome, whether or not it is segmented.

Determination of polypeptides containing conserved sequences may be useful for selecting probes which bind the HGBV genome, thus allowing its isolation. In addition, conserved sequences in conjunction with those derived from the HGBV nucleic acid sequences, may be used to design primers for use in
10 systems which amplify genomic sequences. Further, the structure of HGBV also may be determined and its components isolated. The morphology and size may be determined by electron microscopy, for example. The identification and localization of specific viral polypeptide antigens such as envelope (coat) antigens, or internal antigens such as nucleic acid binding proteins or core antigens, and
15 polynucleotide polymerase(s) also may be determined by ascertaining whether the antigens are present in major or minor viral components, as well as by utilizing antibodies directed against the specific antigens encoded within isolated nucleic acid sequences as probes. This information may be useful for diagnostic and therapeutic applications. For example, it may be preferable to include an exterior
20 antigen in a vaccine preparation, or perhaps multivalent vaccines may be comprised of a polypeptide derived from the genome encoding a structural protein as well as a polypeptide from another portion of the genome, such as a nonstructural polypeptide.

Cell Culture Systems and Animal Model Systems for HGBV Replication

25 Generally, suitable cells or cell lines for culturing HGBV may include the following: monkey kidney cells such as MK2 and VERO, porcine kidney cell lines such as PS, baby hamster kidney cell lines such as BHK, murine macrophage cell lines such as P388D1, MK1 and Mm1, human macrophage cell lines such as U-937, human peripheral blood leukocytes, human adherent monocytes, hepatocytes
30 or hepatocytic cell lines such as HUH7 and HepG2, embryos or embryonic cell such as chick embryo fibroblasts or cell lines derived from invertebrates, preferably from insects such as *Drosophila* cell lines or more preferably from arthropods such as mosquito cell lines or tick cell lines. It also is possible that primary hepatocytes can be cultured and then infected with HGBV. Alternatively,
35 the hepatocyte cultures could be derived from the livers of infected individuals (human or tamarins). ~~That latter~~ case is an example of a cell line which is infected in vivo being passaged in vitro. In addition, various immortalization methods can

be used to obtain cell lines derived from hepatocyte cultures. For example, primary liver cultures (before and after enrichment of the hepatocyte population) may be fused to a variety of cells to maintain stability. Also, cultures may be infected with transforming viruses, or transfected with transforming genes in order to create permanent or semipermanent cell lines. In addition, cells in liver cultures may be fused to established cell lines such as PehG2. Methods for cell fusion are well-known to the routineer, and include the use of fusion agents such as PEG and Sendai Virus, among others.

It is contemplated that HGBV infection of cell lines may be accomplished by techniques such as incubating the cells with viral preparations under conditions which allow viral entry into the cell. It also may be possible to obtain viral production by transfecting the cells with isolated viral polynucleotides. Methods for transfecting tissue culture cells are known in the art and include but are not limited to techniques which use electroporation and precipitation with DEAE-Dextran or calcium phosphate. Transfection with cloned HGBV genomic or cDNA should result in viral replication and the *in vitro* propagation of the virus. In addition to cultured cells, animal model systems may be used for viral replication. HGBV replication thus may occur in chimpanzees and also in, for example, marmosets and suckling mice.

20 Screening for Anti-Viral Agents For HGBV

The availability of cell culture and animal model systems for HGBV also renders screening for anti-viral agents which inhibit HGBV replication possible, and particularly for those agents which preferentially allow cell growth and multiplication while inhibiting viral replication. These screening methods are known in the art. Generally, the anti-viral agents are tested at a variety of concentrations, for their effect on preventing viral replication in cell culture systems which support viral replication, and then for an inhibition of infectivity or of viral pathogenicity, and a low level of toxicity, in an animal model system. The methods and composition provided herein for detecting HGBV antigens and HGBV polynucleotides are useful for screening of anti-viral agents because they provide an alternative, and perhaps a more sensitive means, for detecting the agent's effect on viral replication than the cell plaque assay or ID₅₀ assay. For example, the HGBV polynucleotide probes described herein may be used to quantitate the amount of viral nucleic acid produced in a cell culture. This could be performed by hybridization or competition hybridization of the infected cell nucleic acids with a labelled HGBV polynucleotide probe. Also, anti-HGBV antibodies may be used to identify and quantitate HGBV antigen(s) in the cell culture utilizing

the immunoassays described herein. Also, since it may be desirable to quantitate HGBV antigens in the infected cell culture by a competition assay, the polypeptides encoded within the HGBV nucleic acid sequences described herein are useful for these assays. Generally, a recombinant HGBV polypeptide derived from the HGBV genomic or cDNA would be labelled, and the inhibition of binding of this labelled polypeptide to an HGBV polypeptide due to the antigen produced in the cell culture system would be monitored. These methods are especially useful in cases where the HGBV may be able to replicate in a cell lines without causing cell death.

10 Preparation of Attenuated Strains of HGBV

It may be possible to isolate attenuated strains of HGBV by utilizing the tissue culture systems and/or animal models systems provided herein. These attenuated strains would be useful for vaccines, or for the isolation of viral antigens. Attenuated strains are isolatable after multiple passages in cell culture and/or an animal model. Detection of an attenuated strain in an infected cell or individual is achievable by following methods known in the art and could include the use of antibodies to one or more epitopes encoded in HGBV as a probe or the use of a polynucleotide containing an HGBV sequence of at least about 8 nucleotides in length as a probe. Also or alternatively, an attenuated strain may be constructed utilizing the genomic information of HGBV provided herein, and utilizing recombinant techniques. Usually an attempt is made to delete a region of the genome encoding a polypeptide related to pathogenicity but not to viral replication. The genomic construction would allow the expression of an epitope which gives rise to neutralizing antibodies for HGBV. The altered genome then could be used to transform cells which allow HGBV replication, and the cells grown under conditions to allow viral replication. Attenuated HGBV strains are useful not only for vaccine purposes, but also as sources for the commercial production of viral antigens, since the processing of these viruses would require less stringent protection measures for the employees involved in viral production and/or the production of viral products.

30 Hosts and Expression Control Sequences

Although the following are known in the art, included herein are general techniques used in extracting the genome from a virus, preparing and probing a genomic library, sequencing clones, constructing expression vectors, transforming cells, performing immunological assays, and for growing cell in culture.

Both prokaryotic and eukaryotic host cells may be used for expression of desired coding sequences when appropriate control sequences which are

compatible with the designated host are used. Among prokaryotic hosts, E. coli is most frequently used. Expression control sequences for prokaryotics include promoters, optionally containing operator portions, and ribosome binding sites. Transfer vectors compatible with prokaryotic hosts are commonly derived from the plasmid pBR322 which contains operons conferring ampicillin and tetracycline resistance, and the various pUC vectors, which also contain sequences conferring antibiotic resistance markers. These markers may be used to obtain successful transformants by selection. Commonly used prokaryotic control sequences include the beta-lactamase (penicillinase), lactose promoter system (Chang et al., Nature 198:1056 [1977]) the tryptophan promoter system (reported by Goeddel et al., Nucleic Acid Res 8:4057 [1980]) and the lambda-derived P1 promoter and N gene ribosome binding site (Shimatake et al., Nature 292:128 [1981]) and the hybrid Tac promoter (De Boer et al., Proc. Natl. Acad. Sci. USA 292:128 [1983]) derived from sequences of the trp and lac UV5 promoters. The foregoing systems are particularly compatible with E. coli; however, other prokaryotic hosts such as strains of Bacillus or Pseudomonas may be used if desired, with corresponding control sequences.

Eukaryotic hosts include yeast and mammalian cells in culture systems. Saccharomyces cerevisiae and Saccharomyces carlsbergensis are the most commonly used yeast hosts, and are convenient fungal hosts. Yeast compatible vectors carry markers which permit selection of successful transformants by conferring protrophy to auxotrophic mutants or resistance to heavy metals on wild-type strains. Yeast compatible vectors may employ the 2 micron origin of replication (as described by Broach et al., Meth. Enz. 101:307 [1983]), the combination of CEN3 and ARS1 or other means for assuring replication, such as sequences which will result in incorporation of an appropriate fragment into the host cell genome. Control sequences for yeast vectors are known in the art and include promoters for the synthesis of glycolytic enzymes, including the promoter for 3 phosphophycerate kinase. See, for example, Hess et al., J. Adv. Enzyme Reg. 7: 149 (1968), Holland et al., Biochemistry 17:4900 (1978) and Hitzeman J. Biol. Chem. 255:2073 (1980). Terminators also may be included, such as those derived from the enolase gene as reported by Holland, J. Biol. Chem. 256:1385 (1981). It is contemplated that particularly useful control systems are those which comprise the glyceraldehyde-3 phosphate dehydrogenase (GAPDH) promoter or alcohol dehydrogenase (ADH) regulatable promoter, terminators also derived from GAPDH, and if secretion is desired, leader sequences from yeast alpha factor. In addition, the transcriptional regulatory region and the transcriptional initiation

region which are operably linked may be such that they are not naturally associated in the wild-type organism.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines which are available from the American Type Culture Collection. These include HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney (BHK) cells, and others. Suitable promoters for mammalian cells also are known in the art and include viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), bovine papilloma virus (BPV), cytomegalovirus (CMV). Mammalian cells also may require terminator sequences and poly A addition sequences; enhancer sequences which increase expression also may be included, and sequences which cause amplification of the gene also may be desirable. These sequences are known in the art. Vectors suitable for replication in mammalian cells may include viral replicons, or sequences which insure integration of the appropriate sequences encoding non-A, non-B, non-C, non-D, non-E epitopes into the host genome. An example of a mammalian expression system for HCV is described in U.S. Patent Application Serial No. 07/830,024, filed January 31, 1992.

Transformations

Transformation may be by any known method for introducing polynucleotides into a host cell, including packaging the polynucleotide in a virus and transducing a host cell with the virus, and by direct uptake of the polynucleotide. The transformation procedures selected depends upon the host to be transformed. Bacterial transformation by direct uptake generally employs treatment with calcium or rubidium chloride. Cohen, Proc. Natl. Acad. Sci. USA 69:2110 (1972). Yeast transformation by direct uptake may be conducted using the calcium phosphate precipitation method of Graham et al., Virology 52:526 (1978), or modification thereof.

Vector Construction

Vector construction employs methods known in the art. Generally, site-specific DNA cleavage is performed by treating with suitable restriction enzymes under conditions which generally are specified by the manufacturer of these commercially available enzymes. Usually, about 1 microgram (μ g) of plasmid or DNA sequence is cleaved by 1-10 units of enzyme in about 20 μ l of buffer solution by incubation at 37°C for 1 to 2 hours. After incubation with the restriction enzyme, protein is removed by phenol/chloroform extraction and the DNA recovered by precipitation with ethanol. The cleaved fragments may be

separated using polyacrylamide or agarose gel electrophoresis methods, according to methods known by the routineer.

Sticky end cleavage fragments may be blunt ended using E. coli DNA polymerase 1 (Klenow) in the presence of the appropriate deoxynucleotide triphosphates (dNTPs) present in the mixture. Treatment with S1 nuclease also
5 may be used, resulting in the hydrolysis of any single stranded DNA portions.

Ligations are performed using standard buffer and temperature conditions using T4 DNA ligase and ATP. Sticky end ligations require less ATP and less ligase than blunt end ligations. When vector fragments are used as part of a
10 ligation mixture, the vector fragment often is treated with bacterial alkaline phosphatase (BAP) or calf intestinal alkaline phosphatase to remove the 5'-phosphate and thus prevent religation of the vector. Or, restriction enzyme digestion of unwanted fragments can be used to prevent ligation. Ligation mixtures are transformed into suitable cloning hosts such as E. coli and successful
15 transformants selected by methods including antibiotic resistance, and then screened for the correct construction.

Construction of Desired DNA Sequences

Synthetic oligonucleotides may be prepared using an automated oligonucleotide synthesizer such as that described by Warner, DNA 3:401 (1984).
20 If desired, the synthetic strands may be labelled with ^{32}P by treatment with polynucleotide kinase in the presence of ^{32}P -ATP, using standard conditions for the reaction. DNA sequences including those isolated from genomic or cDNA libraries, may be modified by known methods which include site directed mutagenesis as described by Zoller, Nucleic Acids Res. 10:6487 (1982). Briefly,
25 the DNA to be modified is packaged into phage as a single stranded sequence, and converted to a double stranded DNA with DNA polymerase using, as a primer, a synthetic oligonucleotide complementary to the portion of the DNA to be modified, and having the desired modification included in its own sequence. Culture of the transformed bacteria, which contain replications of each strand of the phage, are
30 plated in agar to obtain plaques. Theoretically, 50% of the new plaques contain phage having the mutated sequence, and the remaining 50% have the original sequence. Replicates of the plaques are hybridized to labelled synthetic probe at temperatures and conditions suitable for hybridization with the correct strand, but not with the unmodified sequence. The sequences which have been identified by
35 hybridization are recovered and cloned.

Hybridization With Probe

HGBV genomic or DNA libraries may be probed using the procedure described by Grunstein and Hogness, Proc. Natl. Acad. Sci. USA 73:3961 (1975). Briefly, the DNA to be probed is immobilized on nitrocellulose filters, denatured and prehybridized with a buffer which contains 0-50% formamide, 0.75 M NaCl, 75 mM Na citrate, 0.02% (w/v) each of bovine serum albumin (BSA), polyvinyl pyrrolidone and Ficoll, 50 mM Na Phosphate (pH 6.5), 0.1% SDS and 100 µg/ml carrier denatured DNA. The percentage of formamide in the buffer, as well as the time and temperature conditions of the prehybridization and subsequent hybridization steps depends on the stringency required. Oligomeric probes which require lower stringency conditions are generally used with low percentages of formamide, lower temperatures, and longer hybridization times. Probes containing more than 30 or 40 nucleotides such as those derived from cDNA or genomic sequences generally employ higher temperatures, for example, about 40 to 42°C, and a high percentage, for example, 50% formamide. Following prehybridization, a ³²P-labelled oligonucleotide probe is added to the buffer, and the filters are incubated in this mixture under hybridization conditions. After washing, the treated filters are subjected to autoradiography to show the location of the hybridized probe. DNA in corresponding locations on the original agar plates is used as the source of the desired DNA.

20 Verification of Construction and Sequencing

For standard vector constructions, ligation mixtures are transformed into E. coli strain XL-1 Blue or other suitable host, and successful transformants selected by antibiotic resistance or other markers. Plasmids from the transformants then are prepared according to the method of Clewell et al., Proc. Natl. Acad. Sci. USA 62:1159 (1969) usually following chloramphenicol amplification as reported by Clewell et al., J. Bacteriol. 110:667 (1972). The DNA is isolated and analyzed usually by restriction enzyme analysis and/or sequencing. Sequencing may be by the well-known dideoxy method of Sanger et al., Proc. Natl. Acad. Sci. USA 74:5463 (1977) as further described by Messing et al., Nucleic Acid Res. 9:309 (1981), or by the method reported by Maxam et al., Methods in Enzymology 65:499 (1980). Problems with band compression, which are sometimes observed in GC rich regions, are overcome by use of T-deazoguanosine according to the method reported by Barr et al., Biotechniques 4:428 (1986).

Enzyme-Linked Immunosorbent Assay

35 Enzyme-linked immunosorbent assay (ELISA) can be used to measure either antigen or antibody concentrations. This method depends upon conjugation of an enzyme label to either an antigen or antibody, and uses the bound enzyme

activity (signal generated) as a quantitative label (measurable generated signal). Methods which utilize enzymes as labels are described herein, as are examples of such enzyme labels.

Preparation of HGBV Nucleic Acid Sequences

- 5 The source of the non-A, non-B, non-C, non-D, non-E agent is an individual or pooled plasma, serum or liver homogenate from a human or tamarin infected with the HGBV virus meeting the clinical and laboratory criteria described herein. A tamarin alternatively can be experimentally infected with blood from another individual with non-A, non-B, non-C, non-E hepatitis meeting the criteria
- 10 described hereinbelow. A pool can be made by combining many individual plasma, serum or liver homogenate samples containing high levels of alanine transferase activity; this activity results from hepatic injury due to HGBV infection. The TID (tamarin infective dose) of the virus has been calculated from one of our experiments to be $\geq 4 \times 10^5/\text{ml}$ (see Example 2, below).
- 15 For example, a nucleic acid library from plasma, serum or liver homogenate, preferably but not necessarily high titer, is generated as follows. First, viral particles are isolated from the plasma, serum or liver homogenate; then an aliquot is diluted in a buffered solution, such as one containing 50 mM Tris-HCl, pH 8.0, 1 mM EDTA, 100 mM NaCl. Debris is removed by centrifugation,
- 20 for example, for 20 minutes at $15,000 \times g$ at 20°C . Viral particles in the resulting supernatant then are pelleted by centrifugation under appropriate conditions which can be determined routinely by one skilled in the art. To release the viral genome, the particles are disrupted by suspending the pellets in an aliquot of an SDS suspension, for example, one containing 1% SDS, 120 mM EDTA, 10 mM Tris-HCl, pH 7.5, which also contains 2 mg/ml proteinase K, which is followed by
- 25 incubation at appropriate conditions, for example, 45°C for 90 minutes. Nucleic acids are isolated by adding, for example, $0.8 \mu\text{g}$ MS2 bacteriophage RNA as carrier, and extracting the mixture four times with a 1:1 mixture of phenol:chloroform (phenol saturated with 0.5M Tris-HCl, pH 7.5, 0.1% (v/v) beta-mercaptoethanol, 0.1% (w/v) hydroxyquinolone, followed by extraction two
- 30 times with chloroform. The aqueous phase is concentrated with, for example, 1-butanol prior to precipitation with 2.5 volumes of absolute ethanol overnight at -20°C . Nucleic acids are recovered by centrifugation in, for example, a Beckman SW41 rotor at 40,000 rpm for 90 min at 4°C , and dissolved in water that is treated
- 35 with 0.05% (v/v) diethylpyrocarbonate and autoclaved.

Nucleic acid obtained by the above procedure is denatured with, for example, 17.5 mM CH_3HgOH ; cDNA then is synthesized using this denatured

nucleic acid as template, and is cloned into the EcoRI site of phage lambda-gt11, for example, by using methods described by Huynh (1985) supra, except that random primers replace oligo(dT) 12-18 during the synthesis of the first nucleic acid strand by reverse transcriptase (see Taylor et al., [1976]). The resulting
5 double stranded nucleic acid sequences are fractionated according to size on a Sepharose CL-4B column, for example. Eluted material of approximate mean size 400, 300, 200 and 100 base-pairs are pooled into genomic pools. The lambda-gt11 cDNA library is generated from the cDNA in at least one of the pools. Alternatively, if the etiological agent is a DNA virus, methods for cloning genomic
10 DNA may be useful and are known to those skilled in the art.

The so-generated lambda-gt11 genomic library is screened for epitopes that can bind specifically with serum, plasma or a liver homogenate from an individual who had previously experienced non-A, non-B, non-C, non-E hepatitis (one which meets the criteria as set forth hereinbelow). About 10^4 - 10^7 phage are
15 screened with sera, plasma, or liver homogenates using the methods of Huynh et al. (supra). Bound human antibody can be detected with sheep anti-human Ig antisera that is radio-labelled with ^{125}I or other suitable reporter molecules including HRPO, alkaline phosphatase and others. Positive phage are identified and purified. These phage then are tested for specificity of binding to sera from a
20 pre-determined number of different humans previously infected with the HGBV agent, using the same method. Ideally, the phage will encode a polypeptide that reacts with all or a majority of the sera, plasma or liver homogenates that are tested, and will not react with sera, plasma or liver homogenates from individuals who are determined to be "negative" according to the criteria set forth herein for the
25 HGBV agent as well as hepatitis A, B, C, D and E. By following these procedures, a clone that encodes a polypeptide which is specifically recognized immunologically by sera, plasma or liver homogenates from non-A, non-B, non-C, non-D and non-E-identified patients can be isolated.

The present invention will now be described by way of examples, which
30 are meant to illustrate, but not to limit, the spirit and scope of the invention.

EXAMPLES

The examples provided herein describe in detail methods which led to the discovery of the HGBV group of viruses. The examples are provided in
35 chronological order so that the discovery of the HGBV-A, HGBV-B and HGBV-C viruses of the HGBV group can be followed. Generally, transmissibility and infectivity studies were initially performed; these studies and subsequent ones

described herein led to evidence for the existence of two HCV-like viruses in HGBV: GB-A and GB-B. Subsequent experiments also detailed herein utilizing degenerative primers led to the discovery of HGBV-C. The prevalence of this group of viruses in humans as evidenced by serological studies, the viral
5 characterization of this group of viruses, the relatedness of HGBV to other viruses in its proposed genus and the interrelatedness of HGBV-A, HGBV-B and HGBV-C also is taught.

Example 1. Transmissibility of HGBV

10 A. Experimental Protocol. Sixteen tamarins (*Saguinus labiatus*) were secured through LEMSIP (Laboratory for Experimental Medicine and Surgery in Primates, Tuxedo, New York) for the transmissibility and infectivity studies. All animals were maintained and monitored at LEMSIP according to protocols approved by LEMSIP. (Note: one animal died of natural causes and one ailing animal was
15 euthanized prior to the initiation of infectivity studies). Baseline serum liver enzyme values were established for serum liver enzymes alanine transaminase (ALT), gamma-glutamyltransferase (GGT) and isocitric dehydrogenase (ICD) for two to three months on serum specimens obtained weekly or bi-weekly. A minimum of eight serum liver enzyme values were obtained for each animal prior
20 to inoculation. Cutoff values (CO) were determined for each animal, based on the mean liver enzyme value plus 3.75 times the standard deviation. Liver enzyme values above the cutoff value were interpreted as abnormal and suggestive of liver damage. Several tamarins were inoculated as described hereinbelow and monitored for changes in ALT, GGT and ICD serum levels. At specified times
25 thereafter during the monitoring process, certain animals were sacrificed in order to obtain serum and tissues for further studies.

B. Inoculation of Animals (Initial Study). A pool of known infectious tamarin GB serum (passage 11, designated as H205 GB pass 11) was prepared from
30 serum collected during the early acute phase (19-24 days post inoculation) of hepatitis from nine tamarins inoculated with the HGBV. This pool had been previously described and studied in an effort to determine the etiological agent involved. J. L. Dienstag et al., Nature 264 supra; E. Tabor et al., J. Med. Virol. 5, supra. Aliquots of this pool were maintained at Abbott Laboratories (North
35 Chicago, IL 60064) under liquid nitrogen storage conditions until utilized in this study. Other aliquots of HGBV are available from the American Type Culture

Collection (A.T.C.C.), 12301 Parklawn Drive, Rockville, MD 20852, under A.T.C.C. Deposit.No. VR-806.

On day one, four tamarins of the initial group of remaining 14 tamarins, identified as T-1053, T-1048, T-1057 and T-1061, were inoculated intravenously with 0.25 ml of pool H205, passage 11, previously diluted 1:50. These animals were monitored weekly for changes in the liver enzymes ALT, GGT and ICD. TABLE 2 presents the pre- and post- inoculation liver enzyme data on these four tamarins (T-1053, T-1048, T-1057 and T-1061); FIGURES 1-4 present the pre- and post- inoculation ALT and ICD levels of these four tamarins. As the data demonstrate, significant rises in ALT, GGT and ICD above the CO were obtained in the four tamarins inoculated with the 1:50 dilution of pool H205.

On the same day (day one), one tamarin (T-1047) was inoculated intravenously with 0.25 ml of pooled normal tamarin serum and used as a negative control, and another tamarin (T-1042) was inoculated intravenously with 0.25 ml of pooled normal human serum and served as an additional negative control. FIGURES 5-6 and TABLE 3 present the pre- and post- inoculation ALT and ICD levels of the two control tamarins (T-1047 and T-1042). As the data demonstrate, no rise in ALT or ICD was documented post-inoculation for the two control tamarins for a period of eight weeks.

On the same day (day one), one tamarin (T-1044) was inoculated intravenously with 0.2 ml of convalescent sera obtained from the surgeon (original GB source) approximately three weeks following the onset of acute hepatitis. This specimen had been stored at -20°C. F. Deinhardt et al., J. Exper. Med. 125:673-688 (1967). Another tamarin (T-1034) was inoculated with 0.1 ml of this convalescent sera. As FIGURES 7-8 and TABLE 4 demonstrate, no rise in serum liver enzymes was observed in these tamarins for a period of eleven weeks post inoculation. Thus, these data demonstrate that infective HGBV was not detectable in the convalescent sera obtained from the original patient and stored at -20°C, which could indicate that the individual had recovered from infection and that the virus had been cleared from the patient's serum or that the viral titer had been reduced to non-detectable levels upon storage at -20°C.

C. Further Studies. Tamarin T-1053 showed a significant rise in serum liver enzymes one week post-inoculation, and was retested for liver enzymes on day 11 post-inoculation. At day 12 it was determined that significant elevations in serum liver enzymes were present, and the animal was sacrificed on that day. Plasma, liver and spleen tissue samples were obtained for further studies. The plasma from

T-1053 served as the source for the RDA procedure discussed in Example 3 below; the liver tissue was utilized in Example 8 below.

5 Tamarins T-1048, T-1057 and T-1061 were monitored for serum liver enzyme values; all were observed to exhibit elevated serum liver enzyme levels within two weeks following inoculation; these elevated values were noted for six or more weeks post inoculation. All three tamarins were observed to have decreasing serum liver enzyme levels below the CO by 84 days post inoculation. On day 97 post inoculation, these three tamarins (T-1048, T-1057 and T-1061) were re-challenged with 0.10 ml of neat plasma obtained from tamarin T-1053 (shown to be infectious, see Example 2) to determine whether hepatitis as documented by elevations in serum liver enzymes could be re-induced. The data are presented in TABLE 2 and FIGURES 1, 3 and 4. As the data indicates, serum liver enzyme levels of two tamarins (T-1057 and T-1061) remained below the CO for three weeks post reinoculation. One tamarin (T-1048) exhibited mild elevations in serum liver enzyme levels two weeks immediately post-reinoculation. It was hypothesized that the mild elevations in T-1048 were attributable to either reinfection of liver tissue by HGBV or incomplete recovery from the initial inoculation with H205.

20 Example 2. Infectivity Studies

A. Experimental Protocol. Baseline readings on four tamarins were obtained as described in Example 1(A). Briefly, baseline serum liver enzymes (ALT, GGT and ICD) were established for each animal prior to inoculation. Cutoff values (CO) were determined for each animal, based on the mean liver enzyme value plus 3.75 times the standard deviation. Liver enzyme values above the cutoff were interpreted as abnormal and suggestive of liver damage.

B. Inoculation of Tamarins. The plasma from Tamarin T-1053, sacrificed at day 12 post inoculation (see Example 1[C]), was used as the inoculum for further studies. On day one, one tamarin (T-1055) was inoculated intravenously with 0.25 ml of neat T-1053 plasma. On the same day, two tamarins (T-1038 and T-1051) were inoculated intravenously with 0.25 ml of T-1053 plasma which had been serially diluted to either 10^{-4} (T-1038) or 10^{-5} (T-1051) in pooled normal tamarin plasma. On the same day, tamarin T-1049 was inoculated intravenously with 0.25 ml of plasma T-1053 which had been filtered through a series of filters of decreasing pore size (0.8 μ m, 0.45 μ m, 0.22 μ m and 0.10 μ m) and diluted at 10^{-4} in pooled normal tamarin plasma.

All tamarins (T-1055, T-1038, T-1051 and T-1049) were monitored weekly as described in Example 1 for changes in serum liver enzymes ALT, GGT and ICD. TABLE 5 presents the pre- and post- inoculation liver enzyme data on these four tamarins. FIGURE 9 presents the pre- and post- inoculation ALT and ICD values T-1055. Referring to FIGURE 9, it can be seen that elevations above the CO in serum liver enzymes ALT and ICD occurred. This tamarin was sacrificed on day 12 post-inoculation. FIGURES 10 and 11 present the pre- and post-inoculation serum levels of ALT and ICD for tamarins T-1051 and T-1038, respectively. Referring to FIGURES 10 and 11, it can be seen that elevations in serum liver enzymes ALT and ICD occurred in both animals by 11 days post-inoculation. T-1038 was sacrificed on day 14 post inoculation. TABLE 5 and FIGURE 12 present the data obtained on T-1049. As can be seen from TABLE 5 and FIGURE 12, elevations in serum liver enzymes above the CO were observed in T-1049 within 11 days post-inoculation.

The filtration study conducted on T-1049 indicates that HGBV can pass through a 0.10 μ m filter, thereby suggesting that HGBV is likely to be viral in nature, and less than 0.1 μ m in diameter. In addition, the infectivity titration experiment conducted on T-1038 demonstrates that the T 1053 serum contains at least 4×10^5 tamarin infectious doses per ml.

In order to show the transmissibility of a single HGBV agent, tamarin T-1044 was inoculated with 0.25 ml of an inoculum consisting of T-1057 serum that had been obtained 7 days after the H205 inoculation and diluted 1:500 in normal tamarin serum. Mild elevations in ALT levels above the cutoff were observed from days 14-63 PI (that is, elevations in the range of 82 to 106).

Tamarins T-1047 and T-1056 were subsequently inoculated with 0.25ml of T-1044 serum obtained 14 days PI and diluted 1:2 in normal tamarin serum. Elevations in ALT levels above the cutoff were first observed in T-1047 and T-1056 at 42 days PI and returned to normal levels at days 64 and 91 PI, respectively. Tamarin T-1058 was inoculated with 0.25ml of neat T-1057 serum obtained 22 days after the challenge with T-1053 serum. Elevations in ALT levels have not been observed for 112 days PI.

Example 3. Representational Difference Analysis (Subtractive Hybridization)

A. Generation of double-stranded DNA for Amplicons

Using the procedure described herein in Materials and Methods above and referring to FIGURE 13, tester amplicon was prepared from total nucleic acid obtained from tamarin T-1053 infectious plasma on day 12 post inoculation with

H205 serum (see Examples 1C and 2B). Driver amplicon was prepared from Tamarin T-1053 pre-inoculation plasma pooled from days -17 to -30 (see Example 1A). Briefly, both plasmas were filtered through a 0.1 μ m filter as described in Example 2B. Next, 50 μ l of each filtered plasma was extracted using
5 a commercially available kit [United States Biochemical (USB), Cleveland, OH, cat. #73750] and 10 μ g yeast tRNA as a carrier. This nucleic acid was subjected to random primed reverse transcription followed by random primed DNA
10 synthesis using commercially available kits. Briefly, an 80 μ l reverse transcription reaction was performed using Perkin Elmer's (Norwalk, CT) RNA PCR kit (cat. # N808-0017) as directed by the manufacturer using random hexamers and incubating for 10 minutes at 20°C followed by 2 hours incubation at 42°C. The reactions then were terminated and cDNA/RNA duplexes denatured by incubation at 99°C for 2 minutes. The reactions were supplemented with 10 μ l
15 10x RP buffer [100 mM NaCl, 420 mM Tris (pH 8.0), 50 mM DTT, 100 μ g/ml BSA], 250 pmoles random hexamers and 13 units Sequenase[®] version 2.0 polymerase (USB, cat. #70775) in a total volume of 20 μ l. The reactions were incubated at 20°C for 10 minutes followed by 37°C for 2 hours. After phenol:chloroform extraction and ethanol precipitation, the double stranded DNA products of these reactions were digested with 4 units of restriction endonuclease
20 Sau3A I (New England Biolabs [NEB], cat. #169L) in 30 μ l reaction volumes for 30 minutes, as directed by the supplier.

B. Generation of amplicons.

Sau3AI-digested DNA was extracted and precipitated as described above. The entire Sau3AI-digested product was annealed to 465 pmoles R Bgl 24
25 (SEQUENCE I.D. NO. 1) and 465 pmoles R Bgl 12 (SEQUENCE I.D. NO. 2) in a 30 μ l reaction volume buffered with 1x T4 DNA ligase buffer (NEB) by placing the reaction in a 50-55°C dry heat block which was then incubated at 4°C for 1 hour. The annealed product was ligated by adding 400 units T4 DNA ligase (NEB, cat. # 202S). After incubation for 14 hours at 16°C, a small scale PCR was
30 performed. Briefly, 10 μ l of the ligation reaction was added to 60 μ l H₂O, 20 μ l 5x PCR buffer (335 mM Tris, pH 8.8, 80 mM [NH₄]₂SO₄, 20 mM MgCl₂, 0.5 μ g/ml bovine serum albumin, and 50 mM 2-mercaptoethanol), 8 μ l of 4 mM dNTP stock, 2 μ l (124 pmoles) R Bgl 24 (SEQUENCE I.D. NO. 3) and 3.75 units of AmpliTaq[®] DNA polymerase (Perkin Elmer, cat. # N808-1012). The
35 PCR amplification was performed in a GeneAmp[®] 9600 thermocycler (Perkin Elmer). Samples were incubated for 5 min. at 72°C to fill-in the 5'-protruding ends of the ligated adaptors. The samples were amplified for 25 to 30 cycles (1

min. at 95°C and 3 min. at 72°C) followed by extension of 72°C for 10 min. After agarose gel confirmation of successful amplicon generation (ie. a smear of PCR products ranging from approximately 100 bp to over 1500 bp), a large scale amplification of tester and driver amplicons was performed. Forty 100 µl PCRs and eight 100 µl PCRs were set up as described above for the preparation of driver and tester amplicons, respectively. Two µl from the small scale PCR product per 100 µl reaction served as the template for the large scale amplicon generation. Thermocycling was performed as described above for an additional 15 to 20 cycles of amplification. The PCR reactions for both driver and tester DNA were then phenol/chloroform extracted twice, isopropanol precipitated, washed with 70% ethanol and digested with Sau3AI to cleave away the adaptors. The tester amplicon was further purified on a low melting point agarose gel. Briefly, 10 µg of tester amplicon DNA was run on a 2% SeaPlaque® gel (FMC Bioproducts, Rockland, ME). Fragments of 150-1500 base pairs were excised from the gel, the gel slice was melted at 72°C for 20 minutes with 3 ml H₂O, 400 µl 0.5 M MOPS and 400 µl NaCl. DNA was recovered from the melted gel slice using a Qiagen-tip 20 (Qiagen, Inc., Chatsworth, CA) as directed by the manufacturer.

C. Hybridization and Selective Amplification of amplicons

Approximately 2 µg of purified tester DNA amplicon was ligated to N Bgl 24 (SEQUENCE I.D. NO.3) and N Bgl 12 (SEQUENCE I.D. NO. 4) as described above. For the first subtractive hybridization, tester amplicon ligated to the N Bgl primer set (0.5 µg) and driver amplicon (20 µg) were mixed, phenol/chloroform extracted and ethanol precipitated. The DNA was resuspended in 4 µl of EE x 3 buffer (30 mM EPPS, pH 8.0 at 20°C [Sigma, St. Louis, MO], 3 mM EDTA) and overlaid with 35 µl of mineral oil. Following heat denaturation (3 min at 99°C), 1 µl of 5 M NaCl was added to the denatured DNA and the DNA was allowed to hybridize at 67°C for 20 hours. The aqueous phase was removed to a new tube and 8 µl of tRNA (5 mg/ml) was added to the sample followed by 390 µl TE (10 mM Tris, pH 8.0 and 1 mM EDTA). Eighty µl of the hybridized DNA solution was added to 480 µl H₂O, 160 µl 5x PCR buffer (above), 64 µl 4 mM dNTPs and 6 µl (30 units) AmpliTaq® polymerase. This solution was incubated at 72°C for 5 min. to fill in the 5' overhangs created by the ligated N Bgl 24 primer. N Bgl 24 (SEQUENCE I.D. NO. 3, 1.24 nmoles in 20 µl H₂O) was added, the reaction was aliquoted (100 µl/tube) and subjected to 10 cycles of amplification as described above. The reaction was pooled, phenol/chloroform extracted twice, isopropanol precipitated, washed with 70% ethanol and resuspended in 40 µl H₂O. Single-stranded DNA was removed by mung bean

nuclease (MBN) . Briefly, 20 µl amplified DNA was digested with 20 units MBN (NEB) in a 40 µl reaction as described by the supplier. One hundred and sixty µl 50 mM Tris, pH 8.8 was added to the MBN digest. The enzyme was heat inactivated at 99°C for 5 min. Eighty µl of the MBN-digested DNA was PCR
5 amplified as described above for an additional 15 cycles. Again, the reaction was pooled, phenol/chloroform extracted twice, isopropanol precipitated, washed with 70% ethanol and resuspended in H₂O. The amplified DNA (3 to 5 µg) was then digested with Sau3A I, extracted and precipitated as described above. The final DNA pellet was resuspended in 100 µl TE.

10 D. Subsequent hybridization/amplification steps

One hundred ng of the DNA from the previous hybridization/selective amplification was ligated to the J Bgl primer set (SEQUENCE I.D. NO. 5 and SEQUENCE I.D. NO. 6) as described previously. This DNA (50 ng) was mixed with 20 µg of driver amplicon and the hybridization and amplification procedures
15 were repeated as described above except that the extension temperature during the thermocycling was 70°C and not 72°C as for the N Bgl primer set (SEQUENCE I.D. NO. 3 and SEQUENCE I.D. NO. 4) and the final amplification step (after MBN digestion) was for 25 cycles. One hundred ng of the second hybridization-amplification product was then ligated to the N Bgl primer set (SEQUENCE I.D.
20 NO. 3 and SEQUENCE I.D. NO. 4), and 200 pg of this material together with 20 µg of driver amplicon was taken for the third round of hybridization/amplification as described above with the final amplification for 25 cycles.

A 2% agarose gel of the products from the representational difference analysis (RDA) performed on pre-HGBV inoculated and acute phase T-1053
25 plasma is shown in FIGURE 14. Referring to FIGURE 14, Lane 1 contains 150 ng of HaeIII digested Phi-X174 DNA marker (NEB) with the appropriate size (in bp) of the DNA fragments. The complexity of the driver amplicon (lane 2) and the tester amplicon (lane 3) is evidenced by the smear of DNA products seen in these samples. This complexity drops dramatically as the tester sequences are subjected
30 to one (lane 4), two (lane 5) or three (lane 6) rounds of hybridization/selective amplification.

E. Cloning of the difference products

The difference products were cloned into the BamHI site of pBluescript II KS+ (Stratagene, La Jolla, CA, cat. # 212207), as follows. Briefly, 0.5 µg
35 pBluescript II was digested with BamHI (10 units, NEB) and 5' dephosphorylated with calf intestinal phosphatase (10 units, NEB) as directed by the supplier. The plasmid was phenol:chloroform extracted, ethanol precipitated, washed with 70%

ethanol and resuspended in 10 μ l H₂O (final concentration approximately 50 ng pBluescript II per μ l). The four largest bands from the second hybridization/amplification products were excised from a 2% low melting point agarose gel as described above. Four μ l of the melted (72°C, 5 min.) gel slices
5 were ligated to 50 ng of the BamHI-cut, dephosphorylated pBluescript II in a 50 μ l reaction using the Takara DNA ligation kit (Takara Biochemical, Berkeley, CA). After incubating at 16°C for 3.5 hours, 8 μ l of the ligation reactions were used to transform *E. coli* competent XL-1 Blue cells (Stratagene) as directed by the supplier. The transformation mixtures were plated on LB plates supplemented
10 with ampicillin (150 μ g/ml) and incubated overnight at 37°C. The resulting colonies were grown up in liquid culture and miniprep plasmid DNA was analyzed as described in the art to confirm the existence of cloned product.

In addition to the cloning of the four largest products from the second hybridization/amplification step, the entire population of products from the third
15 hybridization/amplification step was cloned into pBluescript II. Briefly, 50 ng pBluescript II vector (prepared as above) was ligated to 10 ng of the third hybridization/amplification products in a 50 μ l reaction as described above. After incubation at 16°C for 2 hours, 10 μ l ligation product was used to transform *E. coli* competent XL-1 Blue cells as before. Sixty colonies from the resultant
20 transformation were grown up, and miniprep DNA was prepared and analyzed as described and known in the art. Restriction endonuclease digestion and dot blot hybridization experiments were used to identify unique clones.

25 Example 4. Immunoisolation of a cDNA Clone Encoding an Antigenic Region of the HGBV Genome

A. Preparation of Concentrated Virus as a Source of Cloning Material

The following isolation scheme was employed to isolate the HGBV genome in addition to the procedures exemplified in Example 3. Three tamarins (T-1055, T-1038 and T-1049) were inoculated with serum prepared from tamarin
30 T-1053 as described in Example 2. Referring to TABLE 5, elevated liver enzyme values were noted in all 3 tamarins by day 11 PI. Tamarin T-1055 was sacrificed on day 12 PI and tamarins T-1038 and T-1049 were sacrificed on day 14 PI. Approximately 3-4 ml of serum from each of these three tamarins were pooled, providing a total volume of approximately 11.3 ml. The pooled serum was
35 clarified by centrifugation at 10,000 x g for 15 min at 15°C. It was then passed successively through 0.8, 0.45, 0.2, and 0.1 μ m syringe filters. This filtered material was then concentrated by centrifugation through a 0.3 ml CsCl cushion

(density 1.6 g/ml, in 10 mM Tris, 150 mM NaCl, 1mM EDTA, pH 8.0) in a SW41-Ti rotor at 41,000 rpm at 4°C for 68 min. The CsCl layer, approximately 0.6 ml, was removed following centrifugation and stored in three 0.2 ml aliquots at -70°C.

5 Tamarin T-1034 was subsequently inoculated with 0.25 ml of a 10^{-6} dilution of this pelleted material (prepared in normal tamarin serum). Elevated ALT liver enzyme values were first noted in T-1034 at 2 weeks PI, and remained elevated for the next 7 weeks, finally normalizing by week 10 PI (see FIGURE 30, Example 14). This experiment demonstrated the infectivity of the material
10 concentrated from the pooled tamarin sera. Since this material was shown to be of a relatively high titer, this concentrated source of virus was used as the source of nucleic acid for the preparation of a cDNA library, as described below.

B. cDNA Library Construction

An aliquot (0.2 ml) of the concentrated virus (described above) was
15 extracted for RNA using a commercially available RNA extraction kit (Stratagene, La Jolla, CA) as instructed by the supplier. The sample was divided into four equal aliquots prior to the final precipitation step, and then precipitated in the presence of 5 µg/ml yeast tRNA. Only one of these aliquots was used for cDNA synthesis; the others were stored at -80°C. Phosphorylated, blunt-ended, double-
20 stranded cDNA was prepared from the RNA using a commercially available kit (Stratagene, La Jolla, CA) as directed by the manufacturer. A double-stranded linker/primer was then ligated to the cDNA ends (sense strand, SEQUENCE I.D. NO. 7; antisense strand, SEQUENCE I.D. NO. 8) in a 10 µl reaction volume using a T4 DNA ligase kit (Stratagene, La Jolla, CA) as directed by the
25 manufacturer. This provided all cDNAs in the mixture with identical 5' and 3' ends containing Not I and Eco RI restriction enzyme recognition sites. G. Reyes and J. Kim, Mol. Cell. Probes 5:473-481 (1991); A. Akowitz and L. Manuelidis, Gene 81:295-306 (1989); and G. Inchauspe et al., in Viral Hepatitis and Liver Disease, F.B. Hollinger et al., Eds., pp. 382-387 (1991). The sense-strand
30 oligonucleotide of the linker/primer was then used as a primer in a PCR reaction such that all cDNAs were amplified independent of their sequence. This procedure allowed for the amplification of rare cDNAs present within the total cDNA population to a level which allowed them to be efficiently cloned, thus producing a cDNA library that is representative of the sequences within the starting material.

35 PCR was performed on a 1 µl aliquot of the above ligate in the presence of the sense-strand oligonucleotide primer (final concentration: 1 µM; reaction volume: 50µl) using the GeneAmp PCR kit (Perkin-Elmer) as directed by the

manufacturer in a PE-9600 thermocycler. Thirty cycles of PCR were performed as follows: denaturation at 94°C for 0.5 min, annealing at 55°C for 0.5 min, and extension at 72°C for 1.5 min. A 1 µl aliquot of the resulting products was then re-amplified as described above. The final PCR reaction products were then
 5 extracted once with an equal volume of phenol-chloroform (1:1, v/v) and once with an equal volume of chloroform, and then precipitated on dry ice for 10 min following the addition of sodium acetate (final concentration, 0.3 M) and 2.5 volumes of absolute ethanol. The resulting DNA pellet was resuspended in water and digested with the restriction enzyme Eco RI (New England Biolabs) as
 10 directed by the manufacturer. The digested cDNAs were then purified from the reaction mixture using a DNA binding resin (Prep-a-Gene, BioRad Laboratories) as directed by the manufacturer and eluted in 20 µl of distilled water.

The cDNAs (8 µl) were ligated to 3 µg lambda gt11 vector DNA arms (Stratagene, La Jolla, CA) in a reaction volume of 30 µl at 4°C for 1-5 days.
 15 Eleven microliters of the ligate was packaged into phage heads using GigaPack III Gold packaging extract (Stratagene, La Jolla, CA) as directed by the manufacturer. The resulting library contained a total of approximately 1.73 million members (PFU) at a recombination frequency of 89.3% with an average insert size of approximately 350 base pairs.

20 C. Immunoscreening of the Recombinant GB cDNA Library

The antiserum used for immunoscreening of the cDNA library was obtained from tamarins that had demonstrated elevations in their serum liver enzyme levels following inoculation. Two separate pools of antisera were used for immunoscreening. The first pool contained serum from two animals (T-1048 and
 25 T-1051; see Example 1, TABLE 2, and Example 2, TABLE 5, respectively) while the second pool contained serum from a single animal (T1034; see FIGURE 30, Example 14). The specific sera used are shown in TABLE 6.

At the time that these samples were chosen for use in cDNA library immunoscreening, they had not been tested for their immunoreactivity with either
 30 the 1.4 or 1.7 recombinant CKS proteins (Example 13). Therefore, the results shown herein were obtained independent of any information regarding the presence or absence of HGBV antibodies against these recombinant proteins within the antiserum used.

TABLE 6

35 Tamarin Sera used for Immunoscreening of GB cDNA Library

Tamarin 1048 ^a	Tamarin 1051 ^b	Tamarin 1034 ^c
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<u>Days Post-Inoculate</u>	<u>Volume in Pool</u>	<u>Days Post-Inoculate</u>	<u>Volume in Pool</u>	<u>Days Post-Inoculate</u>	<u>Volume in Pool</u>
63	0.2 ml	63	0.2 ml	42	0.1 ml
77	0.2 ml	69	0.1 ml	49	0.1 ml
91	0.2 ml	91	0.2 ml	63	0.1 ml
97	0.2 ml	98	0.2 ml	70	0.1 ml
126	2.0 ml	105	0.2 ml	77	0.08 ml
		109	5.3 ml		

^aTotal T-1048 pool volume is 2.8 ml. ^bTotal T-1051 pool volume is 6.4 ml. One ml of each pool was saved and the remainder of each was combined and used as the primary antiserum for immunoscreening. ^cTotal T-1034 pool volume is 0.48 ml; the entire pool was used for immunoscreening.

5

The procedure used for the immunoisolation of recombinant phage was based upon the method described by Young and Davis with modifications as described below. R.A. Young and R.W. Davis, PNAS 80:1194-1198 (1983). Two immunoscreening experiments were performed, one utilizing antiserum

10 pooled from T-1048 and T-1051 and the other utilizing antiserum from T-1034. In both cases, the primary antiserum was pre-adsorbed against E. coli extract prior to use in order reduce non-specific interactions of antibody with E. coli proteins. In the first experiment, 1.29 million recombinant phage were immunoscreened with the T-1048/T-1051 antiserum pool; in the second experiment 0.30 million

15 recombinant phage were immunoscreened with T-1034 antiserum. The recombinant phage library was plated on a lawn of E. coli strain Y1090r- and grown at 37°C for 3.5 hours. The plates were then overlaid with nylon filters that were saturated with IPTG (10 mM) and the plates incubated at 42°C for 3.5 hours. The filters were then blocked in Tris-saline buffer containing 1% BSA, 1%

20 gelatin, and 3% Tween-20 ("blocking buffer") for 1 hour at 22°C. The filters were then incubated in primary antiserum (1:100 dilution in blocking buffer) at 4°C for 16 hours. Primary antiserum was then removed and saved for subsequent rounds of plaque purification, and the filters washed four times in Tris-saline containing 0.1% Tween-20. The filters were then incubated in blocking buffer containing

25 125-I-labeled (or alkaline-phosphatase conjugated) goat anti-human IgG (available from Jackson ImmunoResearch, West Grove, PA) for 60 min at 22°C, washed as described above, and then exposed to x-ray film (or subjected to color development according to established procedures, as in J. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd edition, Cold Spring Harbor Press,

30 Cold Spring Harbor, N.Y. , 1989). Five immunopositive phage (4-3B1, 48-1A1,

66-3A1, 70-3A1, 78-1C1) were isolated from this library and subsequently tested for specificity of binding to antisera from three infected tamarins (T-1048, T-1051, T-1034) using the method described above. These recombinants encoded polypeptides that reacted with convalescent sera, but not with pre-inoculation sera, from each of the three infected tamarins (data not shown).

In order to verify the specificity of the immunological reactivity of the polypeptide encoded by the recombinant phage, each cDNA was rescued from the lambda phage genome by PCR using primers located 5' (SEQUENCE I.D. NO. 9) and 3' (SEQUENCE I.D. NO. 10) to the Eco RI cloning site. The PCR products were then digested with Eco RI and subsequently ligated into the *E. coli* expression plasmid pJO201 as described in Example 13. Insertion of the cDNAs into the Eco RI site of pJO201 maintained the translational reading frame of this cDNA as present in the lambda phage clone. The subclones in the pJO201 expression vector were designated 4-3B1.1, 48-1A1.1, 66-3A1.49, 70-3A1.37, and 78-1C1.17. Immunoblot analysis (as in Example 13) of *E. coli* lysates prepared from cultures expressing these cDNAs with convalescent sera from tamarins T-1034, T-1048, and T-1051 (1:100 dilution) demonstrated specific immunologic reactivity with a protein of the size predicted for each CKS-fusion protein. (data not shown). The DNA sequence of each of the cDNAs was determined and it was found that these clones possessed nearly 100% sequence identity with that of HGBV-B virus (SEQUENCE I.D. NO. 11). The sequence of the 4-3B1.1 insert (SEQUENCE I.D. NOS. 12 and 13), although not determined in its entirety, those portions that have been sequenced exhibit 99.5% Sequence identity to a portion of the sequence within HGBV-B (SEQUENCE I.D. NO. 11) from base pairs 6834-7458. This region of the HGBV-B (SEQUENCE I.D. NO. 11) sequence showing identity with that of the sequence obtained from clone 4-3B1.1 was translated into the +1 reading frame and is presented in the sequence listing as SEQUENCE I.D. NO. 14. The sequence of the 48-1A1.1 insert (SEQUENCE I.D. NO. 15) exhibits 100% Sequence identity to a portion of the sequence from HGBV-B (SEQUENCE I.D. NO. 11, see Example 9) from base pairs 4523-4752. The DNA sequence corresponding to SEQUENCE I.D. NO. 15 was translated into the +1 reading frame and is presented in the sequence listing as SEQUENCE I.D. NO. 16. The sequence of the 66-3A1.49 insert (SEQUENCE I.D. NO. 17) exhibits essentially 100% sequence identity to that of clone 48-1A1.1 and thus no protein translation is shown in the sequence listing. The sequence of the 70-3A1.37 insert (SEQUENCE I.D. NO. 18) exhibits 100% sequence identity to a portion of the sequence from HGBV-B (SEQUENCE I.D.

NO. 11) from base pairs 6450-6732 except for a three base-pair deletion corresponding to bases 6630-6632 of the HGBV-B sequence (SEQUENCE I.D. NO. 11). The DNA sequence corresponding to SEQUENCE I.D. NO. 18 was translated into the +2 reading frame and is presented in the sequence listing as SEQUENCE I.D. NO. 19. The sequence of the 78-1C1.17 insert (SEQUENCE I.D. NO. 20) exhibits 100% sequence identity to that of clone 70-3A1.37 and thus no protein translation is shown in the sequence listing. These data demonstrate that the cDNA clones isolated from the lambda gt11 cDNA library are derived from the genome of the HGBV agent and that it encodes polypeptides which are specifically recognized immunologically by sera from GB-infected tamarins. Clones 48-1A1.1("clone 48") 4-3B1.1, 66-3A1.49, 70-3A1.37, and 78-1C1.17 have been deposited at the American Type Culture Collection as provided hereinabove.

Example 5. DNA sequence analysis of HGBV clones

Unique clones obtained in Example 3 were sequenced using the dideoxynucleotide chain termination technique (Sanger, et al., *supra*) in a kit form (Sequenase[®] version 2.0, USB). These sequences are non-overlapping and are presented in the Sequence Listing as clone 4 (SEQUENCE I.D. NO. 21), clone 2 (SEQUENCE I.D. NO. 22), clone 10 (SEQUENCE I.D. NO. 23), clone 11 (SEQUENCE I.D. NO. 24), clone 13 (SEQUENCE I.D. NO. 25), clone 16 (SEQUENCE I.D. NO. 26), clone 18 (SEQUENCE I.D. NO. 27), clone 23 (SEQUENCE I.D. NO. 28), clone 50 (SEQUENCE I.D. NO. 29) and clone 119 (SEQUENCE I.D. No. 30). Clones 4, 2, 10, 11, 13, 16, 18, 23, 50 and 119 have been deposited at the A.T.C.C. Clone 2 was accorded A.T.C.C. Deposit No. 69556; Clone 4 was accorded A.T.C.C. Deposit No. 69557; Clone 10 was accorded A.T.C.C. Deposit No. 69558; Clone 16 was accorded A.T.C.C. Deposit No. 69559; Clone 18 was accorded A.T.C.C. Deposit No. 69560; Clone 23 was accorded A.T.C.C. Deposit No. 69561; and Clone 50 was accorded A.T.C.C. Deposit No. 69562; Clone 11 was accorded A.T.C.C. Deposit No. 69613; Clone 13 was accorded A.T.C.C. Deposit No. 69611; and Clone 119 was accorded A.T.C.C. Deposit No. 69612.

The sequences were searched against the GenBank database using the BLASTN algorithm (Altschul et al, *J. Mol. Biol.* 215:403-410 [1990]). None of these sequences were found in GenBank, indicating that these sequences have not been previously characterized in the literature. The DNA sequences were translated into the six possible reading frames and are presented in the sequence

listing (SEQUENCE I.D. NO. 21 translates to SEQUENCE I.D. NOS.31-36,
SEQUENCE I.D. NO. 22 translates to SEQUENCE I.D. NOS. 37-42,
SEQUENCE I.D. NO. 23 translates to SEQUENCE I.D. NOS. 43-48,
SEQUENCE I.D. NO. 26 translates to SEQUENCE I.D. NOS. 49-54,
5 SEQUENCE I.D. NO. 27 translates to SEQUENCE I.D. NOS. 55-60,
SEQUENCE I.D. NO. 28 translates to SEQUENCE I.D. NOS. 61-66, and
SEQUENCE I.D. NO. 29 translates to SEQUENCE I.D. NOS. 67-72).
SEQUENCE I.D. NO. 24 is contained within SEQUENCE I.D. NO. 73
(described in Example 9), which translates to SEQUENCE I.D. NOS. 74-79.
10 SEQUENCE I.D. NOS. 25 and 30 are contained within SEQUENCE I.D. NO. 80
(described in Example 9), which translates to SEQUENCE I.D. NO. 81-86. The
translated sequences were used to search the SWISS-PROT database using the
BLASTX algorithm (Gish et al., Nature Genetics 3:266-272 [1993]). Again, none
of these sequences were found in SWISS-PROT indicating that these sequences
15 have not been previously characterized in the literature.

Homology searches conducted using the BLASTN, BLASTX and
FASTdb algorithms demonstrate some, albeit low, sequence resemblance to
hepatitis C virus (TABLE 7, below). Specifically, translations of clones 4
(SEQUENCE I.D. NO. 35), 10 (SEQUENCE I.D. NO. 44), 11 (residues 1-166
20 of GB-A, frame 3 [SEQUENCE I.D. NO. 76]), 16 (SEQUENCE I.D. NO. 50),
23 (SEQUENCE I.D. NO. 65), 50 (SEQUENCE I.D. NOS. 70 and 72) and 119
(residues 912-988 of GB- A, frame 3 [SEQUENCE I.D. NO. 83]), are between
24.1% and 45.1% homologous to various HCV isolates at the amino acid level. Of
particular interest, translation of clone 10 (SEQUENCE I.D. NO. 44) showed
25 limited homology to the putative RNA-dependent RNA polymerase of HCV. A
comparison of the conserved amino acids present in the putative RNA-dependent
RNA polymerase of other positive strand viruses (Jiang et al. PNAS 90:10539-
10543 [1993]) with the putative amino acid translation of clone 10 (SEQUENCE
I.D. NO. 44) revealed that conserved amino acid residues of other RNA-dependent
30 RNA polymerases are also conserved in clone 10 (SEQUENCE I.D. NO. 44).
This includes the canonical GDD (Gly-Asp-Asp) signature sequence of RNA-
dependent RNA polymerases. Thus, clone 10 (SEQUENCE I.D. NO. 44)
appears to encode a viral RNA-dependent RNA polymerase. Surprisingly, only
clone 10 (SEQUENCE I.D. NO. 44) showed any sequence homology with HCV
35 at the nucleotide level when the BLASTN algorithm was used. Clones 4
(SEQUENCE I.D. NO. 21), 16 (SEQUENCE I.D. NO. 26), 23 (SEQUENCE
I.D. NO.28) and 50 (SEQUENCE I.D. NO. 29) and 119 (SEQUENCE ID. NO.

30) which have low HCV homology at the amino acid level, were not detected by BLASTN in searches of GenBank. In addition, clones 2 (SEQUENCE I.D. NOS. 37-42), 13 (SEQUENCE I.D. NO. 25 and 37-42) and 18 (SEQUENCE I.D. NOS. 27 and 55-60) showed no significant nucleotide or amino acid homology to HCV when searched against GenBank or SWISS-PROT as described hereinabove.

TABLE 7
HCV Homology of HGBV Clones

10

Homology					
Clone	Nucleotide ^a	Amino Acid ^b	Strain ^c	Region ^d	Function ^e
4	none	28/73 (38.4%)	HCVTW	NS4	unknown
10	134/307 (43.6%) ^f	46/102 (45.1%)	HCVJ6	NS5	replicase
11	none	40/166 (24.1%)	HCVJT	NS5	replicase
16	none	55/177 (31.1%)	HCVJ8	NS2/3	protease
23	none	44/121 (36.4%)	HCVJA	NS3	helicase
50	none	29/112 (25.9%)	HCVH	NS4/5	unknown
119	none	27/77 (35.1%)	HCVTW	NS5	replicase

^a Homology found to HCV when GB clones were searched against GenBank using the BLAST algorithm.

15 ^b Homology found to HCV when translated GB clone sequences were searched against SWISS-PROT using the FASTdb algorithm.

^c Most homologous strain of HCV (SWISS-PROT designation)

20 ^{d,e} Region of homology and reputed function of clone compared with HCV according to Houghton et al., *Hepatology* 14(2):381-388 (1991). ^f BLASTN detected a segment of clone 10 that was 64% homologous with HCV NS5 over 132 nucleotides. Alignment of the entire clone 10 sequences with the homologous nucleotide sequence of HCVJ6 shows 43.6% homology.

Example 6. Exogenicity of HGBV clones

The HGBV clones were not detected in normal or HGBV-infected tamarin liver DNA, normal human lymphocyte DNA, yeast DNA or *E. coli* DNA. This was demonstrated for HGBV clones 2 (SEQUENCE I.D. NO. 22) and 16 (SEQUENCE I.D. NO. 26) by Southern blot analysis. In addition, all HGBV clones were analyzed by genomic PCR to confirm the exogenous origin of the HGBV sequences with respect to the tamarin, human, yeast and *E. coli* genomes. These data are consistent with the viral nature of the HGBV sequences described in Example 5.

A. Southern Blot analysis.

Tamarin liver nuclei were obtained from low speed pelleting of liver homogenates of HGBV-infected and normal tamarins (described hereinbelow). DNA was extracted from nuclei using a commercially available kit (USB cat. # 73750) as directed by the supplier. The tamarin DNA was treated with RNase during the extraction procedure. Human placental DNA (Clontech, Palo Alto, CA), yeast DNA (*Saccharomyces cerevisiae*, Clontech) and *E. coli* DNA (Sigma) were obtained from commercial sources.

Each DNA sample was digested with BamHI (NEB) according to the suppliers direction. Digested DNAs (10 µg) and RDA products (0.5 µg each from Example 3B) were electrophoresed on 1% agarose gels and capillary blotted to Hybond-N+ nylon membranes (Amersham, Arlington Heights, IL) as described in Sambrook et al. (pp. 9.34 ff). DNA was fixed to the membrane by alkali treatment as directed by the membrane supplier. Membranes were prehybridized in Rapid Hyb solution (Amersham) at 65°C for 30 min.

Radiolabeled probes of the HGBV sequences were prepared by PCR. Briefly, 50 µl PCRs were set up using 1x PCR buffer II (Perkin Elmer), 2 mM MgCl₂, 20 µM dNTPs, 1 µM each of clone specific sense and antisense primers (for clone 2, SEQUENCE I.D. NOS. 87 and 88; for clone 4, SEQUENCE I.D. NOS. 89 and 90; for clone 10, SEQUENCE I.D. NOS. 91 and 92; for clone 16, SEQUENCE I.D. NOS. 93 and 94; for clone 18, SEQUENCE I.D. NOS. 95 and 96; for clone 23, SEQUENCE I.D. NOS. 97 and 98; and for clone 50, SEQUENCE I.D. NOS. 99 and 100), 1 ng HGBV clone plasmid (described in Example 3[E]), 60 µCi α-³²P-dATP (3000 Ci/mmol) and 1.25 units of AmpliTaq[®] polymerase (Perkin Elmer). The reactions were incubated at 94°C for 30 sec., 55°C for 30 sec., and 72°C for 30 sec. for a total of 30 cycles of amplification followed by a final extension at 72°C for 3 minutes. Unincorporated label was removed by Quick-Spin[®] G-50 spin columns (Boehringer Mannheim, Indianapolis, IN) as directed by the supplier. The probes were denatured (99°C, 2 min.) prior to addition to the pre-hybridized membranes.

Radiolabeled probes were added to the prehybridized membranes (2 x 10⁶ dpm/ml) and filters were hybridized at 65°C for 2.5 hours as directed by the Rapid Hyb[®] supplier. The hybridized membranes were washed under conditions of moderate stringency (1x SSC, 0.1% SDS at 65°C) before being exposed to autoradiographic film for 72 hours at -80°C with an intensifying screen. These conditions were designed to detect a single copy gene with a similar radiolabeled probe.

The results show that clone 2 (SEQUENCE I.D. NO. 22) and clone 16 (SEQUENCE I.D. NO. 26) sequences did not hybridize to DNA from normal or HGBV-infected tamarin liver (FIGURES 15 and 16, lanes 1B and 3B, respectively), human DNA (FIGURES 15 and 16, lane 1A), yeast DNA (FIGURES 15 and 16, lane 2A) or *E. coli* DNA (FIGURES 15 and 16, lane 3A). In addition, no hybridization was detected with the driver amplicon DNA (FIGURES 15 and 16, lanes 4A, derived from pre-HGBV-inoculated tamarin plasma as described in Example 2.B). In contrast, strong hybridization signals were seen with the tester amplicon (FIGURES 15 and 16, lane 6A, derived from infectious HGBV tamarin plasma using total nucleic acid extraction and reverse transcription steps as described in Example 2.B) and the products of the three rounds of subtraction/selective amplification (FIGURES 15 and 16, lanes 7A, 8A and 4B referring to the products from the first, second and third rounds of subtraction/selective amplification, respectively). These data demonstrate that HGBV clones 2 (SEQUENCE I.D. NO. 22) and 16 (SEQUENCE I.D. NO. 26) can be detected in nucleic acid sequences amplified from infectious sources; HGBV clones 2 (SEQUENCE I.D. NO. 22) and 16 (SEQUENCE I.D. NO. 26) are not derived from tamarin, human, yeast or *E. coli* genomic DNA sequences.

B. Genomic PCR analysis.

To further demonstrate the exogenicity of the HGBV sequences and support their viral origin, PCR was performed on genomic DNA from tamarin, human, yeast and *E. coli*. DNA from normal tamarin kidney and liver tissue was prepared as described by J. Sambrook et al., *supra*. Yeast, Rhesus monkey kidney and human placental DNAs were obtained from Clontech. *E. coli* DNA was obtained from Sigma.

PCR was performed using GeneAmp[®] reagents from Perkin-Elmer-Cetus essentially as directed by the supplier's instructions. Briefly, 300 ng of genomic DNA was used for each 100 µl reaction. PCR primers derived from HGBV cloned sequences (for clone 2, SEQUENCE I.D. NOS. 87 and 88; for clone 4, SEQUENCE I.D. NOS. 89 and 90; for clone 10, SEQUENCE I.D. NOS. 91 and 92; for clone 16, SEQUENCE I.D. NOS. 93 and 94; for clone 18, SEQUENCE I.D. NOS. 95 and 96; for clone 23, SEQUENCE I.D. NOS. 97 and 98; and for clone 50, SEQUENCE I.D. NOS. 99 and 100) were used at a final concentration of 0.5 µM. PCR was performed for 35 cycles (94°C, 1 min; 55°C, 1 min; 72°C, 1 min) followed by an extension cycle of 72°C for 7 min. The PCR products were separated by agarose gel electrophoresis and visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide

and/or hybridizaion to a radiolabelled probe after Southern blot transfer to a nitrocellulose filter. Probes were generated as described in Example 6A. Filters were prehybridized in Fast-Pair Hybridization Solution from Digene (Beltsville, MD) for 3-5 hours and then hybridized in Fast-Pair Hybridization Solution with
5 100-200 cpm/cm² at 42°C for 15-25 hours. Filters were washed as described in G. G. Schlauder et al., J. Virol. Methods 37:189-200 (1992) and exposed to Kodak X-Omat-AR film for 15 to 72 hours at -70°C with intensifying screens.

FIGURE 17 shows an ethidium bromide stained 1.5% agarose gel. FIGURE 18 shows an autoradiogram from a Southern blot from the same gel
10 after hybridization to the radiolabeled probe from clone 16 (SEQUENCE I.D. NO. 26). Consistent with its exogenous nature, clone 16 (SEQUENCE I.D. NO. 26) sequences were not detected in tamarin (FIGURE 17 and 18, lanes 9 and 10), Rhesus monkey (lane 11) or human genomic DNAs (lane 12) or in yeast or E. coli DNAs (data not shown) by genomic PCR analysis despite being able to
15 detect clone 16 (SEQUENCE I.D. NO. 26) sequences that have been spiked into normal tamarin liver and kidney DNA at 0.05 genome equivalents (lanes 17 and 18). In addition, primers derived from the human dopamine D1 receptor gene, 1000-1019 base pairs (sense primer) and 1533-1552 base pairs (antisense primer) (GenBank accession number X55760, R. K. Sunahara. et al., Nature
20 347:80-83 [1990]) successfully amplified the dopamine D1 receptor DNA from the primate genomic DNAs (FIGURE 17 lanes 2, 3, 4 and 5 corresponding to tamarin kidney, tamarin liver, rhesus monkey and human DNAs) demonstrating the utility of this method for detecting low copy number (i.e. single copy) sequences. Lanes 1 and 8 are H₂O contols for dopamine D1 receptor and clone
25 16 primers (SEQUENCE I.D. NOS. 93 and 94), respectively. Lane 6 contains 100fg of clone 16 (SEQUENCE I.D. NO. 26) plasmid DNA amplified with the dopamine receptor primers. Lanes 14, 15, 16 and 20 contain 1, 3, 10, and 100fg, respectively, of clone 16 (SEQUENCE I.D. NO. 26) plasmid DNA. Lanes 7 and 19 are markers. Similar results were obtained using PCR primers
30 specific for clones 2, 4, 10, 18, 23 and 50 described above (data not shown). Clones 2 (SEQUENCE I.D. NO. 22), 4 (SEQUENCE I.D. NO. 21), 10 (SEQUENCE I.D. NO. 23), 18 (SEQUENCE I.D. NO. 27), 23 (SEQUENCE I.D. NO. 28) and 50 (SEQUENCE I.D. NO. 29) are inconclusive at this time. However, clones 4 (SEQUENCE I.D. NO. 21), 10 (SEQUENCE I.D. NO. 23),
35 18 (SEQUENCE I.D. NO. 27) and 50 (SEQUENCE I.D. NO. 29) sequences were not detected in tamarin, human, yeast and E. coli DNA, (Rhesus monkey

was not tested) indicating that these sequences are exogenous to the genomic DNA sources tested and supporting the viral origin of these sequences.

Example 7. Presence of HGBV sequences in tamarin sera

5 The presence of the HGBV clone sequences in pre-inoculation and acute phase T-1053 plasma was examined by PCR. Because the HGBV genome could be DNA or RNA, PCR and RT-PCR was performed. Specifically, total nucleic acids were extracted from plasma as described in Example 3(A). PCR was performed on the equivalent of 5 µl plasma nucleic acids as described in Example 10 6(B) and RT-PCR was performed using the GeneAmp® RNA PCR Kit from Perkin-Elmer-Cetus essentially according to the manufacturer's instructions using 1 µM concentration of primers (for clone 2, SEQUENCE I.D. NOS.87 and 88; for clone 4, SEQUENCE I.D. NOS. 89 and 90; for clone 10, SEQUENCE I.D. NOS. 91 and 92; for clone 16, SEQUENCE I.D. NOS. 93 and 94; for clone 18, SEQUENCE I.D. NOS. 95 and 96; for clone 23, SEQUENCE I.D. NOS. 97 and 98; and for clone 50, SEQUENCE I.D. NOS. 99 and 100) in the PCRs. cDNA synthesis was primed with random hexamers.

15 Ethidium bromide staining and hybridization of the PCR products demonstrated the presence of HGBV clone sequences 2 (SEQUENCE I.D. NO. 22), 4 (SEQUENCE I.D. NO. 21), 10 (SEQUENCE I.D. NO. 23), 16 (SEQUENCE I.D. NO. 26), 18 (SEQUENCE I.D. NO. 27), 23 (SEQUENCE I.D. NO. 28) and 50 (SEQUENCE I.D. NO. 29) in the acute phase T-1053 plasma and not the pre-inoculation T-1053 plasma (data not shown). In addition, HGBV clones 2 (SEQUENCE I.D. NO. 22), 4 (SEQUENCE I.D. NO. 21), 10 (SEQUENCE I.D. NO. 23), 18 (SEQUENCE I.D. NO. 27), 23 (SEQUENCE I.D. NO.28) and 50 (SEQUENCE I.D. NO. 29) sequences could be detected in H205, the HGBV inoculum that was injected into tamarin T-1053 (see Example 1B). These results are summarized in TABLE 8. It should be noted that the HGBV clone sequences were only detected by RT-PCR in the acute phase plasma. The fact that the HGBV clone sequences were detected in the acute phase plasma by PCR only after a reverse transcription step to convert RNA to cDNA, taken together with the limited homology of some of these clones with HCV isolates, and the presence of the sequences coding for the conserved amino acids found in the RNA-dependent RNA polymerase in HGBV clone 10 (SEQUENCE I.D. NO. 23; Example 5) suggest that HGBV is an RNA virus.

30 RT-PCR analysis of a panel of tamarin plasmas with HGBV clone 16 sequence (SEQUENCE I.D. NO. 26) was undertaken to confirm the presence of

35

HGBV clone 16 (SEQUENCE I.D. NO. 26) in other individuals who had been experimentally infected with HGBV. Briefly, nucleic acids were isolated as previously described (G. G. Schlauder et al., *J. Virological Methods* 37:189-200 [1992]) from 25 μ l of plasma from tamarins obtained prior to and after
5 experimental infection with the H205 inoculum. Ethanol precipitated nucleic acids were resuspended in 3 μ l of DEPC-treated H₂O. cDNA synthesis and PCR were performed using the GeneAmp RNA PCR Kit from Perkin-Elmer-Cetus essentially according to the manufacturer's instructions. cDNA synthesis was primed with random hexamers. The resulting cDNA was subjected to PCR
10 using clone 16 primers (SEQUENCE I.D. NOS. 93 and 94) at a final concentration of 0.5 μ M. PCR was performed for 35 cycles (94°C, 1 min; 55°C, 1 min; 72°C, 1 min) followed by an extension cycle of 72°C for 7 min. The PCR products were separated by agarose gel electrophoresis and visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide and/or
15 hybridization to a radiolabelled probe after Southern blot transfer to a nitrocellulose filter as describes in Example 6B.

FIGURE 19 shows an ethidium bromide stained 1.5% agarose gel. FIGURE 20 shows an autoradiogram from a Southern blot from the same gel after hybridization to the radiolabeled probe from clone 16 (SEQUENCE I.D. NO. 26). H₂O and normal human serum are shown in lanes 1 and 2. Lanes 3,
20 19 and 20 are markers. Lanes 4, 8, 12, and 16 are from uninfected tamarin sera while lanes 6, 10, 14 and 18 are from infected tamarin sera. These results show that HGBV clone 16 sequence (SEQUENCE I.D. NO. 26) was detected in other individuals infected with HGBV, in addition to tamarin T-1053, and not in
25 uninfected individuals. Acute phase sera from five H205-infected animals were tested. Clone 16 sequences (SEQUENCE I.D. NO. 26) were detected in sera from three of these animals [lane 10, T-1049, 14 days post-inoculation (dpi); lane 14, T-1051, 28 dpi; lane 18, T-1055, 16 dpi.]. The clone 16 sequence (SEQUENCE I.D. NO. 26) was not detected in pre-inoculation sera from any of
30 the five animals (lane 4, T-1048; lane 8, T-1049; lane 12, T-1051; lane 16, T-1055; T-1057 not shown). These results suggest that the clone 16 sequence (SEQUENCE I.D. NO. 26) may be derived from the infectious HGBV agent. The absence of clone 16 sequence (SEQUENCE I.D. NO. 26) in two of five acute phase plasmas (lane 6, T-1048, 28 dpi; T-1057, 14 dpi, not shown) may
35 be explained by the relative low sensitivity of the clone 16 RT-PCR (estimated to be able to detect approximately ≥ 1000 copies of clone 16 sequence (SEQUENCE I.D. NO. 26) coupled with the acute resolving nature of HGBV infection in

tamarins. Thus, the acute plasma from the two negative animals may contain a titer of HGBV that is below the detection level of the RT-PCR assay employed. The observation that these two animals were positive for clone 4 (SEQUENCE I.D. NO.21) by RT-PCR (Example 14) may reflect the presence of RNA
5 sequences of one virus (containing clone 4) and the absence of detectable RNA sequences from a second virus (containing clone 16).

Example 8. Northern blot analysis of HGBV sequences in infected tamarin liver

Because the HGBV clone sequences were detectable by RT-PCR in the
10 acute phase tamarin plasma and the H205 inoculum, it was likely that these sequences originate from the HGBV genome. Additional RT-PCR studies demonstrated the presence of the HGBV sequences in liver RNA extracted from the H205-infected tamarin, T-1053 (data not shown). Therefore, to determine the size of the HGBV genome, Northern analysis of H205-infected and uninfected
15 tamarin liver RNA was performed. Total cellular RNA was extracted from 1.25 g liver of H205-infected tamarin T-1053 and from 1.0 g of liver from a control (i.e. uninfected) tamarin T-1040 using an RNA isolation kit (Stratagene, La Jolla, CA) as directed by the manufacturer. Total RNA (30 µg) was electrophoresed through a 1% agarose gel containing 0.6 M formaldehyde (R.M. Fournay, et al., Focus 10:
20 5-7, [1988]) and then transferred to Hybond-N nylon membrane (Amersham) by capillary action in 20X SCC (pH 7.0) as previously described. J. Sambrook, et al., Molecular Cloning - A Laboratory Manual, 2nd Edition (1989). The RNA was UV-crosslinked to the nylon membrane which was then baked in a vacuum oven at 80°C for 60 min. The blots were prehybridized at 60°C for 2 hours in 25
25 ml of a solution containing 0.05 M PIPES, 50 mM sodium phosphate, 100 mM NaCl, 1 mM EDTA, and 5% SDS. G.D. Virca, et al., Biotechniques 8:370-371 (1990). Prior to hybridization with the radiolabeled DNA probe, the solution was removed and 10 ml of fresh solution was added. The probes used for hybridization were clone 4 (SEQUENCE I.D. NO. 21; 221 bp) and clone 50 (SEQUENCE I.D.
30 NO. 29; 337 bp) and the 2000 bp cDNA encoding human β-actin. P. Gunning, et al., Mol. and Cell. Biol. 3:787-795 (1983). The probes (50 ng) were radiolabeled using a random primer labeling kit (Stratagene, La Jolla, CA) in the presence of [α-³²P]dATP as directed by the manufacturer. The specific activity of each probe was approximately 10⁹ cpm/µg. The blots were hybridized at 60°C for 16 hours
35 and washed as described (G.D. Virca, et al., supra) and then exposed to Kodak X-Omat-AR film at -80°C. Photographs of the resulting autoradiographs are shown in FIGURE 21A. Lanes 1, 3, and 5 contain liver RNA from T-1040 and lanes 2,

4, and 6 contain liver RNA from T-1053. Lanes 1 and 2 were hybridized with the human β -actin cDNA probe; lanes 3 and 4 were hybridized with the clone 4 probe (SEQUENCE I.D. NO. 21); and lanes 5 and 6 were hybridized with the clone 50 probe (SEQUENCE I.D. NO. 29). Exposure times were as follows: lanes 1 and 2, 5 hours at -80°C ; lanes 3-6, 56 hours at -80°C . The positions of the 28S and 18S ribosomal RNAs are indicated by the arrows. The relative sizes of these ribosomal RNAs are 6333 and 2366 nucleotides, respectively. J. Sambrook, et al., supra.

Clone 4 (SEQUENCE I.D. NO. 21) and clone 50 probes (SEQUENCE I.D. NO. 29) hybridized with an RNA species present in RNA extracted from the liver of the infected tamarin (T-1053) (FIGURE 21A, lanes 4 and 6). The size of this hybridizable RNA species was calculated at approximately 8300 nucleotides based on its relative mobility with respect to 28S and 18S ribosomal RNAs. Both probes appear to hybridize to the same RNA species. Neither probe hybridized with RNA extracted from the liver of the uninfected tamarin (T-1040) (FIGURE 21A, lanes 3 and 5). These results suggest that the sequences of clones 4 (SEQUENCE I.D. NO. 21) and 50 (SEQUENCE I.D. NO. 29) are present within the same 8.3 Kb transcript.

In order to determine the strandedness of the HGBV RNA genome, strand-specific radiolabeled DNA probes were prepared by asymmetric PCR using the GeneAmp[®] PCR kit from Perkin-Elmer essentially according to the manufacturer's instructions. Purified clone 50 DNA (SEQUENCE I.D. NO. 29) was used as template in separate reactions containing either the clone 50 negative strand-specific primer (SEQUENCE I.D. NO. 99) or the clone 50 positive strand-specific primer (SEQUENCE I.D. NO. 100) at $1\text{ }\mu\text{M}$ final concentrations. The reaction mixture contained [$\alpha^{32}\text{P}$ -dATP] (Amersham; 3000Ci/mmol) in place of the dATP normally included in the reaction mixture. Following 30-cycles of linear amplification of the template, the unincorporated [$\alpha^{32}\text{P}$ -dATP] was removed by Quick-Spin[®] Sephadex G50 spin columns (Boehringer-Mannheim, Indianapolis, IN) according to the manufacturer's instructions. Hybridization of the radiolabeled probes to DNA dot blots containing ten-fold serial dilutions of double-stranded clone 50 DNA (SEQUENCE I.D. NO. 29) demonstrated that the two probes possessed nearly identical sensitivities (data not shown). The radiolabeled probes were then hybridized to RNA blots containing $30\text{ }\mu\text{g}$ of total liver RNA extracted from uninfected tamarin T-1040 and from infected tamarin T-1053 as described above. Photographs of the resulting autoradiographs are shown in FIGURE 21B. Lanes 1 and 3 contain liver RNA from T-1040 and lanes 2 and 4 contain liver

RNA from T-1053. Lanes 1 and 2 were hybridized with the clone 50 positive strand probe (i.e., the positive strand is radiolabeled and will detect the negative strand; SEQUENCE I.D. NO. 100); lanes 3 and 4 were hybridized with the clone 50 negative strand probe (i.e., the negative strand is radiolabeled and will detect the positive strand; SEQUENCE I.D. NO. 99). The blots were exposed for 18 hours at -80°C. The positions of the 28S and 18S ribosomal RNAs are indicated by the arrows.

As shown in FIGURE 21B, the clone 50 positive and negative strand probes (SEQUENCE I.D. NOS. 100 and 99, respectively) hybridized to an RNA species of approximately 8.3 kilobases extracted from the liver of the infected tamarin T-1053 (FIGURE 21B, lanes 2 and 4), but not to RNA extracted from the liver of the uninfected tamarin T-1040 (FIGURE 21B, lanes 1 and 3). This is consistent with the Northern blot results obtained with the clone 4 (SEQUENCE I.D. NO. 21) and clone 50 (SEQUENCE I.D. NO. 29) double-stranded probes shown above. The more intense signal obtained with the clone 50 negative strand probe (SEQUENCE I.D. NO. 99) (FIGURE 21B, lane 4 vs. lane 2) suggests that the predominant RNA species present in the liver of infected tamarins is the positive (i.e. coding) strand.

20 Example 9. Extending the HGBV clone Sequence

A. Generation of HGBV sequences.

The clones obtained as described in Example 3 and sequenced as described in Example 5 hereinabove appear to be derived from separate regions of the HGBV genome. Therefore, to obtain sequences from additional regions of the HGBV genome that reside between the previously identified clones, and to confirm the sequence of the RDA clones, several PCR walking experiments were performed.

Total nucleic acids were extracted from 50 µl aliquots of infectious T-1053 plasma as described in Example 3(A). Briefly, precipitated nucleic acids were resuspended in 10 µl DEPC-treated H₂O. Standard RT-PCR was performed using the GeneAmp[®] RNA PCR kit (Perkin Elmer) as directed by the manufacturer. Briefly, PCR was performed on the cDNA products of random primed reverse transcription reactions of the extracted nucleic acids with 2 mM MgCl₂ and 1 µM primers. Reactions were subjected to 35 cycles of denaturation-annealing-extension (94°C, 30 sec; 55°C, 30 sec; 72°C 2 min) followed by a 3 min extension at 72°C. The reactions were held at 4°C prior to agarose gel analysis. These products were cloned into pT7 Blue T-vector plasmid (Novagen) as described in

the art. TABLE 9 presents the results obtained when these reactions were performed.

TABLE 9

	<u>Reaction</u>	<u>Primer 1</u>	<u>Primer 2</u>	<u>Product Size</u>
5	1.1	SEQ ID #88	comp. of SEQ ID #93	878 bp
	1.2	comp. of SEQ ID #87	SEQ ID #97	1191 bp
	1.3	SEQ ID #90	SEQ ID #101	864 bp
	1.4	comp. of SEQ ID #99	comp. of SEQ ID #102	1.4 kb
10	1.5	SEQ ID #102	SEQ ID #91	672 bp
	1.6	SEQ ID #98	SEQ ID #99	2328 bp
	1.7	comp of SEQ ID #103	SEQ ID #104	1300 bp
	1.8	comp. of SEQ ID #105	SEQ ID #87	900 bp
	1.9	SEQ. ID. #93	SEQ. ID. #99	2323 bp
15	1.10	SEQ. ID. #92	SEQ. ID. #91	1216 bp
	1.11	SEQ. ID. #90	SEQ. ID. #92	1570 bp
	1.12	comp. of SEQ ID #106	SEQ ID #103	550 bp
	1.13	comp. of SEQ ID #107	SEQ ID #108	900 bp
	1.14	SEQ ID #107	comp. of SEQ ID #96	1100 bp
20	1.15	comp. of SEQ ID #109	SEQ ID #110	410 bp
	1.16	SEQ ID #111	comp. of SEQ #112	600 bp
	1.17	comp. of SEQ ID #113	SEQ ID #114	1000 bp
	1.18	SEQ ID #98	comp. of SEQ ID #115	720 bp
	1.19	comp. of SEQ ID #116	comp. of SEQ ID #117	825 bp
25	1.20	SEQ ID #118	comp. of SEQ ID #119	700 bp
	1.21	SEQ ID #120	SEQ ID #95	900 bp
	1.22	SEQ ID #121	comp. of SEQ ID #122	950 bp
	1.23	SEQ ID #123	SEQ ID #124	420 bp
	1.24	SEQ.ID#87	SEQ.ID#88	130 bp
30	1.25	SEQ.ID#55	SEQ.ID#89	450 bp

A modification of a PCR walking technique described by Sorensen et al. (J. Virol. 67:7118-7124 [1993]) was utilized to obtain additional HGBV sequences. Briefly, total nucleic acid were extracted from infectious tamarin T-1053 plasma and reverse transcribed. The resultant cDNAs were amplified in 50 μ l PCR reactions (PCR 1) as described by Sorensen et al. (supra) except that 2 mM MgCl₂ was used. The reactions were subjected to 35 cycles of denaturation-

annealing-extension (94°C, 30 sec; 55°C, 30 sec; 72°C, 2 min) followed by a 3 min extension at 72°C. Biotinylated products were isolated using streptavidin-coated paramagnetic beads (Promega) as described by Sorensen et al. (*supra*). Nested PCR (PCR 2) were performed on the streptavidin-purified products as described by Sorensen et al. for a total of 20 to 35 cycles of denaturation-annealing-extension as described above. The resultant products and the PCR primers used to generate them are listed in TABLE 10.

TABLE 10

10	<u>Reaction</u>	<u>Primer set PCR 1</u>	<u>Primer set PCR 2</u>	<u>Size of PCR</u>
	<u>product</u>			
	2.1	SEQ ID #103 / SEQ ID #125	SEQ ID #668 / SEQ ID #126	500 bp
	2.2	SEQ ID #114 / SEQ ID #125	SEQ ID #105 / SEQ ID #126	1000 bp
	2.3	SEQ ID #92 / SEQ ID #125	SEQ ID #123 / SEQ ID #126	400 bp
15	2.4	SEQ ID #127 / SEQ ID #128	comp. of SEQ ID #88 / SEQ ID #126	420 bp
	2.5	SEQ ID #108 / SEQ ID #128	SEQ ID #106 / SEQ ID #126	900 bp
	2.6	SEQ ID #129 / SEQ ID #125	SEQ ID #98 / SEQ ID #126	750 bp
	2.7	SEQ ID #116 / SEQ ID #128	SEQ ID #115 / SEQ ID #126	825 bp
20	2.8	SEQ ID #130 / SEQ ID #125	SEQ ID #107 / SEQ ID #126	630 bp
	2.9	SEQ ID #110 / SEQ ID #135	SEQ ID #131 / SEQ ID #126	390 bp
	2.10	SEQ ID #132 / SEQ ID #125	SEQ ID #109 / SEQ ID #126	1000 bp
	2.11	SEQ ID #111 / SEQ ID #128	SEQ ID #133 / SEQ ID #126	600 bp
	2.12	SEQ ID #134 / SEQ ID #135	SEQ ID #112 / SEQ ID #126	580 bp
25	2.13	SEQ ID #136 / SEQ ID #125	SEQ ID #137 / SEQ ID #126	400 bp
	2.14	SEQ ID #138 / SEQ ID #128	SEQ ID #113 / SEQ ID #126	500 bp
	2.15	SEQ ID #139 / SEQ ID #128	SEQ ID #140 / SEQ ID #126	900 bp
	2.16	SEQ ID #121 / SEQ ID #135	SEQ ID #141 / SEQ ID #126	400 bp
	2.17	SEQ ID #142 / SEQ ID #125	comp. of SEQ ID #102 / SEQ ID #126	1000 bp
30	2.18	SEQ ID #143 / SEQ ID #135	SEQ ID #144 / SEQ ID #126	550 bp
	2.19	SEQ ID #87 / SEQ ID #125	SEQ ID #90 / SEQ ID #126	220 bp

These products were isolated from low melting point agarose gels and cloned into pT7 Blue T-vector plasmid (Novagen) as described in the art.

RNA ligase-mediated 5' RACE (rapid amplification of cDNA ends) was employed to obtain the 5' end sequences from viral genomic RNAs as described

hereinabove. Briefly, the 5' AmpliFINDER™ RACE kit (Clontech, Palo Alto, CA) was used as directed by the manufacturer. The source of the viral RNA was acute phase T-1053 plasma that was extracted as described above. The virus-specific oligonucleotides utilized for the reverse transcription (RT), the first PCR amplification (PCR 1) and the second PCR amplification (PCR 2) are listed in TABLE 11. The ligated anchor primer and its complementary PCR primer were provided by the manufacturer. PCRs were performed with the GeneAmp® PCR kit (Perkin Elmer) as directed by the manufacturer.

TABLE 11

<u>Reaction</u>	<u>RT primer</u>	<u>PCR 1 primer</u>	<u>PCR 2 primer</u>	<u>Size of PCR 2 product</u>
3.1	SEQ ID #145	SEQ ID #146	SEQ ID #147	190 bp
3.2	SEQ ID #148	SEQ ID #149	SEQ ID #150	620 bp

The products generated by RNA ligase-mediated 5' RACE were isolated from low melting point agarose gels and cloned into pT7 Blue T-vector plasmid (Novagen) as described in the art.

To obtain additional sequence at the 5' and 3' ends of HGBV-B SEQUENCE (see below, Evidence for the existence of two HCV-like flaviviruses in HGBV), an RNA circularization experiment was performed. (This method is based on that described by C.W. Mandl et al. (1991) Biotechniques, Vol 10 (4): 485-486.) Total nucleic acids were purified from 50 µl of T-1057 plasma (14 days post H205 inoculation except that 1 µg glycogen replaced the tRNA in the precipitation. The nucleic acid pellet was dissolved in 16.3 µl of DEPC-treated water, and 25 µl of 2X TAP buffer (1X=50 mM NaOAC, pH 5.0, 1 mM EDTA, 10 mM 2-mercaptoethanol, 2mM ATP) and 8.7 µl of tobacco acid pyrophosphatase (20 Units; Sigma) were added. The mixture was incubated at 37°C for 60 min. The sample was extracted with phenol (water-saturated) followed by chloroform and then precipitated with NaOAC/EtOH in the presence of glycogen (1 µg). The pellet was dissolved in 83 µl of DEPC water and 10 µl of 10X RNA ligase buffer (New England Biolabs, NEB), 2 µl of RNase inhibitor (Perkin Elmer), and 5 µl of T4 RNA ligase (NEB) was then added. The mixture was incubated at 4°C for 16 hours. The sample was then extracted with phenol (water-saturated) and then chloroform as before and then precipitated with NaOAC/EtOH.

One-tenth of the ligated RNA was used in the reverse transcriptase (RT) reaction using Superscript RT (GIBCO/BRL) and SEQUENCE ID. NO. 146 as the primer as directed by the manufacturer. One-half of the RT reaction mix was

used for PCR1 in the presence of a biotinylated oligonucleotide primer (SEQUENCE ID. NO. 146) and a second oligonucleotide primer (SEQUENCE ID. NO. 133) as described above. PCR1 products were purified from the reaction mixture using streptavidin-magnetic beads as described by Sorensen et al. Purified PCR1 products (2 μ l out of 30 μ l) were used as the template for PCR2. PCR2 using oligonucleotide primers (SEQUENCE ID. NOS. 147 and 154) yielded a 1200 bp product that was cloned into pT7 Blue T-vector plasmid and sequenced as described below. Sequence analysis of two independent clones from this experiment demonstrated 100% identity in the region of overlap with known sequence (although one clone possessed a sequence of 18 T residues and the other a sequence of 27 T residues), and an additional 270 bases of new sequence.

The above circularization experiment provided sequence from both the 5'- and 3'-ends of the HGBV-B viral genome that was not obtained using standard 3'- or 5'-RACE techniques. However, the exact 5'-3' junction is difficult to determine even after additional PCR experiments are performed using primers designed from the newly obtained sequence. Thus, in order to better characterize the 5'-end of the HGBV-B RNA genome a primer extension experiment was performed using RNA isolated from the liver of T-1053.

Total cellular RNA was isolated from the liver of T-1053 and a control (i.e. uninfected) animal (T-1040) as described in Example 7. An antisense oligonucleotide (SEQUENCE I.D. NO. 155) was endlabeled with γ -³²P-ATP using T4 polynucleotide kinase (NEB) to a specific activity of approximately 9.39×10^7 CPM/ μ g as described (Sambrook et al.). The primer was annealed to 30 μ g of T-1053 and T-1040 liver RNA in separate reactions and then extended using MMLV reverse transcriptase (Perkin-Elmer) as previously described (Sambrook et al.). The products were analyzed on a 6% sequencing gel. A sequence ladder generated from one of the HGBV-B circularization clones using the same primer as that utilized for the primer extension served as a size standard.

Primer extension products of 176 bp were obtained from T-1053. These products were not obtained when primer extension was performed using liver RNA from an uninfected animal (T-1040) and therefore represent products derived from the HGBV-B genome. The length of the products obtained indicate that the 5'-end of the genome, as present in the liver of infected animals, is located 442 nucleotides upstream of the initiator AUG codon.

To confirm the 3' location of the sequence obtained in the circularization experiment, RT-PCRs were performed using primers designed to the predicted 3'

termini (see reaction 1.25, TABLE 2). RT-PCR of infectious T-1053 plasma as (described above) using SEQUENCE ID. NOS. 156 and SEQUENCE ID. NO. 157 yielded a product of 450 bp. In contrast, RT-PCR using the complement of SEQUENCE ID. NO. 157 and SEQUENCE ID. NO. 147 did not yield a detectable
5 PCR product (data not shown). These data suggest that the 3' end of the genome is located 50 nucleotides downstream of the poly T tract.

The cloned products from TABLES 9, 10 and 11, and the RNA circularization experiment were sequenced as previously described in Example 5. Interestingly, the cloned products of reactions 1.4, 1.6, 1.9, 1.10 and 1.11 were
10 found to contain only one of the two primer sequences at the termini, suggesting that these products were the result of false priming events. PCR/sequencing experiments have linked sequences detected in products 1.4, 1.6, 1.9, 1.10 and 1.11 with clone 4 (SEQUENCE I.D. NO. 21) and/or clone 50 (SEQUENCE I.D. NO. 29). In addition, sequences derived from each of these reactions contain
15 limited HCV identity. Thus, these products, although a result of false priming at one end of the PCR product, appear to contain authentic HGBV sequence. The product from reaction 1.14 also appeared to be a result of false priming. Here, the complement of SEQUENCE I.D. NO. 160 is found at the 5' end of the product from reaction 1.14 (GB-B, FIGURE 22). This was unexpected because
20 SEQUENCE I.D. NO. 160 was derived from SEQUENCE I.D. NO. 161 which resides in GB-A. However, the sequence identity between products from reactions 1.14 and 2.8, together with additional PCRs/sequencing experiments (data not shown), demonstrate that reaction 1.14 contains authentic HGBV sequence. Apparently, the complement of SEQUENCE I.D. NO. 160 had enough
25 identity to GB-B sequences upstream of SEQUENCE I.D. NO. 162 to act as a PCR primer.

The sequences obtained from the products described in TABLES 9, 10 and 11 hereinabove, and the RNA circularization experiment were assembled into contigs using the GCG Package (version 7) of programs. A schematic of the
30 assembled contigs is presented in FIGURE 22). GB contig A (GB-A) is 9493 bp in length, all of which has been sequenced and is presented in SEQUENCE I.D. NO. 163. GB-A includes clones 2 (SEQUENCE I.D. NO. 22), 16 (SEQUENCE I.D. NO. 26), 23 (SEQUENCE I.D. NO. 28), 18 (SEQUENCE I.D. NO. 27), 11 (SEQUENCE I.D. NO. 24) and 10 (SEQUENCE I.D. NO. 23). SEQUENCE
35 I.D. NO. 163 was translated into three possible reading frames and is presented in the Sequence Listing as SEQUENCE I.D. NOS. 164-392. GB contig B (GB-B) is 9143 bp and is presented in SEQUENCE I.D. NO. 393. GB-B (SEQUENCE

I.D. NO. 393) includes clones 4 (SEQUENCE I.D. NO. 21), 50 (SEQUENCE I.D. NO. 29), 119 (SEQUENCE I.D. NO. 30) and 13 (SEQUENCE I.D. NO. 25). SEQUENCE I.D. NO. 393 was translated into one open reading frame and is presented in the Sequence Listing as SEQUENCE I.D. 396 and 397. The UTRs
5 from the 5' and the 3' ends can each be translated into six reading frames.

B. Evidence for the existence of two HCV-like viruses in HGBV

1. Evidence for GB-A and GB-B representing two distinct RNA species.

Comparison of GB-A (SEQUENCE I.D. NO. 163) GB-B (SEQUENCE
10 I.D. NO. 393) and HCV-1 (GenBank accession # M67463) demonstrate that GB-A (SEQUENCE I.D. NO. 163), GB-B (SEQUENCE I.D. NO. 393) and HCV-1 are all distinct sequences. Dot plot analyses of the nucleic acid sequences of GB-A (SEQUENCE I.D. NO. 163), GB-B (SEQUENCE I.D. NO. 393) and HCV-1 were performed using the GCG Package (version 7). Using a window size of 21
15 and a stringency of 14, GB-A (SEQUENCE I.D. NO. 163), GB-B (SEQUENCE I.D. NO. 393) and HCV-1 were found to clearly contain different nucleotide sequences (FIGURE 23). Therefore, GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) do not represent different strains or genotypes of HCV or of each other. Short regions of limited nucleotide identity are found in
20 the putative NS3-like and NS5b-like sequences of GB-A (SEQ. ID. NO. 163) and GB-B (SEQ. ID. NO. 393) and the NS3 and NS5b sequences of HCV by this analysis. However, nucleotide identity in these regions is not surprising because NS3 and NS5b code for the putative NTP-binding helicase and the RNA-dependent RNA polymerase, respectively, which are conserved in all flaviviruses
25 (see below). That GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) represent separate RNA molecules and not different regions of the same RNA molecule is evidenced by the 5' RACE experiments (above) and supported by the Northern blot data (as described in Example 8. First, the 5' RACE experiments show distinct 5' ends for GB-A (SEQUENCE I.D. NO. 163)
30 and GB-B (SEQUENCE I.D. NO. 393). Because RNA molecules can contain only one 5' end, GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) represent separate RNA molecules. Second, the 8300 base RNA molecule detected in infected tamarin liver RNA by probing Northern blots with clones 4 and 50 (SEQUENCE I.D. NOS. 21 and 29, respectively, both from GB-B [SEQUENCE I.D. NO. 393], see Example 8, corresponds closely to the size of
35 GB-B (SEQUENCE I.D. NO. 393, 9143 bp). If GB-A and GB-B were part of the same RNA molecule, one would expect a Northern blot product of at least

17,000 bases. These data demonstrate that GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) represent the nucleotide sequences of two distinct RNA molecules that are not variants of HCV or each other.

Northern blot analysis and PCR studies of T-1053 provided evidence that the two RNA species corresponding to GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) were not at equivalent levels in the liver. As stated above, clones 4 and 50 (SEQUENCE I.D. NOS. 21 and 29, respectively), both from the GB-B (SEQUENCE I.D. NO. 393), hybridized to an 8.3 kb RNA species present in infected liver of T-1053 (as described in Example 8). In contrast, clones 2 (SEQUENCE I.D. NO. 22), 10 (SEQUENCE I.D. NO. 23), 16 (SEQUENCE I.D. NO. 26 and 23 (SEQUENCE I.D. NO. 28), all from GB-A (SEQUENCE ID. NO. 163), showed no hybridization with T-1053 liver RNA in identical experiments (data not shown). In addition, clone 16 PCR generated much less product than clone 4 PCR on cDNAs generated from T-1053 liver RNA by ethidium staining, despite equivalent sensitivities of clone 4 and clone 16 PCRs demonstrated using plasmid templates (data not shown). This is in contrast to what is found in T-1053 plasma at the time of sacrifice. PCR titration experiments for clone 4 (GB-B-specific, SEQUENCE I.D. NO. 393) and clone 16 (GB-A-specific, SEQUENCE I.D. NO. 163) PCR on cDNAs generated from T-1053 plasma RNA suggest that equivalent amounts of GB-A (SEQUENCE I.D. NO. 163) RNA and GB-B (SEQUENCE I.D. NO. 393) RNA are present in T-1053 plasma (Example 4, E.2). Thus, although GB-A (SEQUENCE I.D. NO. 163) RNA and GB-B (SEQUENCE I.D. NO. 393) RNA were at equivalent levels in T-1053 plasma, there appeared to be a greater amount of GB-B (SEQUENCE I.D. NO. 393) RNA relative to GB-A (SEQUENCE I.D. NO. 163) RNA present in T-1053 liver at the time of sacrifice. Together, these results provide further evidence for the existence of two different RNA molecules corresponding to GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) in T-1053 plasma and suggest that these RNAs are not necessarily present at equivalent levels in infected liver RNA. Therefore, it is unlikely that GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) make up individual segments of a single viral genome.

2. Evidence that GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393) represent the genomes of two distinct viruses.

Infectivity and PCR studies provide evidence for the viral nature of GB-A (SEQUENCE I.D. NO. 163) and B (SEQUENCE I.D. NO. 393). Specifically, tamarins T-1049 and T-1051 which were inoculated with T-1053 plasma that had

been filtered (0.1 μ m) and diluted to 10^{-4} , or unfiltered and diluted to 10^{-5} , respectively, were positive for both clone 4 (GB-B [SEQUENCE I.D. NO. 393]) and clone 16 (GB-A [SEQUENCE I.D. NO. 163]) sequences. Prior to inoculation, both of these animals were negative for clones 4 and 16 (Examples 4, 5 E.4 and 4, E.5). Therefore, the two RNA species present in the acute phase T-1053 plasma corresponding to GB-A and GB-B can be filtered, diluted and passaged to other animals consistent with the proposed viral nature of GB-A (SEQUENCE I.D. NO. 163) and GB-B (SEQUENCE I.D. NO. 393). That GB-A and GB-B represent RNA molecules from separate viral particles is evidenced by PCR studies of the H205-inoculated tamarins. Specifically, four of four tamarins became positive for clone 4 (GB-B [SEQUENCE I.D. NO. 393]) by RT-PCR after H205 inoculation. In contrast, only one of 4 H205-inoculated tamarins (T-1053) became positive for clone 16 (GB-A [SEQUENCE I.D. NO. 163]) by RT-PCR (Example 4.E.2). Therefore, assuming that GB-A (SEQUENCE I.D. NO. 163) sequences were truly absent from T-1048, T-1057 and T-1061, and that the negative clone 16 PCR results were not due to poor sensitivity, it would appear that the virus corresponding to GB-B (SEQUENCE I.D. NO. 393) sequences (i.e. hepatitis GB virus B [HGBV-B]) can be passaged independent of GB-A (SEQUENCE I.D. NO. 163) sequences. An HGBV-B only sample from T-1057 has been passaged two additional times (Example 4). GB-A (SEQUENCE I.D. NO. 163) sequences have not been detected in these animals by RT-PCR. In addition, significant liver enzyme elevations have been noted in these animals (Example 4), demonstrating that HGBV-B alone caused hepatitis in tamarins. GB-A (SEQUENCE I.D. NO. 163) sequences have been identified in tamarins lacking detectable GB-B (SEQUENCE I.D. NO. 393) sequences. Specifically, GB-B only animals (T-1048, T-1057 and T-1061) challenged with T-1053 plasma developed GB-A (SEQUENCE I.D. NO. 163) only viremias as detected by clone 16 specific RT-PCR. The GB-A only plasma from T-1057 has been passaged one additional time (Example 4). Thus, it appears that a virus corresponding to GB-A (SEQUENCE I.D. NO. 163) sequences (hepatitis GB virus A [HGBV-A]) can replicate independent of HGBV-B. Additional passages of HGBV-A in the absence of HGBV-B is ongoing. At this time it is not known whether HGBV-A causes hepatitis in tamarins. However, the lack of elevated liver enzymes noted in the T-1053 challenged tamarins with HGBV-A viremias and in the passage of the HGBV-A only serum from T-1057 argue against the hepatotropic nature of HGBV-B in tamarins.

The presence of two viruses in acute phase T-1053 plasma can be traced back to the H205 inoculum. Specifically, data from Example 7 showed that clone 16 (SEQUENCE I.D. NO.26, found in GB-A [SEQUENCE I.D. NO. 163]) was absent in the preinoculation plasma from all 7 tamarins tested. In addition, clones 2, 10, 18 and 23 (SEQUENCE I.D. NOS. 22, 23, 27 and 28, respectively, all from GB-A [SEQUENCE I.D. NO. 163]) have not been detected in any pre-HGBV-inoculated tamarin plasma tested (Example 7. Similar negative results were found when preinoculation tamarin plasma were tested for clones 4 and 50 (SEQUENCE I.D. NOS. 21 and 29, respectively, all from GB-B [SEQUENCE I.D. NO.393]). Thus, both HGBV-A and HGBV-B were absent in the preinoculation tamarin plasma. In contrast, all of these clones (i.e. clones 2, 10, 16, 18 and 23 from GB-A [SEQUENCE I.D. NO. 163], and clones 4 and 50 from GB-B [SEQUENCE I.D. NO. 393]) were detected in the H205 inoculum (TABLE 7). Interestingly, as found in cDNA made from T-1053 liver (above), several different PCR targets in GB-A (SEQUENCE I.D. NO. 163) all generated less product than similar PCR targets in GB-B (SEQUENCE I.D. NO. 393) using the same random primed cDNAs from H205 (data not shown). Thus, we conclude that HGBV-A and HGBV-B are present in the original GB inoculum, H205. However, HGBV-B appears to be more abundant than HGBV-A in H205. The low relative amount of HGBV-A in the H205 inoculum may explain why only one of four tamarins were positive for the HGBV-A after H205 inoculation (Example 4.E.2).

3. Evidence that HGBV-A and HGBV-B are members of the Flaviviridae.

Searches of the SWISS-PROT database with the three frame translation products of GB-A (SEQUENCE I.D. NO. 165-268, 270-384, 386-392) and GB-B (SEQUENCE I.D. NO. 397) as described in Example 5 show limited, but significant amino acid sequence identity with various strains of HCV. Translation products from GB- A (SEQUENCE I.D. NO. 164) and GB- B (SEQUENCE I.D. NO. 393) show the closest homology to regions of the nonstructural proteins of various HCV isolates (i.e. NS2, NS3, NS4 and NS5). For example, as shown in FIGURE 24, the conserved residues (indicated by *) in the putative NTP-binding helicase domain of flaviviruses (FIGURE 24A) and in the RNA-dependent RNA polymerase domain of all viral RNA-dependent RNA polymerases (FIGURE 24B) are held in common between HCV-1 NS3 and NS5b (SWISS-PROT accession number p26664), respectively, and the predicted translation products of GB-A (SEQUENCE I.D. NO. 390) and GB- B (SEQUENCE I.D. NO. 397). (See Choo et al., PNAS 88:2451-2455 [1991] and Domier et al., Virology 158:20-27

[1987]). Therefore, it appears that both GB- A virus and GB- B virus encode functional NTP-binding helicases and RNA-dependent RNA polymerases. However, GB-A (SEQUENCE I.D. NO. 390) and GB-B (SEQUENCE I.D. NO. 397) do not share complete amino acid identity to each other and/or to HCV in other regions of HCV NS3 and NS5b. Specifically, over the 200 residue region of NS3 shown in FIGURE 24A, GB- A (SEQUENCE I.D. NO. 390, residues 1252-1449) virus and HCV-1 (SEQ. ID. NO.398), GB-B (SEQUENCE I.D. NO. 397, residues 1212-1408) virus and HCV-1 (SEQUENCE I.D. NO.398), and GB- A (SEQUENCE I.D. NO. 390, residues 1252-1449) virus and GB- B (SEQUENCE I.D. NO. 397, residues 1212-1408) virus are 47%, 55% and 43.5% identical, respectively. In addition, over the 100 residue region of NS5b shown in FIGURE 24B, GB-A (SEQUENCE I.D. NO. 390, residues 2644-2739) virus and HCV-1 (SEQUENCE I.D. NO. 398), GB- B (SEQUENCE I.D. NO. 397, residues 2513-1612) virus and HCV-1 (SEQUENCE I.D. NO.398), and GB-A (SEQUENCE I.D. NO. 390, residues 2644-2739) virus and GB- B (SEQUENCE I.D. NO. 397, residues 2599-2698) virus are 36%, 41% and 44% identical, respectively. Lower levels of homology are found in other putative nonstructural genes of GB- A (SEQUENCE I.D. NO. 390) and GB-B (SEQUENCE I.D. NO. 397) when compared to HCV. The overall level of homology of the putative nonstructural proteins of GB- A virus and GB- B virus compared with HCV sequences present in GenBank suggests that both GB-A (SEQUENCE I.D. NO. 164) and GB-B (SEQUENCE I.D. NO. 393) are derived from two separate members of the Flaviviridae. Flaviviruses contain a single genomic RNA molecule which code for one NTP-binding helicase domain and one RNA-dependent RNA polymerase domain. The presence of two contigs, each containing a putative RNA helicase domain and a putative RNA-dependent RNA polymerase is consistent with the presence of two HCV-like flaviviruses in the acute phase T-1053 plasma.

Example 10. PCR

In order to determine the sequence relatedness of HGBV to hepatitis C virus the following PCR-based experiment was performed. PCR primers based on the 5'-untranslated region (UTR) sequence of the HCV genome (J.H. Han, *PNAS* 88:1711-1715 [1991]), which are highly conserved in HCV isolates from a variety of geographic origins (Cha, T.-A., et al., *J. Clin. Microbiol.* 29:2528-2534 [1991]) were utilized in attempts to detect similar sequences in H205-infected tamarin T-1053 liver RNA. Total cellular RNA was extracted from the liver of infected tamarin T1053 and from the liver of an uninfected tamarin (T-1040) as described in Example 8A. Thirty micrograms of each RNA sample was reverse transcribed and PCR amplified using a kit available from Perkin-Elmer essentially as described in the manufacturer's instructions. An antisense primer (primer 1) was used for the reverse transcriptase reaction and comprised bases 249-268 of the HCV 5'-UTR. Primer 1 and a primer comprising bases 13-46 of the HCV 5'-UTR (primer 2) were then used for PCR amplification of the intervening sequence. The conditions used for thermocycling were essentially as described by Cha et al., *supra*.

In order to increase the sensitivity of this assay for the detection of HCV 5'-UTR sequences in H205 infected tamarin T-1053, the above PCR reaction was subjected to a second amplification reaction which utilized "nested" PCR primers. These primers are derived from sequences found internal to the sequences of primers 1 and 2 above in the HCV 5'-UTR: Primer 3 comprised sequences from 47-69 and primer 4, an antisense primer, comprised bases 188-210 of the HCV 5'-UTR. In this "nested" PCR reaction, PCR products (2 μ l out of a total of 100 μ l reaction volume) from the first PCR reaction were used as the source of DNA template. The thermocycling parameters were essentially the same as described above except that the annealing temperature was 55°C instead of 60°C. The resulting PCR products from the second PCR reaction were then analyzed for the expected DNA products by agarose gel electrophoresis and ethidium bromide staining. The expected DNA fragment sizes, based on the sequence of the HCV 5'UTR (Han et al., *supra*) is 253 bp for the product of the first PCR reaction and 163 bp for the product of the nested PCR reaction. PCR products of the anticipated size were obtained in control experiments performed using 30 μ g of total cellular RNA extracted from the liver of an HCV infected chimpanzee as described in Example 8A (data not shown), thus demonstrating that this experimental procedure was able to detect the 5-UTR of HCV. However, neither of the expected products were observed on the resulting ethidium bromide stained agarose gel when either

T-1053 liver RNA or T-1040 liver RNA were used (data not shown). This inability to produce the predicted result may suggest that (i) the sequence of the 5'-UTR of the agent differs significantly from that of HCV such that the oligonucleotide primers used would not be able to anneal efficiently thereby disallowing PCR amplification from occurring or (ii) the agent lacks a 5'-UTR. In either case it appears from these results that the nucleotide sequence of the agent is significantly different from that of HCV.

In addition, nucleic acids were isolated as in Example 7 from a chimpanzee plasma pool obtained during the acute phase of an experimental infection of HCV (G. Schlauder et al., *J. Clin. Microbiology* 29:2175-2179 [1991]): RT-PCR was performed as described in Example 7 using clone 16 primers (SEQUENCE I.D. NOS. 93 and 94). No bands of the expected size for these primers were detected by ethidium bromide staining or after hybridization to a clone 16 specific probe (data not shown). These results support the unrelatedness of clone 16 sequence (SEQUENCE I.D. NO. 26) to HCV.

Example 11. Reactivity of HGBV Infected Serum to Other Hepatitis Viruses

Serum specimens were obtained prior to, and after, inoculation with HGBV using either the H205 inoculum (T-1048, T-1057, T-1061) or the T-1053 inoculum (T-1051) and tested for antibodies frequently detected following exposure to known hepatitis viruses. Specimens were tested for antibodies to hepatitis A virus (using the HAVAB assay, available from Abbott Laboratories, Abbott Park, IL), the core protein of hepatitis B core (using the Corzyme® test available from Abbott Laboratories, Abbott Park, IL), hepatitis E virus (HEV) (using the HEV EIA, available from Abbott Laboratories, Abbott Park, IL) and hepatitis C virus (HCV) (utilizing HCV second generation test, available from Abbott Laboratories, Abbott Park, IL). These tests were performed according to the manufacturer's package inserts.

None of the tamarins tested positive for antibodies to HCV or to HEV either prior to or after HGBV inoculation (see TABLE 12). Therefore, HGBV infection does not elicit detectable antisera against HCV or HEV.

One of the tamarins (T-1061) was positive for antibodies to HAV prior to and after inoculation with HGBV, suggesting a previous exposure to HAV (TABLE 9, T-1061). However, the three remaining tamarins (T-1048, T-1057 and T-1051) show no HAV-specific antibodies after HGBV inoculation. Therefore, HGBV infection does not elicit an anti-HAV response. One of the tamarins (T-1048) was negative for antibodies to HBV core both prior to and after

inoculation with HGBV. Two of the tamarins (T-1061 and T-1057) were positive prior to inoculation with HGBV. One of the tamarins (T-1051) was borderline positive for antibodies to HBV prior to inoculation, but was negative after inoculation. Based on these data, there is no evidence that infection with the HGBV agent induces an immune response to HBV core. Taken together, these data support that the HGBV agent is a unique viral agent, and is not related to any of the viral agents commonly associated with hepatitis in man.

Example 12. Western Blot Analysis of HGBV Infected Liver.

As noted in Examples 1 and 2 above, elevated liver enzyme values are noted in tamarins inoculated with HGBV. If HGBV is indeed a hepatotropic virus, it would be expected that viral protein(s) would be produced in infected liver cells, and that an immune response to those proteins would be generated. In this example, evidence is presented which suggests that a unique protein appears in livers obtained from HGBV-infected tamarins; this protein appears to be specifically recognized via Western blot utilizing tamarin serum obtained in the convalescent stage following infection with HGBV.

HGBV-infected tamarin livers and various control tamarin and chimpanzee livers were diced and homogenized in PBS (approximately 1 g liver to 5 ml) using a Omni-mixer homogenizer. The resulting suspension was clarified by centrifugation (10,000 x g, 1 hour, 4°C) and by micro-filtration through 5 µm, 0.8 µm and 0.45 µm filters. The clarified homogenate was centrifuged under conditions pelleting all components of 100S or greater. Pellets (100S liver fractions) were taken up in a small volume of buffer and stored at -70°C.

SDS polyacrylamide gel electrophoresis (PAGE) was carried out using standard methods and reagents (Laemmli discontinuous gels). 100S liver fractions were diluted 1:20 in a sample buffer containing SDS and 2-mercaptoethanol and heated at 95°C for 5 minutes. The proteins were electrophoresed through either 12% acrylamide or 4-15% acrylamide linear gradient gels, 7cm x 8cm, at 200 volts for 30 to 45 minutes. Proteins were electro-transferred to nitrocellulose membranes using standard methods and reagents.

Western blots were developed using standard methods. Briefly, the nitrocellulose membrane was briefly rinsed in TBS/Tween and blocked overnight in TBS/CS (100 mM Tris, 150 mM NaCl, 10 mM EDTA, 0.18% Tween-20, 4.0% calf serum, pH 8.0) at 4°C. The nitrocellulose was placed in the Multi-screen apparatus and 600 µl of sera was placed in the channels and followed with a 2 hour room temperature and an overnight 4°C incubation. After removing the

membrane from the Multi-screen apparatus, it was washed 3 times, 5 minutes each, in 15 ml TBS/Tween (50 mM Tris, 150 mM NaCl, 0.05% Tween-20, pH 8.0). The membrane was incubated for 1 hour at room temperature in 15 ml goat anti-human:HRPO conjugate (0.2 µg/ml TBS/CS). After washing as before, the
5 membrane was incubated in the TMB enzyme substrate solution, rinsed in water and dried.

Proteins isolated from T-1053 liver at sacrifice (12 days post-GB inoculation) and blotted as described above showed a unique immunogenic protein with an apparent molecular weight of approximately 50 to 80 kDa when reacted
10 with T-1057 sera from 5, 6, 7, 9 or 11 weeks post-GB inoculation. The band was not present when reacted with T-1057 sera pre-inoculation or 3 weeks post-GB inoculation. This band did not appear in the lanes containing liver proteins obtained from an uninoculated tamarin (T-1040) when reacted with any of these T-1057 sera. In addition, a protein of the same size (50 to 80 kDa) was visible when
15 the T-1053 liver proteins were reacted with other post-GB inoculation sera (T-1048 at 11 weeks post-GB inoculation and T-1051 at 8 weeks post-GB inoculation) but not when they were reacted with pre-inoculation sera from these same animals.

An additional Western blot experiment was performed to determine if this
20 immunoreactive band would be detected in liver tissues from other GB-inoculated tamarins, or in liver tissues of chimpanzees infected either with HCV or HBV. In each case, the nitrocellulose strips containing the liver proteins were reacted with a pool of sera from T-1048 (5, 8, and 16 weeks post-GB inoculation) and T-1051 (8 and 12 weeks post-GB inoculation). All 5 sera in the pool were mixed in equal
25 proportion. A reactive protein band of 50-80 kDa was seen with all of the tamarin liver samples obtained from GB inoculated tamarins (T-1038, T-1049, and T-1055 obtained at 14 days post-GB inoculation and T-1053 obtained at 12 days post-GB inoculation). This immunoreactive band was not detected in the liver preparations obtained from T-1040 (uninoculated) nor in any of the chimp liver
30 preparations (CHAS-457 (pre-HCV inoculation), CHAS-457 (HCV+), CRAIG-454 (HCV+) and MUNA-376 (HBV+).

Taken together, these data demonstrate the existence of an immunogenic and antigenic protein with an apparent molecular weight of approximately 50 to 80 kDa specifically associated with HGBV-infected tamarin liver. The nature of this
35 HGBV-associated protein (ie. whether it is viral encoded or of host origin) is currently under investigation. Regardless of the source of the HGBV-associated

protein, these results are consistent with HGBV infection inducing an antibody response to an antigen which is present in HGBV-infected tamarin liver.

Example 13. CKS-based expression and detection of immunogenic

HGBV-A and HGBV-B polypeptides

A. Cloning of HGBV-A and HGBV-B sequences

The cloning vectors pJO200, pJO201, and pJO202 allow the fusion of recombinant proteins to the CMP-KDO synthetase (CKS) protein. Each of these plasmids consists of the plasmid pBR322 with a modified lac promoter fused to a kdsB gene fragment (encoding the first 239 of the entire 248 amino acids of the E. coli CKS protein), and a synthetic linker fused to the end of the kdsB gene fragment. The synthetic linkers include: multiple restriction sites for insertion of genes, translational stop signals, and the trpA rho-independent transcriptional terminator. The unique restriction sites in this linker region include, from 5' to 3', EcoRI, SacI, KpnI, SmaI, BamHI, XbaI, PstI, SphI, and HindIII. Each plasmid allows for insertion in a different reading frame within the multiple cloning site. The CKS method of protein synthesis as well as CKS vectors are disclosed in U.S. Patent No. 5,124,255, which enjoys common ownership and is incorporated herein by reference, and the use of CKS fusion proteins in assay formats and test kits is described in United States Serial No. 07/903,043, which enjoys common ownership and is incorporated herein by reference.

The HGBV-A and HGBV-B sequences obtained from the walking experiments described in TABLES 9 and 10 (Example 9) were liberated from the appropriate pT7Blue T-vector clones using restriction enzymes listed in TABLES 13 and 14 (10 units, NEB), and purified from 1% low melting point agarose gels as described in Example 3B. Plasmids pJO200, pJO201, and pJO202 were digested with the same restriction enzymes (10 units, NEB) and dephosphorylated with bacterial alkaline phosphatase (GIBCO BRL, Grand Island, NY). Each purified HGBV fragment was ligated into the digested, dephosphorylated pJO200, pJO201, and pJO202 and transformed into E. coli XL1 Blue as described in Example 3B. Standard miniprep analyses confirmed the successful construction of the CKS/HGBV expression vectors.

Two additional PCR products were generated specifically for expression. The 2 products, designated 4.1 and 4.2, were predicted to encode the HGBV-B and HGBV-A core regions, respectively (see FIGURE 22). PCR product 4.1 was generated using primers coreB-s and coreB-a1 (SEQUENCE I.D. NOS. 708 and 709) and PCR product 4.2 was generated using primers coreA-s and 2.2.1'

(SEQUENCE I.D. NOS. 710 and 138), as described in Example 9. The 4.1 sense and antisense primers had EcoRI and BamHI restriction sites, respectively, designed into the ends. The 4.1 PCR product was digested, gel isolated, and ligated to pJO200, pJO201, and pJO202 as described above. The sense primer for the 4.2 PCR product had an EcoRI restriction site designed into the end, but the antisense primer did not have a restriction site. Thus, the product was cut with EcoRI, gel isolated, and ligated to pJO200, pJO201, and pJO202 which had been digested with BamHI, end-filled with the Klenow fragment of DNA polymerase and dNTPs, digested with EcoRI, and dephosphorylated with bacterial alkaline phosphatase as described in the art.

B. Expression of HGBV-A and HGBV-B sequences.

E. coli XL1 Blue cultures containing the CKS/HGBV expression vectors were grown at 37°C with shaking in media containing 32 gm/L tryptone, 20 gm/L yeast extract, 5 gm/L NaCl, pH7.4, plus 100 mg/L ampicillin and 3mM glucose. When the cultures reached an OD600 of between 1.0 and 2.0, IPTG was added to a final concentration of 1mM to induce expression from the modified lac promoter. Cultures were allowed to grow at 37°C with shaking for an additional 3 hours, and were then harvested. The cell pellets were resuspended to an OD600 of 10 in SDS/PAGE loading buffer (62.5mM Tris pH6.8, 2% SDS, 10% glycerol, 5% 2-mercaptoethanol, and 0.1 mg/ml bromophenol blue), and boiled for 5 minutes. Aliquots of the prepared whole cell lysates were run on a 10% SDS-polyacrylamide gel, stained in a solution of 0.2% Coomassie blue dye in 40% methanol/10% acetic acid and destained in 16.5% methanol/5% acetic acid until a clear background was obtained.

The whole cell lysates were run on a second 10% SDS-polyacrylamide gel, and electrophoretically transferred to nitrocellulose for immunoblotting. The nitrocellulose sheet containing the transferred proteins was incubated in blocking solution (5% Carnation nonfat dry milk in Tris-buffered saline) for 30 minutes at room temperature followed by incubation for 1 hour at room temperature in goat anti-CKS sera which had been preblocked against E. coli cell lysate then diluted 1:1000 in blocking solution. The nitrocellulose sheet was washed two times with Tris-buffered saline (TBS), then incubated for 1 hour at room temperature with alkaline phosphatase-conjugated rabbit anti-goat IgG, diluted 1:1000 in blocking solution. The nitrocellulose was washed two times with TBS and the color was developed in TBS containing nitroblue tetrazolium and 5-bromo-4-chloro-3-indolyl phosphate. The appropriate reading frame for each fragment was identified based

on expression of an immunoreactive CKS fusion protein of the correct predicted size, and further confirmed by DNA sequencing across the vector-insert junction.

After determining the appropriate reading frame for each of the fragments, samples from cultures containing the appropriate constructs were analyzed by SDS-polyacrylamide gel electrophoresis and Western blot. FIGURE 25A shows 2 Coomassie-stained 10% SDS-polyacrylamide gels containing the CKS fusion protein whole cell lysates. Lanes 1 and 16 contain molecular weight standards with the sizes in kilodaltons shown on the left. The loading order on gel 1 (HGBV-A samples) is as follows: lane 2, clone 1.17 prior to induction; lanes 3-15, clone 4.2, clone 1.17, clone 1.8, clone 1.2, clone 1.18 (SEQUENCE I.D. NO. 390), clone 1.19, clone 1.20, clone 1.21, clone 1.22 (SEQUENCE I.D. NO. 390), clone 2.12, clone 1.5, clone 1.23, and clone 2.18 respectively, all after 3 hours of induction. The loading order on gel 2 (HGBV-B samples) is as follows: lane 17, clone 4.1 prior to induction; lanes 18-29, clone 4.1, clone 1.15, clone 1.14, clone 2.8, clone 1.13, clone 1.12, clone 2.1, clone 1.7, clone 1.3, clone 1.4, clone 1.16, and clone 2.12 respectively, all after 3 hours of induction. These proteins were run on 2 additional 10% gels, in the same loading order, and transferred to nitrocellulose as described above. The samples were analyzed by Western blot using a pool of sera from 2 convalescent tamarins, T-1048 and T-1051, as follows: The nitrocellulose sheets containing the samples were incubated for 30 minutes in blocking solution, followed by transfer to blocking solution containing 10% *E. coli* lysate, 6mg/ml XL1-Blue/CKS lysate, and a 1:100 dilution of the pooled convalescent tamarin sera described in TABLE 6 (Example 4). After overnight incubation at room temperature, the nitrocellulose sheets were washed two times in TBS and then incubated for 1 hour at room temperature in HRPO-conjugated goat anti-human IgG, diluted 1:500 in blocking solution. The nitrocellulose sheets were washed two times in TBS and the color was developed in TBS containing 2 mg/ml 4-chloro-1-naphthol, 0.02% hydrogen peroxide and 17% methanol. As shown in FIGURE 25B, three HGBV-B proteins demonstrated immunoreactivity with the pooled tamarin sera; CKS fusions of clones 1.4, 1.7, and 4.1. Clone 1.7 contains the sequence encoding an HGBV-B immunogenic region (SEQUENCE I.D. NO. 610) and clone 1.4 contains the sequence encoding two HGBV-B immunogenic regions (SEQ. ID. NOS. 12, 13 and 18), identified by immunoscreening of a cDNA library (Example 4) using the same pool of convalescent tamarin sera.

The samples described in the previous paragraph were also analyzed by Western blot as above using a 1:100 dilution of convalescent serum obtained

approximately three weeks following the onset of acute hepatitis from the surgeon GB. The reactivities of the fusion proteins from HGBV-A and HGBV-B with this serum are indicated in TABLES 13 and 14. Only one HGBV-B protein (2.1) showed reactivity with this serum, and the reactivity was quite weak, while two
5 HGBV-A proteins (1.22 [SEQUENCE I.D. NO. 390] and 2.17) exhibited strong reactivity with this serum. These two HGBV-A proteins overlap by 40 amino acids, so this may reflect reactivity with one epitope or more than one epitope. These two HGBV-A proteins were chosen for use in ELISA assays as described in Example 16. It is of interest to note that although tamarins infected with the
10 eleventh passage GB material (H205 GB pass 11) demonstrate an immune response to several HGBV-B epitopes but no HGBV-A epitopes, serum from the original GB source demonstrates significant reactivity with at least one HGBV-A epitope. This suggests that HGBV-A may have been the causative agent of hepatitis in the surgeon GB.

15 Four additional human sera which had indicated the presence of antibodies to one or more of the CKS/HGBV-A or CKS/HGBV-B fusion proteins by the 1.4, 1.7, or 2.17 ELISAS (see Examples 15 and 16) were chosen for Western blot analysis. Three of these sera (G1-41, G1-14 and G1-31) are from the West African "at risk" population and the fourth (341C) is from a nonA-E hepatitis
20 (Egypt) sample (see Example 15 for detailed description of these populations). Additional 10% SDS-polyacrylamide gels containing the whole cell lysates from some of the CKS fusion proteins discussed above were run and transferred to nitrocellulose as described previously. Each of these blots was preblocked as described, then incubated overnight with one of the human serum sample diluted
25 1:100 in blocking buffer containing 10% *E. coli* lysate and 6mg/ml XL1-Blue/CKS lysate. The blots were washed two times in TBS, then reacted with HRPO-conjugated goat anti-human IgG and developed as indicated above.

The CKS/HGBV-B proteins were analyzed with two of these sera, G1-41 and G1-14, and the reactivities are indicated in TABLE 13. In addition to the three
30 proteins which showed reactivity with the tamarin sera, two additional proteins (1.16 and 2.1) showed reactivity with one or the other of the two human sera. The CKS/HGBV-A proteins were analyzed with all four of these human sera and the reactivities are indicated in TABLE 14. In addition to the two proteins which showed reactivity with GB serum, three additional proteins (1.5, 1.18, and 1.19)
35 showed reactivity with one or more of the human sera. Two of these (1.5 and 1.18) were chosen for use in ELISA assays as described in Example 16. It is of particular interest to note that the G1-31 serum, which shows reactivity by Western

blot and/or ELISA (Examples 15 and 16) with two HGBV-A proteins (1.18 and 2.17) and one HGBV-B protein (1.7), is the serum from which the GB-C sequence (SEQUENCE I.D. No. 673, residues 2274-2640) was isolated (Example 17).

TABLE 13
HGBV-B Samples

	PCR product ^a	Restriction digest ^b	Reactivity with T1048 + T1051 sera	Reactivity with GB sera	Reactivity with human G1-41 sera	Reactivity with human G1-14 sera
	1.3	EcoRI, PstI	-	-	-	-
15	1.4	EcoRI, XbaI	+	-	+	+
	1.7	EcoRI, HindIII	+	-	+	-
	1.12	KpnI, PstI	-	-	-	-
	1.13	EcoRI, XbaI	-	-	-	-
	1.14	BamHI, HindIII	-	-	-	-
20	1.15	EcoRI, PstI	-	-	-	-
	1.16	EcoRI, XbaI	-	-	+	-
	2.1	EcoRI, HindIII	-	+/-	-	+
	2.8	EcoRI, XbaI	-	-	-	-
	2.12	KpnI, PstI	-	-	-	-
25	4.1	EcoRI, BamHI	+	-	-	-

^aPCR product is as indicated in TABLE 9, TABLE 10, or Example 13. ^bRestriction digests used to liberate the PCR fragment from pT7Blue T-vector or for direct digestion of 4.1 PCR product.

**Example 14. Epitope mapping of immunoreactive
HGBV-A and HGBV-B proteins**

A. Epitope mapping of HGBV-B protein 1.7

Overlapping subclones within the HGBV-B immunogenic protein 1.7 were generated by RT-PCR from T1053 serum as described in Example 7 in order to determine the location of the immunogenic region or regions. Each PCR primer had six extra bases on the 5' end to facilitate restriction enzyme digestion, followed by either an EcoRI site (sense primers) or a HindIII site (antisense primers). In addition, each antisense primer contained a stop codon just after the coding region. After digestion, each fragment was cloned into EcoRI/HindIII-digested pJO201 as

described in Example 13. The CKS fusion proteins were expressed and analyzed by Western blot with tamarin T1048/T1051 sera as described in Example 13. Five overlapping clones, designated 1.7-1 through 1.7-5, were generated. The clones encoded regions of the 1.7 protein ranging in size from 104 to 110 amino acids.

- 5 The PCR primers used to generate each clone, the sizes of the encoded polypeptides, the location within the 1.7 sequence and the reactivity with tamarin T1048/T1051 sera are shown in TABLE 15. Two further overlapping clones were generated which encompassed the immunogenic region (SEQUENCE I.D. NO. 678) identified by immunoscreening of a cDNA library (Example 4). Each of
10 these clones, designated 1.7-6 and 1.7-7, encoded polypeptides of 75 amino acids. The PCR primers, sizes of encoded polypeptides, location within the 1.7 sequence and reactivity with tamarin T1048/T1051 sera are shown in TABLE 15. Two immunogenic regions were identified within the 507 amino acid long 1.7 protein; one near the N-terminus within residues 1-105, and another near the middle of the
15 protein, encompassing residues 185 to 410. It remains to be determined whether there is a single epitope or multiple epitopes within each of these regions.

B. Epitope mapping of HGBV-B protein 1.4

- Overlapping subclones within the HGBV-B immunogenic protein 1.4 were generated by RT-PCR from T1053 serum as above in order to determine the
20 location of the immunoreactive region or regions. Each PCR primer had six extra bases on the 5' end to facilitate restriction enzyme digestion, followed by either an EcoRI site (sense primers) or a BamHI site (antisense primers). In addition, each antisense primer contained a stop codon just after the coding region. After digestion, each fragment was cloned into EcoRI/BamHI-digested pJO201 as
25 described in Example 13. The CKS fusion proteins were expressed and analyzed by Western blot with tamarin T1048/T1051 sera as described in Example 13. Four overlapping clones, designated 1.4-1 through 1.4-4, were generated. The clones encoded regions of the 1.4 protein ranging in size from 137 to 138 amino acids. The PCR primers used to generate each clone, the sizes of the encoded
30 polypeptides, the location within the 1.4 sequence and the reactivity with tamarin T1048/T1051 sera are shown in TABLE 15. Two further overlapping clones were generated which encompassed an immunogenic region identified by immunoscreening of a cDNA library (Example 4). Each of these clones, designated 1.4-5 and 1.4-6, encoded polypeptides of 75 amino acids. The PCR
35 primers, sizes of encoded polypeptides, location within the 1.4 sequence and reactivity with tamarin T1048/T1051 sera are shown in TABLE 15. A 265 amino acid sequence was identified as being the immunogenic region within the 522

amino acid long 1.4 protein, encompassing residues 129 to 393. It is likely that there are at least two epitopes within this region, since library immunoscreening (Example 4) identified two immunogenic non-contiguous clones within this sequence.

5 C. Epitope mapping of HGBV-A proteins 1.22 (SEQUENCE I.D. NO. 390) and 2.17

The HGBV-A proteins 1.22 (SEQUENCE I.D. NO. 390) and 2.17 (SEQUENCE I.D. NO. 613) both showed immunoreactivity with GB serum by Western blot (Example 13). Since these two proteins overlap by 40 amino acids, 10 the observed immunoreactivity may have resulted from the presence of one epitope or more than one epitope. The complete 1.22/2.17 sequence is 641 amino acids long. Overlapping subclones within this region were generated by RT-PCR from T1053 serum as above in order to determine the location of the immunogenic region or regions. Each PCR primer had six extra bases on the 5' end to facilitate 15 restriction enzyme digestion, followed by either an EcoRI site (sense primers) or a BamHI site (antisense primers) for 1.22/2.17-2 through 1.22/2.17-6. However, since clone 1.22/2.17-1 had an internal EcoRI site, a BamHI site was used in the sense primer and a HindIII site was used in the antisense primer. In addition, each antisense primer contained a stop codon just after the coding region. After 20 digestion, each fragment was cloned into EcoRI/BamHI-digested (or BamHI/HindIII-digested for 1.22/2.17-1) pJO201 as described in Example 13. The CKS fusion proteins were expressed and analyzed by Western blot with GB serum as described in Example 13. The clones encoded regions of 1.22/2.17 ranging in size from 115 to 116 amino acids. The PCR primers used to generate 25 each clone, the sizes of the encoded polypeptides, the location within the HGBV-A polypeptide sequence and the reactivity with GB serum are shown in TABLE 15. The immunogenic region was narrowed down to a 220 amino acid long region in the middle of the 1.22/2.17 protein. This encompassed the 40 amino acid region of overlap between 1.22 and 2.17, and thus the immunoreactivity seen with the 30 two proteins individually may have been due to a shared epitope or to multiple epitopes.

TABLE 15

	CLONE	SIZE OF ENCODED POLYPEPTIDE	PRIMER SET	T1048/T1051 REACTIVITY	RESIDUES IN SEQ I.D. NO. 120
5	1.7-1	105 aa	SEQ ID #615/SEQID #616	+	1-105
	1.7-2	109 aa	SEQ ID #617/SEQID #618	-	98-206
	1.7-3	110 aa	SEQ ID #619/SEQID #620	+	199-308
	1.7-4	110 aa	SEQ ID #621/SEQID #622	+/-	301-410
	1.7-5	104 aa	SEQ ID #623/SEQID #624	-	403-507
10	1.7-6	75 aa	SEQ ID #625/SEQID #626	+	185-259
	1.7-7	75 aa	SEQ ID #627/SEQID #628	+	251-325
	CLONE	SIZE OF ENCODED POLYPEPTIDE	PRIMER SET	T1048/T1051 REACTIVITY	RESIDUES IN SEQ I.D. NO. 119
15	1.4-1	137 aa	SEQ ID #629/SEQID #630	-	1-137
	1.4-2	137 aa	SEQ ID #631/SEQID #632	+	129-265
	1.4-3	137 aa	SEQ ID #633/SEQID #634	+	257-393
	1.4-4	138 aa	SEQ ID #635/SEQID #636	-	385-522
20	1.4-5	75 aa	SEQ ID #637/SEQID #638	+	138-212
	1.4-6	75 aa	SEQ ID #639/SEQID #640	+	204-278
	CLONE	SIZE OF ENCODED POLYPEPTIDE	PRIMER SET	GB SERUM REACTIVITY	RESIDUES IN SEQ I.D. NO. 390
25	1.22/2.17-1	115 aa	SEQ ID #641/SEQID #642	-	1862-1976
	1.22/2.17-2	115 aa	SEQ ID #643/SEQID #644	-	1967-2081
	1.22/2.17-3	115 aa	SEQ ID #645/SEQID #646	+	2072-2186
	1.22/2.17-4	115 aa	SEQ ID #647/SEQID #648	+	2177-2291
30	1.22/2.17-5	115 aa	SEQ ID #649/SEQID #650	-	2282-2396
	1.22/2.17-6	116 aa	SEQ ID #651/SEQID #652	-	2387-2505

Example 15. Serological Studies HGBV-B

A. Recombinant Protein Purification Protocol

Bacterial cell cultures expressing the CKS fusion proteins were frozen and stored at -70°C. The bacterial cells from each of the three constructs were thawed and disrupted by treating with lysozyme and DNase, followed by sonication in the presence of phenylmethanesulfonyl fluoride and other protease inhibitors to produce mixtures of the individual recombinant antigen and *E. coli* proteins. Individually for each of the three cultures, the insoluble recombinant antigen was concentrated by centrifugation and subjected to a series of sequential washes to eliminate the majority of non-recombinant *E. coli* proteins. The washes used in this protocol included distilled water, 5% Triton X-100 and 50 mM Tris (pH 8.5). The resulting pellets were solubilized in the presence of sodium dodecyl sulfate (SDS). After determining protein concentration, 2-mercaptoethanol was added and the mixtures were subjected to gel filtration column chromatography, with Sephacryl S300 resin used to size and separate the various proteins. Fractions were collected and analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). The electrophoretically separated proteins were then stained with Coomassie Brilliant Blue R250 and examined for the presence of a protein having a molecular weight of approximately 75 kD (CKS-1.7/SEQUENCE I.D. NO. 610), 80 kD (CKS-1.4/SEQUENCE I.D. NO. 611), 42 kD (CKS-4.1/SEQUENCE I.D. NO. 612). Fractions containing the protein of interest were pooled and re-examined by SDS-PAGE.

The immunogenicity and structural integrity of the pooled fractions containing the purified antigen were determined by immunoblot following electrotransfer to nitrocellulose as described in Example 13. In the absence of a qualified positive control, the recombinant proteins were identified by their reactivity with a monoclonal antibody directed against the CKS portion of each fusion protein. When the CKS-1.7 protein (SEQUENCE I.D. NO. 610) was examined by Western blot, using the anti-CKS monoclonal antibody to detect the recombinant antigen, a single band at approximately 75 kD was observed. This corresponds to the expected size of the CKS-1.7 protein (SEQUENCE I.D. NO. 610). For the CKS-1.4 protein (SEQUENCE I.D. NO. 611), the anti-CKS monoclonal antibody detects a quadruplet banding pattern between 60 and 70 kD. These observed bands are smaller than the expected size of the full length protein and probably represent truncation products. When the CKS-4.1 protein (SEQUENCE I.D. NO. 52) was examined by Western blot, the anti-CKS monoclonal antibody detected the recombinant antigen as a single band at

approximately 42 kD. This corresponds to the expected size of the CKS-4.1 protein (SEQUENCE I.D. NO. 612).

B. Polystyrene Bead Coating Procedure

5 The proteins were dialyzed and evaluated for their antigenicity on polystyrene coated beads as described below. Separate enzyme-linked immunosorbent assays (ELISA's) were developed for detecting antibodies to HGBV using each of the three purified HGBV recombinant proteins (CKS-1.7 (SEQUENCE I.D. NO. 610); CKS-1.4 (SEQUENCE I.D. NO. 611); and the
10 CKS-4.1 protein (SEQUENCE I.D. NO. 612). The ELISA's developed with these proteins are referred to as the 1.7 ELISA (utilizing the CKS-1.7 (SEQUENCE I.D. NO. 610) recombinant protein), the 1.4 ELISA (utilizing the CKS-1.4 (SEQUENCE I.D. NO. 611) recombinant protein), the 4.1 ELISA (utilizing the CKS-4.1 [SEQUENCE I.D. NO. 612]) recombinant protein. In the
15 first study, one-quarter inch polystyrene beads were coated with various concentrations with each of the purified proteins (approximately 60 beads per lot) and evaluated in an ELISA test (described below) using serum from an uninoculated tamarin as a negative control and convalescent sera from an
20 inoculated tamarin as a positive control. Additional controls included the a pool of human serum from individuals testing negative for various hepatitis viruses. An additional positive control consisted of monoclonal antibodies to the CKS protein to monitor the efficiency of bead coating. The bead coating conditions providing the highest ratio of positive control signal to negative control signal were selected for scaling up the bead coating process. For each of the four ELISA's at least two
25 lots of 1,000 beads were produced and utilized for serological studies.

Briefly, polystyrene beads were coated with the purified proteins by adding the washed beads to a scintillation vial and immersing the beads (approximately 0.233 ml per bead) in a buffered solution containing the recombinant antigen. Several different concentrations of each of the recombinant antigens were evaluated
30 along with several different buffers prepared at pHs ranging from pH 5.0 to pH 9.5. The vials were then placed on a rotating device in a 40°C incubator for 2 hours after which the fluids were aspirated and the beads were washed three times in phosphate buffered saline (PBS), pH 6.8. The beads were then treated with 0.1% Triton X-100 for 1 hour at 40°C and washed three times in PBS. Next, the beads
35 were overcoated with 5% bovine serum albumin and incubated at 40°C for 1 hour with agitation. After additional washing steps with PBS, the beads were overcoated with 5% sucrose for 20 minutes at room temperature and the fluids

were aspirated. Finally, the beads were air dried and then utilized for developing ELISA's for detection of antibodies to HGBV.

C. ELISA Protocol for Detection of Antibodies to HGBV

5 An indirect assay format was utilized for the ELISA's. Briefly, sera or plasma was diluted in specimen diluent and reacted with the antigen coated solid phase. After a washing step, the beads were reacted with horseradish-peroxidase (HRPO) labeled antibodies directed against human immunoglobulins to detect tamarin or human antibodies bound to the solid phase. Specimens which produced signals above a cutoff value were considered reactive. Additional details pertaining to the ELISA's are described below.

10 The format for the ELISA's entails contacting the antigen-coated solid phase with tamarin serum pre-diluted in specimen diluent (buffered solution containing animal sera and non-ionic detergents). This specimen diluent was formulated to reduce background signals obtained from non-specific binding of immunoglobulins to the solid phase while enhancing the binding of specific antibodies to the antigen-coated solid phase. Specifically, 10 µl of tamarin serum was diluted in 150 µl of specimen diluent and vortexed. Ten microliters of this pre-diluted specimen was then added to the well of a reaction tray, followed by the addition of 200 µl of specimen diluent and an antigen coated polystyrene bead.

15 The reaction tray was then incubated in a Dynamic Incubator (Abbott Laboratories) set for constant agitation at room temperature. After a 1 hour incubation, the fluids were aspirated, and the wells containing the beads were washed three times in distilled water (5 ml per wash). Next, 200 µl of HRPO-labeled goat anti-human immunoglobulins diluted in a conjugate diluent (buffered solution containing animal sera and non-ionic detergents) was added to each well and the reaction tray was incubated again as above for 1 hour. The fluids were aspirated and the wells containing the beads were washed three times in distilled water as above. The beads containing antigen and bound immunoglobulins were removed from the wells, each was placed in a test tube and reacted with 300 µL of a solution of

20 0.3% *o*-phenylenediamine-2 HCl in 0.1 M citrate buffer (pH 5.5) with 0.02% H₂O₂. After 30 minutes at room temperature, the reaction was terminated by the addition of 1 N H₂SO₄. The absorbance at 492 nm was read on a spectrophotometer. The color produced was directly proportional to the amount of antibody present in the test sample.

25 For each group of specimens, a preliminary cutoff value was set to separate those specimens which presumably contain antibodies to the HGBV epitope from those which did not.

D. Detection of HGBV derived RNA in Serum from Infected Individuals.

In order to correlate serological data obtained for 1.7 and 1.4 ELISA's with the presence of HGBV RNA in tamarin serum or in human serum/plasma, RT-PCR was performed as described in Example 7 of U.S. Serial No. 08/283,314, previously incorporated herein by reference utilizing oligonucleotides derived from HGBV cloned sequences, at a final concentration of 0.5 μ M for clone 4 (as described in Example 7) derived from the HGBV-B genome and for clone 16, derived from the HGBV-A genome.

E. Tamarin Serological Profiles.

Serum was obtained from tamarins housed at LEMSIP on a weekly basis and tested for liver enzyme levels; the remaining volume from these specimens was sent to Abbott Laboratories for further studies.

1. ELISA Results on Tamarins (Initial Infectivity Studies)

Four tamarins (T-1053, T-1048, T-1057 and T-1061) were inoculated with GB serum (designated as H205 GB passage 11). Elevated liver enzymes were noted in Tamarin T-1053 during the first week post-inoculation (PI): this tamarin was euthanized on day 12 PI. Tamarins T-1048, T-1057 and T-1061 exhibited elevated liver enzyme values within two weeks following their inoculation; these elevated values persisted until 8-9 weeks PI (FIGURES 2-4) before returning to pre-inoculation levels. On week 14 PI, these three tamarins were re-challenged with 0.10 ml of neat serum obtained from tamarin T-1053 (which was shown to be infectious - Example 2).

Sera from three convalescing tamarins (T-1048, T-1057 and T-1061) were tested for antibodies to the CKS-1.7 (SEQUENCE I.D. NO. 610) recombinant protein, the CKS-1.4 (SEQUENCE I.D. NO. 611) recombinant protein, and the CKS 4.1 (SEQUENCE I.D. NO. 612) recombinant protein, using separate ELISA's (FIGURES 3, 4 and 5). Specific antibodies to 1.7 (SEQUENCE I.D. NO. 610), 1.4 (SEQUENCE I.D. NO. 611), 4.1 (SEQUENCE I.D. NO. 612, or 1.5 (SEQUENCE I.D. NO. 614) recombinant proteins were not detected in any of the pre-inoculation specimens.

As shown in FIGURE 26, specific antibodies were detected in T-1048 sera with the 1.7 and 1.4 ELISA's on days 56-84 but not on days 97 and 137 PI. Specific antibodies were not detected in T-1048 sera tested with the 4.1 ELISA. As shown in FIGURE 27, antibodies to the 1.7 protein (SEQUENCE I.D. NO. 610) were detected in T-1057 serum at 56 and 63 days PI, but not after 63 days PI. Antibodies to the 4.1 protein (SEQUENCE I.D. NO. 612) were detected on days 28-63 PI but not on days 84-97 PI. As noted above, tamarins were

challenged with a second dose of the H205 inoculum on day 97 PI. Specific antibodies to the 4.1 protein (SEQUENCE I.D. NO. 612) were detected on days 112 and 126 PI, suggesting an anamnestic response to the inoculum. No antibody reactivity was noted for the 1.4 recombinant protein (SEQUENCE I.D. NO. 611).

Specific antibodies to the recombinant 1.4 protein (SEQUENCE I.D. NO. 611) were detected in the serum of tamarin T-1061 between 84 and 112 days PI, but were not detected after 126 days PI. As shown in FIGURE 28, Tamarin T-1061 sera were negative for antibodies to the 1.7 protein (SEQUENCE I.D. NO. 610) and to the 4.1 protein (SEQUENCE I.D. NO. 612) for 350 days PI.

2. PCR Results on Tamarins (Initial Infectivity Studies)

Selected sera obtained from tamarins T-1048 and T-1057 were tested for HGBV RNA via RT-PCR using primers from clone 4 as described in Example 7) and from clone 16 as described in Example 7.

HGBV RNA was not detected via RT-PCR with either set of primers in the serum obtained 10 and 17 days prior to inoculation (T-1048) as shown in FIGURE 26, or 17, 37 and 59 days prior to inoculation (T-1057), as shown in FIGURE 27. For T-1048, HGBV RNA was detected via RT-PCR using primers from clone 4 on fifteen of seventeen different sera obtained between 7-137 days PI. HGBV RNA was not detected via RT-PCR using primers from clone 16 in any of the 10 sera obtained on days 7-97 PI. After the challenge with T-1053 plasma, four of five sera obtained between 8 and 40 days after the challenge were positive for clone 16. For T-1057, positive RT-PCR results were obtained on four sera obtained on days 7-28 PI, using primers from clone 4, as shown in FIGURE 27. RT-PCR performed on specimens drawn beyond day 28 PI were negative for clone 4, except for day 287 which showed a weak hybridization signal. Neither of the six specimens obtained from T-1057 on day 7-97 PI were positive via RT-PCR using primers from clone 16. However, sera obtained between 8-85 days after the T-1053 challenge were positive using primers from clone 16.

3. ELISA Results on Tamarins (Titration/Transmissibility Studies)

As described in Example 2, serum from tamarin T-1053 was inoculated into four tamarins. Three of these four tamarins were euthanized during the acute stage of the disease (between days 12 and 14 PI). The RT-PCR results obtained on these three tamarins are described below. The surviving tamarin (T-1051) first developed elevated liver enzyme values by day 14 PI and these values persisted for at least 8 weeks PI. Specimens from tamarin T-1051 were tested in the 1.7 and 1.4 ELISA's; the results are shown in FIGURE 29. Specific antibodies were not detected in the pre-inoculation serum nor in serum drawn in the first 41 days PI.

However, an antibody response was noted against the 1.4 protein (SEQUENCE I.D. NO. 611), and the 1.7 protein (SEQUENCE I.D. NO. 610) between 49 and 113 days PI and the 4.1 protein (SEQUENCE I.D. NO. 612) between 28 and 105 days PI. The tamarin was euthanized during the 113th day PI.

5 Tamarin (T-1034) was previously inoculated with 0.1 ml of potentially infectious serum obtained from a patient (original GB source) who was recovering from a recent hepatitis infection as described in Example 1 and in TABLE 4. No elevations in liver enzyme values were noted in T-1034 for nearly 10 weeks after inoculation. For this reason, it was decided that tamarin T-1034 could be used in
10 an additional study. Tamarin T-1034 was inoculated with a preparation of HGBV prepared as described in Example 4 ?? from a pool of serum obtained from three tamarins (T-1055, T-1038 and T-1049) previously inoculated with serum from tamarin T-1053.

These three tamarins (T-1055, T-1038 and T-1049) were inoculated with
15 serum prepared from tamarin T-1053 as described in Example 2. Elevated liver enzyme values were noted in all 3 tamarins by day 11 PI. Tamarin T-1055 was sacrificed on day 12 PI; tamarins T-1038 and T-1049 were sacrificed on day 14 PI. Serum from these tamarins was pooled, clarified and filtered. Tamarin T-1034 was inoculated with 0.25 ml of a 10^{-6} dilution (prepared in normal tamarin
20 serum) of this filtered material.

Elevated ALT liver enzyme values were first noted in T-1034 at 2 weeks PI, and remained elevated for the next 7 weeks, finally normalizing by week 10 PI. As demonstrated in FIGURE 30, a specific antibody response to the 1.4 (SEQUENCE I.D. NO. 22) recombinant protein was first detected on day 49 PI
25 and continued to be detected on days 56-118 PI. The antibody response to the 4.1 (SEQUENCE I.D. NO. 52) recombinant protein was first detected on day 49 PI and continued to be detected between days 56-77 PI, but was not detected on between days 84-118 PI. The antibody response to the 1.7 (SEQUENCE I.D. NO. 610) recombinant protein was first detected on day 56 PI and continued to be
30 detected between days 63-118 PI. The tamarin was sacrificed on day 118 PI.

As described in Example 2, tamarin T-1044 was inoculated with serum obtained from T-1057 that had been obtained 7 days after the H205 inoculation. This inoculum was positive only for sequences detected with clone 4 primers. The inoculum was negative by RT-PCR with clone 16 primers. Mild elevations in
35 ALT levels above the cutoff were observed from days 14-63 PI. As demonstrated previously, a specific antibody response to the 1.7 (SEQUENCE I.D. NO. 610) recombinant protein was detected between 63-84 days PI. No antibody response

to the 4.1 (SEQUENCE I.D. NO. 612) recombinant protein or to the 1.4 (SEQUENCE I.D. NO. 611) recombinant protein was detected. The tamarin was sacrificed on 161 days PI.

4. PCR Results on Tamarins (Titration/Transmissibility Studies)

5 Sera obtained from T-1049 and T-1055 during the 8th week prior to inoculation and T-1038 on the day of inoculation, were negative by RT-PCR for sequences to clone 16 (SEQUENCE I.D. NO. 26) and clone 4 (SEQUENCE I.D. NO. 21). Tamarins T-1049 and T-1055 were positive for clone 4 sequences (SEQUENCE I.D. NO. 21) by RT-PCR 1 week after inoculation (clone 16 PCR was not done). Prior to the day of sacrifice, T-1049 (14 days PI) as well as T-1055 (11 days PI) were positive by RT-PCR for both clone 4 (SEQUENCE I.D. NO. 21) and clone 16 sequences (SEQUENCE I.D. NO. 26). Tamarin T-1038 was positive with both sets of primers on the day of sacrifice (14 days PI).

15 As seen in FIGURE 30, T-1034 was positive by RT-PCR for sequences detected with clone 4 primers on the first serum sample obtained after inoculation (7 days PI) and remained positive to day 70 PI. A sample obtained on day 112 PI was negative. All of these samples were negative by RT-PCR with clone 16 primers. Samples obtained 70 and 101 days prior to inoculation were negative with both sets of primers.

20 As can be seen in FIGURE 29 for tamarin T-1051, HGBV RNA was not detected with either set of primers (from clones 4 and 16 as described above) in the serum specimen obtained 8 weeks prior to inoculation. HGBV RNA was detected by RT-PCR using primers from clone 4 on six sera obtained between days 7-69 PI, but not on days 77, 84, 91, or 105 PI. HGBV RNA was detected by RT-PCR using primers from clone 16 on nine samples obtained after inoculation.

25 As seen in FIGURE 7, T-1044 was positive by RT-PCR for sequences detected with clone 4 primers on the first serum sample obtained after inoculation (7 days PI) and remained positive to day 63 PI. Samples obtained between days 77-119 were negative. All of these samples were negative by RT-PCR with clone 16 primers. A sample obtained 42 days prior to inoculation was negative for both sets of primers.

30 Tamarins T-1047 and T-1056 were inoculated with T-1044 serum obtained 14 days PI. Nine samples obtained between 7- 64 days PI from both of these animals were positive by RT-PCR with clone 4 primers (SEQUENCE I.D. NOS. 8 and 9) but negative with clone 16 primers.

35 Tamarin T-1058 was inoculated with neat T-1057 serum obtained 22 days after the challenge with T-1053 serum. This inoculum was positive for sequences

detected with clone 16 primers but negative with clone 4 primers. Serum samples obtained from this animal were tested with primers derived from GBV- sequences [clone 16 , clone 2 clone 10 and clone 18]] and GB-B sequences [clone 4 and clone 50]. A sample obtained 9 days prior to inoculation was negative with all primer sets. A sample obtained 14 days PI was positive only with clone 10 and 18 primers. A sample obtained 21 days PI was positive only with clone 16 , 10 and 18 primers. A sample obtained 28 days PI was positive only with clone 18 primers. A sample obtained 35 days PI was positive only with clone 2, 16 (and 18 primers. A sample obtained 41 days PI was positive only with clone 16 and 18 primers. All samples tested were negative with primers from clone 4 and clone 50

5. Summary of Serological Studies in Tamarins

Five tamarins were inoculated with various preparations of HGBV and developed elevated liver enzyme values by two weeks PI. These elevations persisted for the next six to eight weeks. A specific antibody response to one or more HGBV recombinant antigens, 1.7, 1.4, and 4.1 was noted in all five tamarins. In all cases, the antibodies were first detected by six to ten weeks PI, and persisted for two to seven or more weeks. In general, the antibody levels peaked and then declined rapidly over the next several weeks. It is observed that the antibodies become detectable shortly after the liver enzyme values returned to normal levels, suggesting that the generation of antibodies may play a role in clearing the viral infection.

6. Summary of PCR Studies on Tamarins

The results of the genomic walking experiments suggest that clone 4 (SEQUENCE I.D. NO.21) and clone 16 (SEQUENCE I.D. NO. 26) reside on separate RNA molecules. We previously provided arguments that supported the idea that there are two distinct viral genomes, one comprised partly of clone 4 (SEQUENCE I.D. NO.21) and one comprised partly of clone 16 (SEQUENCE I.D. NO. 26). The observation that some animals are positive with primers from clone 4 and not with primers from clone 16 supported the existence of two distinct viral genomes. However, it can also be argued that the inability to detect clone 16 (SEQUENCE I.D. NO. 26) sequence in some of the infected tamarins may reflect a lower limit of sensitivity of the clone 16 primer set relative to the clone 4 primer set. If this latter possibility was the case, then a tamarin positive for both primer sets should exhibit a difference in sensitivity with these two primer sets. In order to support the explanation that these results are explained by the existence of two separate viruses, and not differences in sensitivities of these two primer sets, PCR

was performed on a dilution series of cDNA from tamarins T-1057 and T1053. T-1057 serum was positive at 5×10^{-3} but negative at 5×10^{-4} ul serum equivalents with clone 4 primers. As much as 20 ul of T-1057 serum was used for RT-PCR with clone 16 primers with negative results. If this difference was due to the relative sensitivity of the two primer sets (clone 4 vs. clone 16), one would expect that other specimens would also show a 4000 fold higher endpoint dilution when tested by PCR. However, cDNA derived from T-1053 serum was found to be positive at 2.5×10^{-4} but negative at 2.5×10^{-5} ul serum equivalents for both clone 4 (SEQUENCE I.D. NO.21) and clone 16 (SEQUENCE I.D. NO. 26) sequences. These observations are therefore not consistent with a difference in sensitivity of primer sets but are consistent with the existence of contig B-clone 4 (SEQUENCE I.D. NO.21) and contig A-clone 16 (SEQUENCE I.D. NO. 26) sequences on separate viral genomes of roughly equal titer in T-1053 but differing in titer by at least 4000 fold in T-1057. This data is therefore consistent with the existence of two separate viruses which may have different relative endpoint titers in different specimens.

The observation that HGBV-B viremia alone was sufficient to cause elevations in liver enzyme levels and that no elevations were observed during a GBV-A-only viremic stage, indicated that HGBV-B was the probable causative agent for hepatitis in these tamarins. The immune response to the HGBV-B antigens appeared to be for a short duration, at most 150 days PI. One explanation could be that the selection of epitopes used in these ELISAs was not from the dominant epitopes to which the immune response is generated. Another explanation could be that in tamarins the hepatic challenge may not be significant enough to necessitate a long-lived response. This is consistent with histological evidence from animals that were sacrificed during the acute phase of the disease or had died of natural causes some time after the acute phase which showed that hepatic inflammation ranged from mild to not significant (results not shown).

Five of six animals described in this study resolved viremia of HGBV-B by 112 days PI. In contrast, Tamarin T-1048 remained viremic for 136 days and was found to be viremic at the time of death (137 days PI). Of the four animals that were positive for GBV-A sequence, three showed resolution by 77 days after the first appearance of GBV-A sequence. In contrast, tamarin T-1061 was viremic for 245 days up to the time the animal was sacrificed. In addition, tamarin T-1051 was viremic up to the time of sacrifice (day 113 PI), however, it is unclear if this persistent viremia is due to the initial inoculation with T-1053 plasma or a result of the subsequent challenge with additional T-1053 plasma 69 days later.

The average peak ALT value for the six animals positive for both HGBV-A and HGBV-B was higher than the average value for the four HGBV-B-only animals. In addition, the peak value occurred, on average, earlier in animals positive for GBV-A and GBV-B than for animals positive only for GBV-B. These results suggest that the intensity of the hepatitis may be related to the presence of both agents at significant levels. The observation from the additional passage of GBV-B into tamarins T-1047 and T-1056 that minimal elevation in liver enzymes occurred with GBV-B viremia supports this assumption that both agents may be necessary for major elevations in ALT levels to occur in tamarins. In addition to the passage of HGBV-B alone, initial results from the inoculation of T-1058 with HGBV-A inoculum suggest that HGBV-A can be transmitted independent of any detectable HGBV-B as indicated by the absence of any detectable GB-B sequences with clone 4 and clone 50 primers.

F. Experimental Protocol for demonstrating exposure to HGBV in human populations

Specimens were obtained from various human populations and tested for antibodies to HGBV utilizing three separate ELISA's utilizing recombinant proteins derived from HGBV-B. The 1.7 ELISA utilized the CKS-1.7 recombinant protein (SEQUENCE I.D. NO.610) coated onto the solid phase; the 1.4 ELISA utilized the CKS-1.4 recombinant proteins (SEQUENCE I.D. NO.611) coated on the solid phase and the 4.1 ELISA utilized the 4.1 recombinant protein (SEQUENCE I.D. NO.612) coated on the solid phase as described in Example 15.B. As also noted in Example 15.E, tamarins inoculated with HGBV produce a specific, but short-lived antibody response to these proteins. In view of the transient nature of this detectable immune response, a negative result in human populations would not necessarily exclude previous exposure to HGBV.

The objective of the serological studies conducted with human specimens was two-fold. First, the seroprevalence of antibodies to the current HGBV recombinant antigens in various human populations was to be determined. These studies included testing (1) populations considered at "low risk" for exposure to HGBV (e.g. healthy volunteer blood donors in U.S.); (2) populations considered to be "at risk" for exposure to HGBV (e.g. specimens obtained from intravenous drug users and hemophiliacs are frequently seropositive for parenterally transmitted hepatitis viruses (HBV and HCV); specimens obtained from individuals residing in developing nations are frequently seropositive for enterically transmitted viruses (HAV and HEV); (3) panels of specimens obtained from individuals with "non-A-E hepatitis" that is not associated with exposure to

known hepatitis viruses (HAV, HBV, HCV, HDV or HEV) or to other viruses associated with hepatitis such as cytomegalovirus (CMV) or Epstein-Barr Virus (EBV). In some cases, members of the panels under the general heading of non A-E hepatitis were not tested for antibodies to HEV. Therefore, all specimens in the non A-E group which were reactive with the 1.7, 1.4 or 4.1 ELISA's were retested with an HEV ELISA assay (available from Abbott Laboratories, Abbott Park, IL). Positive anti-HEV results were noted with samples from three sites (Pakistan, U.S. and New Zealand), as explained hereinbelow.

One would expect to observe higher seroprevalence rates among populations "at risk" for exposure to HGBV and among individuals with non-A-E hepatitis, than among populations considered to be at "low risk" for exposure to HGBV.

The second objective of the serological studies was to examine specimens found to be positive for antibodies to one or more HGBV epitopes by RT-PCR to determine if the virus is present in serum. It is well known that HBV and HCV can establish a viremic state which persists for months or years, and in general, that HAV and HEV establish a short-lived viremia persisting in general for several weeks. In cases of HBV and HCV infection which are acute, resolving hepatitis, the viremic stage may also be short-lived persisting for several weeks. Thus, RT-PCR can be used to provide evidence that the virus is present in an infected individual. However, because the viremic state can be short-lived, a negative RT-PCR result for a given agent can be observed in individuals who are infected with that agent.

G. Cutoff Determination

Previous experience with other ELISA's utilizing the indirect assay format indicated that a preliminary cutoff value can be calculated based on the absorbance values obtained on a population presumably negative for antibodies to the protein being studied. A preliminary cutoff value was calculated as the sum of the mean absorbance value of the population plus 10 standard deviations from the population mean. Since the cutoff value was to be used every time a panel was run, a more convenient method to express the cutoff was as a factor of the negative control (pool of normal human plasma - NHP) which was run in replicates of five for each assay run. For the 1.7, 1.4 and 4.1 ELISA's, the negative control typically had an absorbance value of between 0.030 and 0.060. As described below, the cutoff values were calculated to be at an absorbance value of approximately 0.300 to 0.600, which was equivalent to an absorbance signal of ten times the negative control value. Thus, in order for a specimen to be considered reactive, the ratio of

the sample (S) absorbance value to the negative (N) control absorbance value (S/N ratio) had to be equal to or greater than 10.0.

H. Supplemental Testing

Specimens which were initially reactive were typically retested in duplicate.

5 If one or both of the retest absorbance values were above the cutoff value, the specimen was considered repeatably reactive. Specimens which were repeatably reactive were then tested with supplemental assays which may further support the ELISA data. Repeatably reactive specimens which had sufficient volume may be tested by Western blot to determine that the antibody response was directed against
10 the CKS-1.7 (SEQUENCE I.D. NO. 610), a CKS-1.4 (SEQUENCE I.D. NO. 611) or CKS 4.1 (SEQUENCE I.D. NO. 612) antigens and not to E. coli proteins which may have been co-coated on the solid phase with the major protein of interest. For a Western blot result to be considered positive, a visible band had to be detected at 80kD for the 1.7 protein (SEQUENCE I.D. NO. 610), 60-70 kD
15 for the 1.4 protein (SEQUENCE I.D. NO. 611) or at 42 kD for the 4.1 protein (SEQUENCE I.D. NO. 612). Since the Western blot has not been optimized to match or exceed the sensitivity of the ELISA's, a negative result was not used to discard the ELISA data. However, a positive result reinforced the reactivity detected by the ELISA's.

20 Repeatably reactive specimens which had sufficient volume may be tested by RT-PCR (performed as described in Example 15.D using clone 4 primers to identify HGBV specific nucleotide sequences in serum. A positive result would indicate a viremic specimen and would ultimately help in establishing the role of HGBV in human hepatitis. A negative result, however, was not to be construed to
25 indicate that the ELISA results was incorrect. As noted in the tamarin study in Example 15.E, RT-PCR results were positive in the first several weeks after infection and then became negative at about the time when antibodies were just beginning to be detected with the current ELISA's. These later specimens may be RT-PCR negative but positive in one or both of the ELISA's.

30 I. Serological Data Obtained with Low-Risk Specimens

A population consisting of 100 sera and 100 plasma was obtained from healthy, volunteer blood donors in Southeastern Wisconsin and tested for antibodies to the 1.7 (SEQUENCE I.D. NO. 610) and 1.4 (SEQUENCE I.D. NO. 611) and 4.1 (SEQUENCE I.D. NO. 612) recombinant proteins utilizing the
35 ELISA's described above. The absorbance values obtained with the 1.7, 1.4 and 4.1 ELISA's for serum and plasma were plotted separately (FIGURES 9-14).

For the 1.7 ELISA, the mean absorbance values for the serum and plasma specimens were 0.072 [with a standard deviation (SD) of 0.061] and 0.083 (SD=0.055), respectively. Thus, for the 1.7 ELISA's, the tentative cutoff values for serum and plasma were 0.499 and 0.468, respectively. As discussed above, the cutoff also was expressed as a factor of the negative control absorbance value; specimens having S/N values above 10.0 were considered reactive. Using this cutoff value, 0 of 200 specimens tested for antibodies to 1.7 (SEQUENCE I.D. NO. 610).

For the 1.4 ELISA, several specimens (three from the serum population and six from the plasma population) had absorbance values greater than 0.300 (S/N's of 6-12, near or above the expected cutoff value). When retested, all nine of these specimens produced S/N values of less than 10.0. The mean absorbance value for the serum and plasma specimens were 0.072 (SD=0.052) and 0.108 (SD=0.062), respectively. The cutoff for the 1.4 ELISA was calculated using the formula described above; the cutoff values for serum and plasma populations were 0.436 and 0.542, respectively. One specimen from the serum population was initially reactive and when re-tested in duplicate was negative. Two specimens from the plasma population were initially reactive but were negative upon re-test. A second population of 200 normals was tested including 100 plasma and 100 serum. Using the proposed cutoff, two plasma and two sera were repeatably reactive.

For the 4.1 ELISA, the mean absorbance values for the serum and plasma specimens were 0.070 [with a standard deviation (SD) of 0.037] and 0.063 (SD=0.040), respectively. Thus, for the 4.1 ELISA, the tentative cutoff values for serum and plasma were 0.329 and 0.511, respectively. As discussed above, the cutoff also was expressed as a factor of the negative control absorbance value; specimens having S/N values above 10.0 were considered reactive. Using this cutoff value, 0 of 100 plasma specimens and 0 of 100 serum specimens were initially reactive for antibodies to 4.1 (SEQUENCE I.D. NO.612).

An additional 760 plasma donors from the Interstate Blood Bank (Ohio) were tested with the 1.7 and 1.4 ELISAs. A total of 9 specimens were repeatably reactive. None of the specimens were reactive in both ELISAs. All 9 specimens were repeatably reactive with the 1.4 ELISA.

In total, 960 specimens from plasma or blood donors residing in the U.S. were tested for antibodies to the 1.7 and 1.4 proteins. A total of 13 specimens were repeatably reactive by the 1.4 ELISA. None of the specimens were repeatably reactive with the 1.7 ELISA.

In summary, these data indicate that, with the existing ELISA's, a total of 13 of 960 specimens obtained from U.S. blood donors were reactive for antibodies in one or more of the ELISA's employing recombinant antigens from HGBV-B. These data suggest that HGBV may be endemic in the U.S.

5 These data are summarized in TABLE 16.

J. Specimens Considered "At Risk" for Hepatitis

The data for these studies is summarized in TABLE 16.

(i) Specimens from West Africa

10 A total of 181 of 1300 specimens obtained from West Africa were repeatedly reactive in one or more of the ELISA's. One specimen was repeatedly reactive in all 3 ELISA's. A total of 43 specimens were repeatedly reactive with the 1.7 ELISA, 91 specimens were repeatedly reactive with the 1.4 ELISA and 51 specimens were repeatedly reactive in the 4.1 ELISA.

15 One of six specimens repeatedly reactive in the 1.7 ELISA was reactive by Western blot for the 1.7 protein (SEQUENCE I.D. NO.610). Nine of 9 specimens (100%) which were repeatedly reactive in the 1.4 ELISA were positive by Western blot for antibodies to the 1.4 protein (SEQUENCE I.D. NO. 611). One specimen was positive by Western blot for both proteins. Twelve of 12 specimens (100%) repeatedly reactive in the 4.1 ELISA were positive by Western
20 blot for the 4.1 protein (SEQUENCE I.D. NO.612).

Three repeatedly reactive specimens (including one specimen positive in the 1.4 ELISA and one specimen positive in both ELISA's and both Western blots) were tested for HGBV RNA by RT-PCR using primers from clone 4 as described above. All three specimens were negative by RT-PCR.

25 These data suggest that HGBV may be endemic in West Africa.

(ii) Specimens from Intravenous Drug Users (IVDU's)

Set 1: Three of 112 specimens were positive with the 1.4 ELISA. Five specimens were reactive on 4.1 ELISA and three on 1.7 ELISA. Two samples were positive on more than one ELISA.

30 Set 2: A total of 99 specimens were obtained from a population of intravenous drug users, as part of a study being conducted at Hines Veteran's Administration Hospital, in Chicago, IL. None of these specimens were reactive in the 1.7 or 4.1 ELISA. One specimen was repeatedly reactive in the 1.4 ELISA. This repeatedly reactive specimen was tested for HGBV RNA by RT-PCR using
35 primers from clone 4 as described above. This specimen was RT-PCR negative.

K. Specimens obtained from individuals with non A-E Hepatitis

The data for these studies is summarized in TABLE 16.

Various populations of specimens were obtained from individuals diagnosed as having non-A-E hepatitis and tested with the 1.7, 1.4, and 4.1 ELISA's described in Example 15.C. These specimens included: 180 specimens obtained from a Japanese clinic; 56 specimens from a clinic in New Zealand; 73 specimens obtained from a clinic in Greece; 132 specimens from a clinic in Egypt; 64 specimens from a U.S. clinic in Texas (set T), 72 specimens from a research center in Minesota (set M); 62 specimens from U.S. (set #1); 82 specimens obtained from a clinic in Pakistan; 10 specimens from a clinic in Italy. (Due to insufficient volumes of some sera, certain specimens from these groups were not tested on all of the available ELISAs).

(i) Specimens from Japan

These 180 specimens were obtained from 85 different patients. These two reactive specimens came from 2 individuals. A total of 2 of 180 specimens were repeatably reactive in the 1.7 ELISA. These 2 specimens were tested by RT-PCR using primers from clone 4 as described above. None of the specimens were positive.

None of the specimens were positive in the 1.4 ELISA.

For the 4.1 ELISA, seven of 89 specimens were repeatably reactive in the 4.1 assay. (Note: these 89 specimens were obtained from 29 different patients). Five of the reactive specimens were obtained from one patient. The remaining two were from a different patient.

(ii) Specimens from New Zealand

A total four of 56 specimens were repeatably reactive in one or more of the ELISA's 1.7, 1.4, and 4.1. None of these specimens were reactive in two or more ELISA's. One specimen was repeatably reactive in the 1.7 ELISA and two specimens were repeatably reactive in the 1.4 ELISA. One specimen was repeatably reactive with the 4.1 ELISA. PCR was performed on two repeatably reactive specimens; both specimens were negative. One specimen which was repeatably reactive in the 1.4 ELISA was also reactive for antibodies to HEV.

(iii) Specimens from Greece

A total of 5 of 73 specimens were found to be reactive for antibodies in the 1.7 and/or 1.4 ELISA's. These 73 specimens were obtained from a total of 11 patients. Two of the five repeatably reactive specimens were repeatably reactive for both ELISA's and were obtained from one individual on different dates. Two repeatably reactive specimens were tested by RT-PCR and were negative. None of these specimens were reactive for antibodies with the 4.1 ELISA.

(iv) Specimens from Egypt

A total of 11 of 132 specimens were reactive in the 1.7, 1.4, or 4.1 ELISA's. Eight specimens were positive in both the 1.7 and 1.4 ELISA's. Nine specimens were reactive for antibodies in the 1.7 ELISA and 9 specimens were reactive in the 1.4 ELISA. One specimen repeatedly reactive in the 4.1 ELISA but negative in the 1.7 and 1.4 ELISAs. One specimen repeatedly reactive in the 1.7 ELISA was tested by Western blot and was negative for antibodies to the 1.7 recombinant protein (SEQUENCE I.D. NO. 610). Six of nine specimens repeatedly reactive in the 1.4 ELISA tested positive by Western blot for antibodies to the 1.4 recombinant protein (SEQUENCE I.D. NO. 611). Seven of the repeatedly reactive specimens were tested by RT-PCR; none of the specimens were reactive. These 132 specimens were obtained on different dates from 25 different individuals. The 11 repeatedly reactive specimens were obtained from five different individuals. For one of these individuals (patient #101), the immune response clearly mimics that observed with the tamarins (FIGURE 31). Note that in FIGURE 31, the ALT levels were elevated at the time of presentation of symptoms to the physician. In subsequent specimens, the ALT levels declined and antibodies were detected utilizing the 1.4 and 1.7 ELISA's. The antibody response declined over the next several weeks as was noted with the serologic profiles observed in the tamarins. Three additional patients (257, 260, and 340) exhibited serologic patterns similar to patient #101 (as shown in FIGURES 32-34. These data provide supportive evidence that HGBV may be the etiologic agent in these cases of hepatitis.

None of the seven specimens obtained from these four patients were positive for HGBV RNA by RT-PCR. There are several potential reasons for these results. First, the viremic phase may have been very short-lived: the virus may have been cleared from the serum by the time of the first bleed date. Secondly, these specimens were shipped from Egypt and may potentially have been frozen and thawed or otherwise compromised during the storage and shipping process, thus reducing the potential to detect HGBV RNA.

(v) Specimens from U.S. (Set T)

None of 64 specimens from the U.S. (set T) were repeatedly reactive in the 1.7, 1.4 or 4.1 ELISA.

(vi) Specimens from U.S. (Set M)

A total of 4 of 72 specimens from U.S. specimens (set M) were repeatedly reactive in one or more of the ELISA's. Two specimens were reactive with the 1.7 and 4.1 ELISA's. One specimen was reactive only with 1.7 and one specimen was reactive only with the 4.1 ELISA.

vii) Specimens from the United States (set 1)

A total of three of 51 specimens from non A-E hepatitis U.S. set 1 were repeatably reactive in one or both of the ELISA's. One specimen was repeatably reactive in both ELISA's. One specimen was reactive in the 1.7 ELISA and three
5 specimens were repeatably reactive in the 1.4 ELISA. The specimen positive in both ELISA's was positive by Western blot for the 1.4 recombinant protein (SEQUENCE I.D. NO. 22) but negative for the 1.7 recombinant protein (SEQUENCE I.D. NO. 23). One additional specimen was positive in the 1.4
10 ELISA and Western blot positive for the 1.4 recombinant protein (SEQUENCE I.D. NO.611). One specimen which was repeatably reactive in the 1.4 ELISA was reactive for antibodies to HEV.

(viii) Specimens from Pakistan

A total of four of 82 specimens were repeatably reactive for antibodies in 1.4 and/or 1.7 ELISAs. None of the specimens were reactive in both ELISA's.
15 Two specimens were repeatably reactive in the 1.7 ELISA and two specimens were repeatably reactive in the 1.4 ELISA. Two specimens repeatably reactive in the 1.4 ELISA were also reactive for antibodies to HEV. None of these 82 specimens were positive with the 4.1 ELISA.

(ix) Specimens from Italy

20 None of the ten specimens were repeatably reactive in the 1.7, 1.4, or 4.1 ELISA.

L. Statistical Significance of Serological Results

These data indicate that specific antibodies to HGBV proteins (i.e. specimens repeatably reactive for antibodies in 1.7, 1.4, or 4.1 ELISA's can be
25 detected in all three categories of populations studied. Serological results obtained with the various categories of specimens ("low risk", "at risk" and non A-E hepatitis patients) were grouped together and analyzed for statistical significance using the Chi square test. The data indicated that there is a significant difference in comparing the seroprevalence of anti-HGBV in volunteer blood donors with either
30 the individuals considered "at risk" for exposure to HGBV or to individuals diagnosed with hepatitis of an unknown etiology.

Among West Africans, the seroprevalence rate is 13.9% and is significantly higher than the baseline group (TABLE 17) with a p value of 0.000. Similiarly, for the IVDU's, there was a statistically significant difference (p value
35 of 0.000) when the results from IVDU's were compared with volunteer donors. In countries (including Japan, New Zealand, U.S., Egypt, and Pakistan), there

were significant differences in antibody prevalence in patients with non A-E hepatitis when compared to the volunteer blood donors from the US.

H. Summary

These data suggest that the ELISA's described herein may be useful in
5 diagnosing cases of hepatitis in humans in various geographical regions including Japan, New Zealand, U.S., Egypt, and Pakistan. It is likely that these data underestimate the seroprevalence of antibodies to HGBV among all categories of specimens tested. It is expected that as additional HGBV epitopes are discovered and evaluated, the utility of tests derived from the HGBV genome(s) will become
10 more important in diagnosing hepatitis among patients whose diagnosis cannot currently be made. NOTE: Although the results of RT-PCR were negative in these initial studies, subsequent data revealed flavi-like viral sequences in serum of seropositive individuals (see Example 17).

As we have discussed supra, more than one strain of the HGBV is present.
15 These are considered to be within the scope of the present invention and are termed "hepatitis GB Virus ("HGBV").

Example 16. Serological studies with HGBV-A

A. Recombinant Protein Purification Protocol

20 Bacterial cells expressing the CKS fusion proteins were frozen and stored at -70°C. The bacterial cells from each of the GBV-A constructs were thawed and disrupted as described in Example 15 for GBV-B constructs. Further, the recombinant proteins were purified as described for GBV-B recombinant proteins in example 15.

25 The fractions which were collected during the purification protocol were electrophoretically separated and stained with Coomassie Brilliant Blue R250 and examined for the presence of a protein having a molecular weight of approximately 60kD (CKS 1.5/SEQUENCE NO. 614), 65kD (CKS 2.17/ SEQUENCE NO. 613), 55kD (CKS 1.18/SEQUENCE NO. 390) and 66kD (CKS
30 1.22/SEQUENCE NO. 390). Fractions containing the protein of interest were pooled and re-examined by SDS-PAGE.

The immunogenicity and structural integrity of the pooled fractions containing the purified antigen were determined by immunoblot following electrotransfer to nitrocellulose as described in Example 13. In the absence of a
35 qualified positive control, the recombinant proteins were identified by their reactivity with a monoclonal antibody directed against the CKS portion of each fusion protein. When the CKS-1.5 protein (SEQUENCE I.D. NO. 614) was

examined by Western blot, using the anti-CKS monoclonal antibody to detect the recombinant antigen, a single band at approximately 60 kD was observed. This corresponds to the expected size of the CKS-1.5 protein (SEQUENCE I.D. NO. 614). Similarly, bands of the expected sizes were noted for the CKS-2.17 protein (SEQUENCE I.D. NO. 613), the the CKS 1.18 protein (SEQUENCE NO. 390) and the CKS-1.22 protein (SEQUENCE I.D. NO. 390) when examined by immunoblot.

B. Polystyrene Bead Coating Procedure

The proteins were dialyzed and evaluated for their antigenicity on polystyrene beads described in Example 15.

C. ELISA Protocol for Detection of Antibodies to HGBV

The ELISA's were performed as described in Example 15.

D. Detection of HGBV RNA in Serum of infected Individuals

Specimens which were repeatably reactive in the ELISAs were tested for HGBV RNA as described in section D. of Example 15.

E. Tamarin Serological Profiles

None of the sera from the tamarins produced a specific immune response when tested in the ELISA utilizing the CKS 1.5 protein, the CKS 2.17 protein, the CKS 1.18 protein or the CKS 1.22 protein, all derived from the HGBV-A genome. However, HGBV-A RNA was detected in several of the infected tamarins as described in the previous example. (See Example 15 for a summary of the tamarin serological profiles).

F. Experimental Protocol for Serologic Studies on Human Populations

In Example 15, ELISA's employing recombinant antigens from HGBV-B were utilized to evaluate the presence of antibodies to HGBV-B in various human populations. Many of the same specimens were then tested for antibodies to HGBV-A utilizing the 1.5 ELISA employing the CKS-1.5 recombinant protein (SEQUENCE I.D. NO. 614), the 2.17 ELISA employing the CKS-2.17 recombinant protein (SEQUENCE I.D. NO. 613), the 1.18 ELISA employing the CKS-1.18 recombinant protein (SEQUENCE I.D. NO. 390), and the ELISA employing the CKS-1.22 recombinant protein (SEQUENCE I.D. NO. 390), coated on the solid phase (as described in Example 15). As noted in Example 15, all five of the convalescing tamarins inoculated with HGBV produced a specific but short-lived antibody response to the HGVB-B recombinant proteins (as detected with the 1.7, 1.4 and 4.1 ELISA's). Although none of the tamarins produced a detectable antibody response in the 1.5, 2.17, 1.18 or 1.22 ELISAs, some human specimens from West Africa produced a specific antibody response to

one or more of these recombinant proteins when tested via Western blot and one of the specimens obtained from the surgeon (who was the source of the GB agent) at 22 days after onset of hepatitis produced a specific antibody response to the 2.17 recombinant protein when tested by Western blot (see Example 3). In the current
5 example, we evaluated the utility of the 1.5, 2.17, 1.18 and 1.22 ELISA's in detecting antibodies in various human populations.

G. Cutoff Determination

The cutoff for the 1.5, 2.17, 1.18, and 1.22 ELISAs were determined as described in Example 15.

H. Supplemental Testing

As noted in Example 15, specimens which were initially reactive were typically retested; if the specimen was repeatably reactive, additional tests (e.g. Western blot) may be performed to further support the ELISA data. For a Western blot result to be considered positive, a visible band should be observed at 60 kD
15 for the 1.5 protein (SEQUENCE I.D. NO. 614) at 65 kD for the 2.17 protein (SEQUENCE I.D. NO. 613), at 55kD for the 1.18 protein (SEQUENCE I.D. NO. 390) at 66 kD for the 1.22 protein (SEQUENCE I.D. NO. 390).. Since the Western blot had not been optimized to match or exceed the sensitivity of the ELISA's, a negative result was not used to discard the ELISA data. However, a
20 positive result reinforced the reactivity detected by the ELISA's.

As also noted in Example 15, repeatably reactive specimens which have sufficient volume may be tested by RT-PCR (performed as described in Example 15) using primers to identify HGBV specific nucleotide sequences in serum.

I. Serological Data Obtained with Low-Risk Specimens

25 A total of 252 plasma specimens were obtained from the Interstate Blood Bank in Ohio and tested for antibodies with the 1.5 ELISA which utilizes the 1.5 recombinant protein (SEQUENCE I.D. NO. 614). The mean absorbance value for the population was 0.036 (SD=0.022). The cutoff was calculated to be 0.168, corresponding to an S/N value of 10.0. A total of 760 plasma specimens
30 (including the 252 specimens utilized to determine the cutoff) were tested for antibodies with the 1.5 ELISA. None of the specimens were repeatably reactive. In addition, 100 plasma specimens were obtained from Southeastern Wisconsin and tested for antibodies with the 1.5 ELISA. None of the specimens were repeatably reactive.

35 Thus, there is no evidence that antibodies to the 1.5 protein were present in U.S. blood donors.

A total of 200 specimens were obtained from Wisconsin blood donors and tested for antibodies with the 2.17 ELISA which utilizes the 2.17 recombinant protein (SEQUENCE I.D. NO. 60). The mean absorbance value for the population was 0.058 (SD=0.025). The cutoff was calculated to be 0.208, corresponding to an S/N value of approximately 10.0. One of the specimens was repeatably reactive. Thus, the seroprevalence in U.S. blood donors (N=200) is relatively low.

The same 200 specimens described in the above paragraph were tested for antibodies with the 1.18 and 1.22 ELISAs. None of the specimens were repeatably reactive. Thus, there is no evidence that specimens from volunteer blood donors are antibody positive for HGBV-A proteins as determined by the 1.5, 2.17, 1.18 and 1.22 ELISAs.

J. Specimens Considered "At Risk" for Hepatitis

The data for these studies is summarized in TABLE 18.

(i) Specimens from West Africa

A total of 58 of 1300 specimens were reactive with the 1.5 ELISA. Twelve of 18 repeatably reactive specimens were positive by Western blot for antibodies to the 1.5 protein (SEQUENCE I.D. NO. 614). A total of 43 of 817 specimens were reactive in the 2.17 ELISA. These repeatably reactive specimens were not tested by Western blot for antibodies to the 2.17 protein (SEQUENCE I.D. NO. 613).

Six of the 817 specimens were reactive with the 1.22 ELISA. Nine of the 353 specimens were reactive for 1.18 ELISA. Twenty-one specimens reactive with the 2.17 ELISA were tested by Western blot and 13 were reactive. All eight specimens that were repeatably reactive with the 1.18 ELISA was positive by Western blot.

These data suggest that HGBV may be endemic in West Africa.

(ii) Specimens from Intravenous Drug Users

A total of 112 specimens were obtained from a population of intravenous drug users, as part of a study being conducted at Hines Veteran's Administration Hospital, in Chicago, IL. One specimen was repeatably reactive in the 2.17 ELISA and an additional specimen was reactive in the 1.18 ELISA. None of these specimens were positive in the 1.5 or 1.22 ELISA.

K. Specimens obtained from individuals with non A-E Hepatitis

The data for these studies is summarized in TABLE 18.

Various populations of specimens (described in Example 15.K) were obtained from individuals with non-A-E hepatitis and tested with the 1.5, 2.17,

1.18 and 1.22 ELISAs (described in Example 15.C). Due to insufficient sample volume, not all specimens were tested in all of the ELISAs.

(i) Specimens from Japan

5 A total of four of 89 specimens were repeatably reactive in the 1.5 ELISA, with three of the specimens being from one individual and one of the specimens from a second individual. One specimen which had tested negative for the 1.5 ELISA, the 1.18 ELISA and the 1.22 ELISA was reactive in the 2.17 ELISA. None of the specimens were reactive in the 1.18 ELISA. These specimens were not tested with the 1.22 ELISA.

10 (ii) Specimens from New Zealand

None of these 56 specimens were reactive in the 1.5 ELISA. These specimens were not tested in the 2.17 ELISA, the 1.18 ELISA or the 1.22 ELISA..

(iii) Specimens from Greece

15 None of the 67 specimens (obtained from a total of 10 patients) were reactive for antibodies with the 1.5, 2.17 or 1.22 ELISA.

(iv) Specimens from Egypt

20 None of 132 specimens were reactive in the 1.5 ELISA. A total of 7 of 132 specimens available for testing were reactive in the 2.17 ELISA. These specimens were obtained from 25 individuals with acute non A-E hepatitis. Three of the 25 patients were seropositive in the 2.17 ELISA on one or more separate dates following the onset of hepatitis. None were reactive in the 1.18 or 1.22 ELISA.

(v) Specimen from the U.S. (Set M)

25 None of the 72 specimens were reactive with the 1.5 ELISA. Three of the 72 specimens were reactive for the 1.18 ELISA. Two of the specimens were reactive in the 2.17 ELISA and four specimens were reactive with the 1.22 ELISA. Two of the samples were reactive in one of more of the ELISAs.

(vi) Specimens from U.S. (Set T)

30 None of the 64 specimens were reactive with the 1.5, 1.22 or 2.17 ELISAs. One specimen was reactive for the 1.18 ELISA.

(vii) Specimens from U.S. (Set I)

35 A total of 3 of 62 specimens were reactive in one or more of the GBV-A ELISAs. One specimen was repeatly reactive in both the 2.17 and 1.22 ELISA. One specimen was reactive only in the 2.17 ELISA and an additional specimen was reactive only in the 1.22 ELISA. None of the specimens were reactive in the 1.5 or 1.18 ELISA.

As we have discussed supra, it is possible that more than one strain of the HGBV may be present, or that more than one distinct virus may be represented by the sequences disclosed herein. These are considered to be within the scope of the present invention and are termed "hepatitis GB Virus ("HGBV").

5 L. Statistical Significance of Serological Results

These data indicated that specific antibodies to HGBV-A proteins (i.e. specimens repeatably reactive for antibodies in 1.5, 2.17, 1.18 and 1.22 ELISA's) were detected among individuals considered "at risk" for exposure to HGBV and among individuals diagnosed with non A-E hepatitis, but were not frequently
10 detected either among volunteer or paid blood donors from the U.S. In TABLE 19, the serological results obtained with the various categories of specimens ("low risk", "at risk" and non A-E hepatitis patients as shown in TABLE 18) were grouped together and analyzed for statistical significance using the Chi square test. Unlike the data in TABLE 18, which compiled the seroprevalence of antibodies to
15 HGBV proteins in the total number of specimens tested, the data in TABLE 19 reflect the results obtained with different individuals (persons). For the GBV-A ELISAs, the data indicate that there is a significant difference (with a p value of 0.000) in comparing the seroprevalence of anti-HGBV in volunteer blood donors with the individuals considered "at risk" for exposure to HGBV (West Africa) but
20 not in the IVDUs. In addition, there was a statistically significant difference between the seroprevalence of antibodies to HGBV-A in individuals with non A-E hepatitis in Egypt and the U.S. when compared to volunteer donors. These data suggest that exposure to HGBV-A was associated with non-A through E hepatitis. NOTE: although the results of RT-PCR were negative in these initial studies,
25 subsequent data revealed flavi-like viral sequences in serum of seropositive individuals (see Example 19).

M Summary

These data suggest that the ELISA described herein may be useful in detecting antibodies among individuals residing in West Africa and among
30 individuals with non-A through E hepatitis. The risk for hepatitis among the West Africans is relatively high; nearly 85% of these individuals are seropositive for antibodies to Hepatitis B virus, and approximately 5% are positive for antibodies to hepatitis C virus. It is likely that these data underestimate the seroprevalence of antibodies to HGBV among all categories of specimens tested. It is expected that
35 as additional HGBV epitopes are discovered and evaluated, the utility of tests derived from the HGBV genome(s) will become more important in diagnosing hepatitis among patients whose diagnosis cannot currently be made.

Example 18. Identification of a GB-related virus in humans

A. Theory

Epitopes from both HGBV-A and HGBV-B have been identified (Example 3). These have been used as serologic markers to screen human serum and plasma samples (Examples 5 and 6). A significant correlation between seroreactivity with some of these markers and the incidence of nonA-E hepatitis has suggested that HGBV-B is the causative agent of nonA-E hepatitis in humans (Example 5.G). However, Western blot analysis of GB human sera gave no indication of reactivity to HGBV-B epitopes (Example 3). Instead, at least one HGBV-A epitope was identified with the GB human sera suggesting that HGBV-A was the causative agent of hepatitis in GB. Neither HGBV-A nor HGBV-B sequences have been identified in patients with nonA-E hepatitis by RT-PCR (Example 5.E). Therefore, proof of HGBV-A and/or HGBV-B infection in humans with nonA-E hepatitis remains to be determined.

The failure to identify HGBV-A and/or HGBV-B sequences in human sera or plasma sources may be due to several factors. First, we have looked at only a limited number of HGBV-A and/or HGBV-B-seropositive samples by RT-PCR, and the complete storage history of many of these samples is unknown. Thus, it is possible that viral RNA present in these samples was compromised by incorrect storage. Second, GB infection appears to be resolving in nature. As such, the window of time in which GB sequences are present in an infected individual's serum may be very narrow. Thus, the chances of obtaining serum samples containing GB sequences may be extremely low. Finally, a limited number of PCR primer sets were used to look for HGBV-A and/or HGBV-B sequences. HGBV-A and/or HGBV-B are RNA viruses and, therefore, are likely to have high rates of mutation (Holland, et al. (1982) Science 215:1577-1585). Thus, the sequence of HGBV-A and/or HGBV-B present in the examined human sera may be different enough from the sequence of our PCR primers such that HGBV-A and/or HGBV-B may be not be detected.

To address the possibility that the genomic variability of HGBV-A and/or HGBV-B prevented these viruses in our PCR studies, degenerate PCR primers were designed to the highly conserved NS3-like regions of HGBV-A and HGBV-B (see Fig.17). It was reasoned that these highly conserved regions serve a necessary function in the viral replicative cycle. Therefore, these sequences should be maintained in HGBV-A and HGBV-B variants. PCR primers designed within this region should be able to detect HGBV-A and/or HGBV-B genomic RNA by

RT-PCR. In addition, by designing degenerate PCR primers that can specifically amplify HGBV-A, HGBV-B and HCV sequences, we reasoned that we might be able to amplify sequences from viruses related to HGBV-A, HGBV-B and HCV. Thus, if the limited seroreactivity detected in human serum and plasma samples (Examples 5 and 6) is the result of cross-reactive antibodies to antigens from distinct HGBV-A- or HGBV-B-related viruses, we may be able to obtain sequences from these GB-related viruses. [This is similar to the experimental approach that Nichol and colleagues took to identify the unique Hantavirus associated with the recent outbreak of acute respiratory illness in the Southwest United States. Nichol, et al. *Science* 262:914-917 (1993)]

B. Cloning the NS3-like region of hepatitis GB virus C (HGBV-C).

In several models of virus infections, viremia occurs during the early stages of infection and is often associated with the detection of IgM class antibodies to viral proteins. As noted in examples 5 and 6, several specimens were immunoreactive in ELISA's which detected IgG class antibodies to recombinant proteins derived from HGBV-A and HGBV-B. Additional ELISA's were performed to determine if IgM class antibodies could be detected to these proteins. Several seropositive specimens obtained from West African individuals (Example 5.E.i) were reactive for IgM class antibodies to the recombinant proteins (data not shown). These specimens were thought to have a high probability of containing virus. In addition, specimens obtained from HGBV-A- and HGBV-B-seropositive Egyptian individuals (Example 5.F.vii) suffering from acute hepatitis in the absence of detectable IgM class antibodies to HGBV-A or HGBV-B recombinant proteins were also examined due to the likelihood that acute liver disease is most likely linked to viral presence. A "hemi-nested" RT-PCR was performed on the nucleic acids from these samples with degenerate oligonucleotide primers which will amplify HGBV-A, HGBV-B and HCV-1 sequences using the GeneAmp[®] RNA PCR kit (Perkin Elmer) as directed by the manufacturer. Briefly, the first set of amplifications were performed on the cDNA products of random-primed reverse transcription reactions of the extracted nucleic acids with 2 mM MgCl₂ and 1 μ M primers ns3.1-s and ns3.1-a (SEQUENCE ID. NOS. 671 and 672, respectively). Reactions were subjected to 40 cycles of denaturation-annealing-extension [three cycles of (94°C, 30 sec; 37°C, 30 sec; 2 min ramp to 72°C; 72°C, 30 sec) followed by 37 cycles of (94°C, 30 sec; 55°C, 30 sec; 72°C, 30 sec)] followed by a 10 min extension at 72°C. Completed reactions were held at 4°C. The second set of amplifications were as described above except that 4% of the first PCR products were used as the template, and ns3.1-s and ns3-a

(SEQUENCE ID. NOS. 671 and 673, respectively) were used as the "hemi-nested" primer set. Products from the first and second sets of PCRs were analyzed by gel electrophoresis.

One sample from West Africa had a PCR product from the hemi-nested reaction that migrated at approximately 386 bp (the expected size of a HGBV-A, HGBV-B or HCV product). This product was cloned into pT7 Blue T-vector plasmid (Novagen) as described in the art. The sequence obtained from this clone (GB contig C [GB-C], SEQUENCE ID. NO. 673, residues 2274-2640) was compared with GB contig A (GB-A, SEQUENCE ID. NO. 163, residues 4438-4804), GB contig B (GB-B, SEQUENCE ID. NO. 393, residues 4218-4587) and HCV-1 (SEQUENCE ID. NO. 398). FIGURE 36 shows a nucleotide alignment of these sequences, while TABLE 20 shows the percent identity between these sequences.

15

TABLE 20

	GB-A	GB-B	GB-C	HCV-1
GB-A	100.0	47.99	61.66	52.55
GB-B		100.0	52.55	54.96
GB-C			100.0	57.37
HCV-1				100.0

As demonstrated in FIGURE 36 and TABLE 20, nucleotide comparisons of GB-A, GB-B and HCV-1 show that these sequences are 47.99 to 61.66% identical to one another. This is not surprising when one considers the conserved amino acid residues present in the NTP-binding helicase of these viruses (Example 2.B.3, FIGURE 17A). The nucleotide comparison of the NS3 PCR product obtained from the West African sample (GB-C, SEQUENCE ID. NO. 673, residues 2274-2640) with the other viruses suggests that the West African NS3 product (GB-C, SEQUENCE ID. NO. 673, residues 2274-2640) is related to, but distinct from the NS3 sequences from GB-A (SEQUENCE ID. NO. 163, residues 4438-4804), GB-B (SEQUENCE ID. NO. 393, residues 4218-4587) and HCV-1 (SEQUENCE ID. NO. 398). This sequence comparison suggests that GB-C may be from a GB-like virus more closely related to GB-A than GB-B or HCV. BLASTN and BLASTX searches of nucleic acid and protein databases in the Wisconsin Sequence Analysis Package (Version 8) with GB-C (SEQUENCE ID. NO. 673, residues 2274-2640) finds limited sequence identity with several strains of HCV. The highest P values (i.e., odds of alignment being made by chance) for nucleotide and amino acid searches were 1.9×10^{-20} and 5.3×10^{-31} , respectively

(data not shown). Together, these data suggest that GB-C (SEQUENCE ID. NO. 673, residues 2274-2640) may be from a unique GB-like virus related to HGBV-A, HGBV-B and HCV which we now designate, HGBV-C.

C. GB-C is exogenous.

5 PCR primers to GB-C sequence were utilized to determine whether this sequence could be detected in the genomes of humans, Rhesus monkeys, S. cerevisiae and E.coli as described, for example, in Example 6.B. PCR was performed using GeneAmp® reagents from Perkin-Elmer-Cetus essentially as directed by the supplier's instructions. Briefly, 300 ng of genomic DNA was used
10 for each 100 µl reaction. PCR primers (SEQUENCE I.D. NOS. 675 and 676) were used at a final concentration of 1.0 µM. PCR was performed for 40 cycles (94°C, 30 sec; 55°C, 30 sec; 72°C, 30 sec) followed by an extension at 72°C for 10 min. PCR products were separated by agarose gel electrophoresis and visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide,
15 followed by hybridization to a radiolabeled probe after Southern transfer to a Hybond-N+ nylon filter. FIGURE 37 shows a PhosphoImage (Molecular Dynamics, Sunnyvale, CA) from a Southern blot of the PCR products after hybridization with the radiolabeled probe from GB-C (SEQUENCE I.D. NO. 673, residues 2274-2640). GB-C (SEQUENCE I.D. NO. 673) sequences were not
20 detected in human (FIGURE 19, lane 1), Rhesus monkey (lane 2), S. cerevisiae (lane 3) or E. coli (lane 4) genomic DNAs despite the detection of ~350 fg (one genome copy equivalent, lane 5) and ~35 fg (0.1 genome copy equivalents, lane 6) of GB-C plasmid template in 300 ng human genomic DNA. (Lane 7 contains the PCR products from ~3.5 fg [0.01 genome copy equivalents] GB-C plasmid
25 template in 300 ng human genomic DNA.) Thus, using genomic PCR that can detect 0.1 genome copy equivalents, GB-C (SEQUENCE I.D. NO. 673) cannot be detected in the genomes of human, Rhesus monkey, S. cerevisiae, and E. coli. These data are consistent with the purported exogenous (i.e. viral) origin of GB-C (SEQUENCE I.D. NO. 673).

30 D. GB-C can be detected in additional human serum samples.

Additional HGBV-A and HGBV-B immunoreactive human serum samples were tested for the presence of GB-C sequences using RT-PCR. As in Example 7, nucleic acids extracted from serum samples were reverse transcribed using random hexamers, and cDNAs were subjected to 35-40 cycles of amplification
35 (94°C, 30 sec; 55°C, 30 sec; 72°C, 30-90 sec) followed by an extension at 72°C for 10 min. GB-C-specific PCR primers (g131-s1 and g131-a1, SEQUENCE ID. NOS. 675 AND 676) were used at 1.0 µM concentration. The PCR products

were separated by agarose gel electrophoresis and visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide and hybridization to a radiolabeled probe after Southern transfer to a Hybond-N+ nylon filter. A total of 48 HGBV-immunopositive samples were tested from West Africa. Including
5 the original sample from which GB-C was identified, eight samples from West Africa were positive for GB-C sequences by RT-PCR. A total of ten GB seronegative West African serum samples were tested, none of which had detectable GB-C sequences. PCR products from four of the positive samples were cloned and sequenced as described above. Over the 156 nucleotides examined,
10 two of four clones examined were identical to GB-C sequence (SEQUENCE I.D. NO. 673, residues 2274-2640), and two clones (SEQUENCE I.D. NOS. 677 and 678) contained sequences that were 88.4% and 83.6% identical to GB-C (SEQUENCE I.D. NO. 673, residues 2274-2640) (FIGURE 38). However, despite the divergence at the nucleotide level, the predicted translation product of
15 each clone is remarkably similar with only one amino acid change occurring in the predicted translation of SEQUENCE ID NO. 678.

Additional serum samples from individuals with nonA-E hepatitis from Greece, Egypt and the United States were tested for GB-C sequences as described above. None of these samples contained detectable GB-C sequences. The lack of
20 detection of GB-C sequences in these samples may be due to several reasons (see above, Theory). However, the sequence variation noted above between GB-C (SEQUENCE I.D. NO. 673, residues 2274-2640) and the two GB-C variants (SEQUENCE I.D. NOS. 678 and 677) suggest that if the closely related HGBV-C's from West Africa can differ by 15.1% at the nucleotide level, it is likely that
25 the GB-C-specific PCR primers (g131-s1, g131-a1, SEQUENCE ID. NOS. 675 and 676) may not hybridize sufficiently to geographically distinct isolates of GB-C virus to generate a detectable PCR product. In this case, PCR primers designed to a more conserved region (5' UTR) of the genome may allow the detection of GB-C sequences in non-West African serum samples.

30 E. Extension of the HGBV-C sequences.

The PCR walking technique described in Example 2.A hereinabove was utilized to obtain additional GB-C sequences. Briefly, total nucleic acid were extracted from the West African human serum originally used to identify GB-C (SEQUENCE I.D. NO. 673, residues 2274-2640). This nucleic acid was reverse
35 transcribed as described supra. The resultant cDNAs were amplified in 50 µl PCR reactions (PCR 1) as described by Sorensen et al. except that 2 mM MgCl₂ was used. Reactions were subjected to 35 cycles of denaturation-annealing-extension

(94°C, 30 sec; 55°C, 30 sec; 72°C, 90 sec) followed by a 10 min extension at 72°C. Biotinylated products were isolated using streptavidin-coated paramagnetic beads (Promega) as described by Sorensen et al. Nested PCRs (PCR 2) were performed on the streptavidin-purified products as described by Sorensen et al. for a total of 35 cycles of denaturation-annealing-extension as described above. The resultant products and the PCR primers used to generate them are listed in TABLE 21.

TABLE 21

	<u>Reaction</u>	<u>Primer set PCR 1</u>	<u>Primer set PCR 2</u>	<u>Size of PCR product</u>
10	C.1	SEQ ID #679/SEQ ID #135	SEQ ID # 680/SEQ ID #126	1250 bp
	C.2	SEQ ID # 681/SEQ ID # 694	SEQ ID # 686/SEQ ID #126	220 bp
	C.3	SEQ ID # 682/SEQ ID # 694	SEQ ID # 683/SEQ ID #126	250bp
	C.4	SEQ ID # 684/SEQ ID #695	SEQ ID # 685/SEQ ID #126	800 bp
15	C.5	comp. of SEQ ID # 679/ SEQ ID #695	SEQ ID # 90/SEQ ID #126	750 bp
	C.6	SEQ ID # 688/SEQ ID #672	SEQ ID # 92/SEQ ID #126	1150 bp
	C.7	SEQ ID # 690/SEQ ID #695	SEQ ID # 94/SEQ ID #126	550 bp
	C.8	SEQ ID # 692/SEQ ID #695	SEQ ID # 96/SEQ ID #126	250 bp
	C.9	653/SEQ ID # 135	654/SEQ ID #126	625 bp
20	C.10	655/SEQ ID # 694	656/SEQ ID #126	350 bp
	C.11	657/SEQ ID # 694	658/SEQ ID #126	550 bp
	C.12	659/SEQ ID # 695	660/SEQ ID #126	450 bp
	C.13	661/665	662/SEQ ID #126	750 bp
	C.14	663/FP3 (SEQ ID #13)	664/SEQ ID #126	550 bp
25	C.15	666/125	667/SEQ ID #126	600 bp

In addition, a 1.3 kb product (C.16) was generated with oligonucleotide primers SEQ ID # 669 and SEQ ID # 670 using PCR 1 conditions described above. This product, together with those described in TABLE 21 were isolated from agarose gels and cloned into pT7 Blue T-vector plasmid (Novagen) as described in the art.

The cloned products were sequenced as described in Example 5. The sequences were assembled using the GCG Package (version 7) of programs. A schematic of the assembled contig is presented in FIGURE 39. GB-C is 9034 bp in length, all of which has been sequenced and is presented in SEQUENCE I.D. NO. 400-606. These SEQUENCE I.D.'s correspond to the three forward translation frames.

Example 19. CKS-based expression and detection of immunogenic

HGBV-C polypeptides

The HGBV-C sequences obtained from the walking experiments described in Example 17 (TABLE 13) were cloned into the CKS expression vectors pJO200, pJO201, and pJO202 using the restriction enzymes listed in TABLE 22 (10 units, NEB) as described in Example 13. Two additional PCR clones, designated C.3/2 and C.8/12, were also expressed (FIGURE 39). PCR product C.3/2 was generated using primers SEQUENCE I.D. NO. 681 and the complement of SEQUENCE I.D. No. 685 and PCR product C.8/12 was generated using primers (SEQUENCE I.D. NO. 693 and its complement) as described in Example 9. The PCR products were cloned into pT7Blue as described previously, then liberated with the restriction enzymes listed in TABLE 22 and cloned into pJO200, pJO201 and pJO202 as above.

Two human sera which had indicated the presence of antibodies to one or more of the CKS/HGBV-A or CKS/HGBV-B fusion proteins by the 1.7, 4.1 or 2.17 ELISAS (see Examples 15 and 16) were chosen for Western blot analysis. One of these sera (240D) was from an individual with nonA-E hepatitis (Egypt) and the other (G8-81) was from a West African individual "at risk" for exposure to HGBV (see Example 15). The CKS/HGBV-C fusion proteins were expressed and transferred to nitrocellulose sheets as described above. The blots were preblocked as described and incubated overnight with one of the human serum sample diluted 1:100 in blocking buffer containing 10% *E. coli* lysate and 6mg/ml XL1-Blue/CKS lysate. The blots were washed two times in TBS, reacted with HRPO-conjugated goat anti-human IgG and developed as indicated above. The results are shown in TABLE 22.

Several of the HGBV-C proteins showed reactivity with one or the other of the two sera, and three (C.1, C.6 and C.7) were chosen for use in ELISA assays (see Example 20). Thus, samples previously identified as reactive with HGBV-A and/or HGBV-B proteins additionally show reactivity with HGBV-C proteins. The reactivity with multiple proteins from the 3 HGBV viruses may be due to cross-reactivity resulting from shared epitopes between the viruses. Alternatively, this may be a result of infection with multiple viruses, or to other unidentified factors.

TABLE 22
HGBV-C Samples

PCR product ^a	Restriction digest ^b	Reactivity with human G8-81 serum	Reactivity with human 240D serum
-----------------------------	------------------------------------	---	--

	GB-C	KpnI, XbaI	+	-
	C.1	EcoRI, XbaI	+	-
5	C.3/2	EcoRI, XbaI	-	-
	C.4	KpnI, XbaI	-	-
	C.9	KpnI, PstI	ND	-
	C.10	EcoRI, XbaI	ND	-
	C.5	KpnI, XbaI	+/-	-
10	C.6	KpnI, PstI	+	-
	C.7	NdeI-fill, BamHI	-	+
	C.8/12	KpnI, XbaI	+	-

15 ^aPCR product is as indicated in previous TABLES or Examples. ^bRestriction digests used to liberate the PCR fragment from pT7Blue T-vector. ND = not done.

Example 20. Serological studies with GBV-C

A. Recombinant Protein Purification Protocol

20 Bacterial cells expressing the CKS fusion proteins were frozen and stored at -70C. The bacterial cells from each of the GBV-C constructs were thawed and disrupted as described in Example 15 for GBV-B constructs. Further, the recombinant proteins were purified as described for GBV-B recombinant proteins in example 15.

25 The fractions which were collected during the purification protocol were electrophoretically separated and stained with Coomassie Brilliant Blue R250 and examined for the presence of a protein having a molecular weight of approximately 75kD (CKS C.1/SEQUENCE I.D. NO. 404), 71kD (CKS C.6/ SEQUENCE I.D. NO. 404), and 49kD (CKS C.7/SEQUENCE I.D. NO.404). Proteins bands of the expected molecular weight were observed for the CKS-C.6 and CKS-C.7

30 recombinant proteins. For the CKS-C.1 protein, a band was observed which corresponded to a molecular weight of 62 kD rather than at the expected molecular weight of 75kD. It is unclear why there are differences between the expected and observed protein band. Fractions containing the protein of interest were pooled and re-examined by SDS-PAGE.

35 The immunogenicity and structural integrity of the pooled fractions containing the purified antigen were determined by immunoblot following electrotransfer to nitrocellulose as described in Example 13. In the absence of a qualified positive control, the recombinant proteins were identified by their

- reactivity with a monoclonal antibody directed against the CKS portion of each fusion protein. When the CKS-C.1 protein (SEQUENCE I.D. NO.404) was examined by Western blot, using the anti-CKS monoclonal antibody to detect the recombinant antigen, a single band at approximately 65kD was observed. This differs from the expected size of 75kD for the CKS-C.1 protein (SEQUENCE I.D. NO.404). Bands of the expected sizes were noted for the CKS-C.6 protein (SEQUENCE I.D. NO. 404), and the CKS C.7 protein (SEQUENCE I.D. NO. 404) were observed when examined by immunoblot.

B. Polystyrene Bead Coating Procedure

- The proteins were dialyzed and evaluated for their antigenicity on polystyrene beads described in Example 15.

C. ELISA Protocol for Detection of Antibodies to HGBV

The ELISA's were performed as described in the previous Example 15.

D. Detection of HGBV RNA in Serum of infected Individuals

- Specimens which were repeatably reactive in the ELISAs were tested for HGBV RNA as described in section D. of the previous example 15.

E. Tamarin Serological Profiles

- None of the sera from the tamarins produced a specific immune response when tested in the ELISA utilizing the CKS-C.1 protein, the CKS-C.6 protein, or the CKS C.7 protein, all derived from the HGBV-C genome. See Example 15 for a description of the tamarin serological profiles.

F. Supplemental Testing

- As noted in Example 15, specimens which were initially reactive were typically retested; if the specimen was repeatably reactive, additional tests (e.g. Western blot) may be performed to further support the ELISA data. For a Western blot result to be considered positive, a visible band should be observed at 65kD for the C.1 protein (SEQUENCE I.D. NO. 404), at 71kD for the C.6 protein (SEQUENCE I.D. NO. 404), or at 49kD for the C.7 protein (SEQUENCE I.D. NO. 404). Since the Western blot had not been optimized to match or exceed the sensitivity of the ELISA's, a negative result was not used to discard the ELISA data. However, a positive result reinforced the reactivity detected by the ELISA's.

- As also noted in Example 15, repeatably reactive specimens which have sufficient volume may be tested by RT-PCR (performed as described in Example 10 using primers corresponding to SEQUENCE I.D. NOS. 8 and 9) to identify HGBV-C specific nucleotide sequences in serum.

G. Experimental Protocol.

In example 15, ELISA's employing recombinant antigens from HGBV-B were utilized to evaluate the presence of antibodies to HGBV-B AND HGBV-A in various human populations. Many of the same specimens were then tested for antibodies to HGBV-C utilizing the C.1 ELISA employing the CKS-C.1 recombinant protein (SEQUENCE I.D. NO. 404), the C.6 ELISA employing the CKS-C.6 recombinant protein (SEQUENCE I.D. NO. 404), the C.7 ELISA employing the CKS-C.7 recombinant protein (SEQUENCE I.D. NO. 404) coated on the solid phase (as described in Example 14). As noted in Example 15, all five of the convalescing tamarins inoculated with HGBV produced a specific but short-lived antibody response to the HGBV-B recombinant proteins (as detected with the 1.7, 1.4 and 4.1 ELISA's). Although none of the tamarins produced a detectable antibody response in the C.1, C.6, C.7 ELISAS, some of the human specimens produced a specific antibody response to the C.1, C.6, and C.7 recombinant protein when tested via Western blot (see Example 13). In the current example, we evaluated the utility of the C.1, C.6, and C.7 ELISA's in detecting antibodies in various human populations.

H. Cutoff Determination

The cutoff for the C.1, C.6, and C.7 ELISAs were determined as described in Example 15.

I. Serological Data Obtained with Low-Risk Specimens

A population consisting of 100 sera and 100 plasma was obtained from healthy, volunteer donors in Southeastern Wisconsin and tested for antibodies to three recombinant proteins from GBV-C including the CKS- C.1 (SEQUENCE I.D. NO. 404) protein in the C.1 ELISA, the CKS- C.6 (SEQUENCE I.D. NO. 404) protein in the C.6 ELISA, and the CKS- C.7 (SEQUENCE I.D. NO. 404) protein in the C.7 ELISA.

For the C.1 ELISA, the mean absorbance values for the serum and plasma specimens were 0.049{ with a standard deviation (SD) of 0.040 } and 0.038 (SD=0.029), respectively. The cutoff for serum and plasma were calculated to be 0.214 and 0.286, respectively. As discussed above, the cutoff value was also expressed as a factor of the negative control absorbance value; specimens having S/N values above 10.0 were considered reactive. Using this cutoff, 0 of 100 plasma specimens and 1 of 100 serum specimens were initially reactive and repeatably reactive for antibodies to the C.1 protein (SEQUENCE I.D. NO. 404).

For the C.6 ELISA, the mean absorbance values for the serum and plasma specimens were 0.102{ with a standard deviation (SD) of 0.046 } and 0.105 (SD=0.047), respectively. Cutoff values were set such that specimens having an

S/N value of 10 or greater were considered reactive. Using this cutoff, three specimens (two from the serum population and one from the plasma population) were repeatably reactive (having S/N values of 10 or greater) for antibodies to the C.6 protein (SEQUENCE I.D. NO. 404).

5 For the C.7 ELISA, the mean absorbance values for the serum and plasma specimens were 0.061 {with a standard deviation (SD) of 0.040} and 0.050 (SD=0.055), respectively. Cutoff values were set such that specimens having an S/N value of 10 or greater were considered reactive. Using this cutoff, none of the specimens were repeatably reactive for antibodies to the C.7 protein (SEQUENCE
10 I.D. NO. 404).

Thus, there is evidence that antibodies to the C.1, C.6, or C.7 proteins are present in approximately 1% of U.S. blood donors (N=200).

J. Specimens Considered "At Risk" for Hepatitis

The data for these studies is summarized in TABLE 23.

15 (i) Specimens from West Africa

A total of 20 of 137 specimens were reactive in one or more of the ELISAs utilizing GBV-C proteins. A total of 12 of 97 were repeatably reactive in the C.1 ELISA, 3 of 52 were repeatably reactive in the C.6 ELISA, 5 of 137 specimens were reactive in the C.7 ELISA. Three of the C.1 reactive specimens were tested
20 on Western blot and found to be reactive.

These data suggest that HGBV may be endemic in West Africa.

(ii) Specimens from Intravenous Drug Users

A total of 112 specimens were obtained from a population of intravenous drug users, as part of a study being conducted at Hines Veteran's Administration
25 Hospital, in Chicago, IL. A total of 2 of 112 specimens were repeatably reactive for one or more proteins. One specimen was repeatably reactive in the C.1 ELISA, one specimen was repeatably reactive in the C.7 ELISA. None of these specimens were positive in the C.6 ELISA.

K. Specimens obtained from individuals with non A-E Hepatitis

30 The data for these studies is summarized in TABLE 23.

Various populations of specimens (described in Example 15.K) were obtained from individuals with non-A-E hepatitis and tested with the 1.5, 2.17, 1.18 and 1.22 ELISAs (described in Example 15.C). Due to insufficient sample volume, not all specimens were tested in all of the ELISAs.

35 (i) Specimens from Japan

None of a total of 89 specimens were repeatably reactive in the C.1 ELISA. Due to lack of specimen volume, the specimens were not tested for antibodies in the C.6 or C.7 ELISAs.

(ii) Specimens from Greece

5 A total of 67 specimens were tested with the C.1 and C.7 ELISAs. None of the specimens were reactive.

(iii) Specimens from Egypt

A total of 18 specimens of 132 specimens were reactive in one or more ELISA. None of the specimens were reactive in the C.1 ELISA. A total of 15
10 specimens were reactive in the C.6 ELISA and three were reactive in the C.7 ELISA.

(iv) Specimens from U.S. (M set)

A total of 6 specimens were reactive in one or more ELISA. Two specimens were repeatably reactive in the C.1 ELISA. Four specimens were
15 repeatably reactive in the C.6 ELISA. None of the specimens were reactive in the C.7 ELISA.

(v) Specimens from U.S. (T set)

None of the 64 specimens were reactive in either the C.1 or the C.6 ELISAs. One specimen was repeatably reactive in the C.7 ELISA.

20 (vi) Specimens from various U.S. clinical sites (set 1)

In total, three of 62 specimens were reactive in one or more ELISA's. One specimen was repeatably reactive in both the C.1 and C.6 ELISA's. Two specimens were repeatably reactive in the C.7 ELISA.

As we have discussed supra, it is possible that more than one strain of the
25 HGBV may be present, or that more than one distinct virus may be represented by the sequences disclosed herein. These are considered to be within the scope of the present invention and are termed "hepatitis GB Virus ("HGBV").

L. Statistical Significance of Serological Results

These data indicated that specific antibodies to HGBV-C proteins (i.e.
30 specimens repeatably reactive for antibodies in C.1, C.6 and C.7 ELISA's) were detected among individuals considered "at risk" for exposure to HGBV and among individuals diagnosed with non A-E hepatitis, and at low rate among volunteer or paid blood donors from the U.S. In TABLE 24, the serological results obtained with the various categories of specimens ("low risk", "at risk" and non A-E
35 hepatitis patients as shown in TABLE 23) were grouped together and analyzed for statistical significance using the Chi square test. Unlike the data in TABLE 23, which compiled the seroprevalence of antibodies to HGBV proteins in the total

- number of specimens tested, the data in TABLE 24 reflect the results obtained with different individuals (persons). For the GBV-C ELISAs, the data indicate that there is a significant difference (with a p value of 0.000) in comparing the seroprevalence of anti-HGBV in volunteer blood donors with the individuals considered "at risk" for exposure to HGBV (West Africa) but not for the IVDUs. In addition, there was a statistically significant difference between the seroprevalence of antibodies to HGBV-C in individuals with non A-E hepatitis in Egypt and the U.S. when compared to volunteer donors. These data suggest that exposure to HGBV-C was associated with non-A through E hepatitis.
- NOTE: although the results of RT-PCR were negative in these initial studies, subsequent data revealed flavi-like viral sequences in serum of seropositive individuals (see Example 19).

Example 21. Presence of HGBV-C in humans with non-A-E hepatitis.

- The generation of HGBV-C-specific ELISAs allowed the identification of immunopositive sera from patients with non-A-E hepatitis (Example for HGBV-C serology). These sera, together with several HGBV-A and/or HGBV-B-immunopositive sera from individuals with documented cases of non-A-E hepatitis (TABLE 25) were examined by RT-PCR for HGBV-C sequences. To increase the likelihood of detecting HGBV-C variants, RT-PCR was performed using degenerate NS3 oligonucleotide primers in a first round of amplification followed by a second round of amplification with nested GB-C-specific primers. Briefly, the first round amplification was performed on serum cDNA products generated as described in Example 6, using 2 mM MgCl₂ and 1 μM primers ns3.2-s1 and ns3.2-a1 (SEQ. ID. NOS. 711 and 712, respectively). Reactions were subjected to 40 cycles of denaturation-annealing-extension [three cycles of (94°C, 30 sec; 37°C, 30 sec; 2 min ramp to 72°C; 72°C, 30 sec) followed by 37 cycles of (94°C, 30 sec; 50°C, 30 sec; 72°C, 30 sec)] followed by a 10 min extension at 72°C. Completed reactions were held at 4°C. A second round of amplification was performed utilizing 2 mM MgCl₂, 1 μM GB-C-specific primers (SEQUENCE I.D. NOS. 675 and 676), and 4% of the first PCR products as template. The second round of amplification employed a thermocycling protocol designed to amplify specific products with oligonucleotide primers that may contain base pair mismatches with the template to be amplified [Roux, Bio/Techniques 16:812-814 (1994)]. Specifically, reactions were thermocycled 43 times (94°C, 20 sec; 55°C decreasing 0.3°C/cycle, 30 sec; 72°C, 1 min) followed by 10 cycles (94°C, 20 sec; 40°C, 30 sec; 72°C, 1 min) with a final extension at 72°C for 10 minutes. PCR

products were separated by agarose gel electrophoresis, visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide, then hybridized to a radiolabeled probe for GB-C after Southern transfer to Hybond-N+ nylon filter. PCR products were cloned and sequenced as described in the art.

5 Using the above methodology, GB-C.4, GB-C.5, GB-C.6 and GB-C.7 were obtained. These sequences are 82.1-86.6% identical to GB-C (SEQUENCE I.D. NO. 400, bases 4167-4365). FIGURE 40 displays the sequence differences of GB-C.4, GB-C.5, GB-C.6 and GB-C.7 aligned to the homologous region of GB-C in the predicted codon triplicates. As demonstrated, a majority of the
10 nucleotide differences do not result in amino acid changes from GB-C. This overall sequence conservation at the amino acid level suggests that GB-C.4, GB-C.5, GB-C.6 and GB-C.7 were derived from different strains of the same virus, HGBV-C. In addition, the level of sequence divergence at the nucleotide level demonstrates that these PCR products are not a result of contamination with any of
15 the previously identified GB-C sequences.

Three of these individuals (the sources of GB-C.4, GB-C.5 and GB-C.7) had no evidence of infection with hepatitis A, hepatitis B or hepatitis C viruses. The presence of GB-C sequences in these individuals with hepatitis of unknown etiology suggests that HGBV-C is one of the causative agents of human hepatitis.
20 Serial samples were available for two of the individuals (containing GB-C.4 and GB-C.5). To follow the HGBV-C sequence in these samples, clone specific RT-PCRs were developed. Briefly, nucleic acids extracted from serum were reverse transcribed using random hexamers as in Example 7. The resultant cDNAs were subjected to 40 cycles of amplification (94°C, 30 sec; 55°C, 30 sec; 72°C, 30 sec)
25 followed by an extension at 72°C for 10 min. GB-C.4- or GB-C.5-specific PCR primers (GB-C.4-s1 and GB-C.4-a1, or GB-C.5-s1 and GB-C.5-a1, respectively) were used at 1.0 µM concentration. PCR products were separated by agarose gel electrophoresis, visualized by UV irradiation after direct staining of the nucleic acid with ethidium bromide, then hybridized to a radiolabeled probe after Southern
30 transfer to Hybond-N+ nylon filter.

GB-C.4 was found in sera from an Egyptian patient with acute non-A-E hepatitis. This patient was seropositive for a HGBV-A protein (see HGBV-A ELISA Example). RT-PCR of five serial samples from the Egyptian patient demonstrated a viremia that persisted for at least 20 days after normalization of the
35 serum ALT values (TABLE 26). The presence of GB-C sequence after serum ALT normalization suggested that HGBV-C may establish chronic infections in some individuals. However, the absence of additional samples from this patient

prevents a conclusion as to the chronic nature of HGBV-C. Additional samples are being pursued to resolve this question.

GB-C.5 was obtained from a Canadian patient with hepatitis associated aplastic anemia. Each sample from this patient was seropositive in the C.7 ELISA (Example 20). GB-C.5 was detected in the samples obtained from the Canadian patient during aplastic anemia (day 13 post-presentation) and at the time of death (day 14, FIGURE. 41) using GB-C.5-specific primers (GB-C.5-s1 and GB-C.5-a1). However, GB-C.5-specific PCR failed to detect GB-C.5 sequence at the time of presentation (day 0, acute hepatitis) and on day 3 (liver failure). Thus, it is unclear whether GB-C.5 was present below the limit of detection in the first samples. If so, HGBV-C may have been the causative agent of this patient's aplastic anemia. However, because GB-C.5 was detected by RT-PCR only during aplastic crisis, GB-C.5 may have been acquired from a blood product administered to combat the anemia. In this case, HGBV-C's association with aplastic anemia would be similar to HCV's [Hibbs, et al. JAMA 267:2051-2054 (1992)].

Due to the distant relation of HGBV-C and HCV, it was of interest to determine whether current methods for detecting HCV infection would recognize human samples containing HGBV-C. Routine detection of individuals exposed to or infected with HCV relies upon antibody tests which utilize antigens derived from three or more regions of HCV-1. These tests allow detection of antibodies to all of the known genotypes of HCV in most individuals[Sakamoto, et al. J. Gen. Virol. 75:1761-1768 (1994); Stuyver, et al. J. Gen. Virol. 74:1093-1102 (1993)]. Second generation ELISAs for HCV were performed on the samples that contain HGBV-C as described in Example 10 (TABLE 25). One of the 4 samples that contain HGBV-C was seropositive for HCV antigens. A limited number of human sera which are seronegative for HCV have been shown to be positive for HCV genomic RNA by a highly sensitive RT-PCR assay[Sugitani, 1992 #65]. A similar RT-PCR assay (as described in Example 9) confirmed the presence of an HCV viremia in the seropositive sample. However, none of the HCV seronegative samples were HCV viremic. Therefore, although 1 of the 4 individuals containing HGBV-C sequences have evidence of HCV infection, the current assays for the presence of HCV did not accurately predict the presence of HGBV-C. The one HCV-positive patient appears to be co-infected with HGBV-C. It is unclear whether the hepatitis noted in this patient was due to HCV, HGBV-C or the presence of both viruses. That HGBV-C and HCV are found in the same patient may suggest that common risk factors exist for acquiring these infections.

Using the PCR protocol described above, GB-C sequences (~85% identical to the previous GB-C isolates shown in FIGURE 41, data not shown) were identified in "normal" units of blood from two volunteer U.S. donor obtained in 1994. These units tested negative for HBV, HCV, and had normal serum ALT values. However, these units tested positive in the 1.4 ELISA. Finding HGBV-C in at least two units of "normal" blood out of ~ 1000 units immunoscreened suggests that this virus is currently in the U.S. blood supply. However, using ELISAs developed from HGBV proteins and nucleotide probes from HGBV sequences, we demonstrate that these units of blood can be identified.

The large amount of sequence variation in the various GB-C sequences (FIGURE 41) should be noted. Although highly sensitive, PCR based assays for viral nucleic acids are dependent on the sequence match between oligonucleotide primers and the viral template. Therefore, because the PCR primers utilized in this study were located in a region of the HGBV-C genome that is not well conserved in various isolates, not all HGBV-C viremic samples tested may have been detected by the RT-PCR assays employed here. Utilization of PCR primers from a highly conserved region of the HGBV-C genome, as have been found in the HCV 5' untranslated region [Cha, et al. *J. Clin. Microbiol.* 29:2528-2534 (1991)], should allow more accurate detection of HGBV-C viremic samples.

TABLE 25
GB-C containing sera

<u>Sequence</u>	<u>Origin</u>	<u>Clinical</u>	<u>GB</u> <u>reactivity</u> ¹	<u>HCV</u> <u>ELISA</u> ²	<u>HCV</u> <u>RNA</u>
GB-C.4	Egyptian	Acute Hepatitis	A	0.25	0
GB-C.5	Canada	HA-AA ³	C	0.15	0
GB-C.6	U.S.	history of hepatitis	C	<u>11.51</u>	+
GB-C.7	U.S.	hepatitis	A	0.26	0

¹ Immunoreactivity detected to recombinant HGBV protein(s) from virus A, B or C.

² Sample to cutoff values reported. Values ≥ 1 (underlined) are considered positive.

³ hepatitis associated aplastic anemia

TABLE 27.
Egyptian Serial Samples

Days post- <u>presentation</u>	<u>ALT (U/l)¹</u>	2.17 ELISA <u>Reactivity²</u>	GB-C.4 <u>RT-PCR</u>
0	128	61.0	+
10	78	62.9	+
20	49	69.4	+
30	33	39.1	+
40	30	55.9	+

¹ Upper limit of normal: 45 U/l.

² Sample to normal reported. Values ≥ 10 are considered positive.

Example 21. Sequence Comparisons and Phylogentic Analysis

- 5 Information about the degree of relatedness of viruses can be obtained by performing comparisons, i.e. alignments, of nucleotide and predicted amino acid sequences. Performing alignments of the HGBV sequences with sequences of other viruses can provide a quantitative assessment of the degree of similarity and identity between the sequences. This information can then be used to develop a
- 10 rationale for the taxonomic classification of the HGBV viruses. In general, the calculation of similarity between two amino acid sequences is based upon the degree of likeness exhibited between the side chains of an amino acid pair in an alignment. The degree of likeness is based upon the physical-chemical characteristics of the amino acid side chains, i.e. size, shape, charge, hydrogen-
- 15 bonding capacity, and chemical reactivity, thus, similar amino acids possess side chains that have similar physical-chemical characteristics. For example, phenylalanine and tyrosine are amino acids containing aromatic side chains and are, therefore, regarded as chemically similar. A discussion of the chemistry of amino acids can be found in any basic biochemistry textbook, for example,
- 20 Biochemistry, Third Edition, Lubert Stryer, Editor, W.H. Freeman and Company, New York, 1988. The calculation of identity between two aligned amino acid sequences is, in general, an arithmetic calculation which counts the number of identical pairs of amino acids in the alignment and divides this number by the length of the sequence(s) in the alignment. Analogous to the method used for
- 25 amino acid sequence alignments, the determination of the degree of identity between two aligned nucleotide sequences is an arithmetic calculation which counts the number of identical pairs of nucleotide bases in the alignment and divides this number by the length of the sequence(s) in the alignment. The calculation of

similarity between two aligned nucleotide sequences sometimes uses different values for transitions and transversions between paired (i.e. matched) nucleotides at various positions in the alignment; however, the magnitude of the similarity and identity scores between pairs of nucleotide sequences are usually very close, i.e.

5 within one to two percent.

As has been stated earlier, limited identity exists between amino acid sequences of the HGBV agents and hepatitis C genotypes. In order to more accurately determine the degree of relatedness between the HGBV agents and HCV, amino acid sequence alignments were performed using the sequence of the
10 entire large open reading frame (ORF) of HGBV-A, B, and C, and the amino acid sequence of the large ORF of several representative HCV isolates. In addition, the degree of relatedness between the HGBV agents and HCV at the nucleotide level was determined using the entire genomic nucleotide sequence of HGBV-A, B, and C, and that of several representative HCV isolates. Alignment of the amino acid
15 and nucleotide sequences was performed using the program GAP of the Wisconsin Sequence Analysis Package (Version 8) which is available from the Genetics Computer Group, Inc., 575 Science Drive, Madison, Wisconsin, 53711. The gap creation and gap extension penalties were 5.0 and 0.3, respectively, for nucleic acid sequence alignments, and 3.0 and 0.1, respectively, for amino acid sequence
20 comparisons. The GAP program uses the algorithm of Needleman and Wunsch (*J. Mol. Biol.* 48:443-453, 1970) to calculate the degree of similarity and identity, expressed as percentages, between the two sequences being aligned.

The nucleotide and amino acid sequences of selected members of the major hepatitis C virus (HCV) genotypes were obtained from GenBank and are shown
25 below with their respective accession numbers:

TABLE 27

	<u>HCV Isolate</u>	<u>Genotype designation</u>	<u>GenBank Accession Number</u>
	HCV-1	1a	M62321
30	HCV-JK1	1b	X61596
	HCV-J6	2a	D00944
	HCV-J8	2b	D10988
	HCV-K3a	3a	D28917
	HCV-Tr	3b	D26556

35

Results of pairwise comparisons of the predicted amino acid sequences of the large open reading frame (i.e. putative precursor polyprotein) and the nucleotide

sequences between each of the above HCV genotypes and each of the HGBV isolates are shown in Tables 28 and 29, respectively. The genotype designation, which is based on the system of nomenclature for HCV isolates described by Simmonds P. et al (1994) Hepatology, 19:1321-1324, of each of the HCV isolates are shown in the top row.

The data shown in TABLE 28 demonstrate that the lower limit of amino acid sequence identity between the HCV genotypes is 69%. This value is very close to that shown by Simmonds et al. [Simmonds, P. et al. Hepatology, 19:1321-1324, 1994] who reported that comparisons of the coding region (i.e. large open reading frame) of eight complete HCV genomes from two major groups showed amino acid sequence similarities of 67.1% to 68.6%; however, these authors did not describe the method by which the similarities were calculated. This value (69%) is also very close to the value of 71-84% identity reported by Okomoto et al., [Virology, 188:331-341, 1992] for comparisons of HCV-J8 with other major HCV isolates; however, these investigators did not describe the method by which the identities were calculated. Comparisons of the HGBV polyprotein sequences with each of the HCV genotypes reveals that the HGBV-encoded polyprotein sequences exhibit no more than 33% identity to any of the HCV polyproteins (TABLE 28). A comparison of the nucleotide sequences (TABLE 29) demonstrates a maximum sequence identity of 44.2% between any HGBV virus and any HCV isolate, whereas, the minimum nucleotide sequence identity between HCV isolates is 64.9%. Therefore, since HGBV-A, B, and C possess nucleotide and predicted amino acid sequence identity with HCV that is well outside the range of identities established for the known HCV genotypes, the HGBV viruses cannot be considered genotypes of the hepatitis C viruses.

The relationship between the hepatitis C viruses and the hepatitis GB viruses can be examined by performing phylogenetic analysis on their aligned nucleotide or deduced amino acid sequences (i.e. large open reading frames) or on a portion of these sequences. This approach has been applied to the hepatitis C viruses and showed that the variability of HCV isolates delineated six equally divergent main groups of sequences [Simmonds, P. et al., J. Gen. Virol. (1993) 74:2391-2399 and Simmonds, P. et al., J. Gen. Virol. (1994) 75:1053-1061]. This analysis resulted in the establishment of a system of nomenclature for the hepatitis C viruses [Simmonds, P. et al. Hepatology, 19:1321-1324, 1994] where the isolates are classified into genotypes based upon the evolutionary distance between sequences.

In order to determine the phylogenetic relationship between the hepatitis GB viruses and the hepatitis C viruses, alignments of amino acid sequences within the putative helicase gene of NS3 and the putative RNA-dependent RNA-polymerase (RdRp) of NS5B were performed. Also included in the alignments were related sequences from other viruses in the Flaviviridae and viruses that have been shown to possess evolutionary relatedness within their helicase or polymerase genes to members of the Flaviviridae [Koonin, E.V. & Dolja, V.V. (1993) Crit. Rev. Biochem. Mol. Biol. 28, 375-430 and Koonin, E.V. (1991) J. Gen. Virol. 72, 2179-2206].

The amino acid sequence alignments were made using the program PILEUP of the Wisconsin Sequence Analysis Package (version 8). Phylogenetic distances between pairs of aligned sequences were determined using the PROTDIST program of the PHYLIP package (version 3.5c, 1993) kindly provided by J. Felsenstein [Felsenstein, J. (1989) Cladistics 5:164-166]. These computed distances were used for the construction of phylogenetic trees using the program NEIGHBOR (neighbor-joining setting). The trees were plotted using the program DRAWTREE. The trees shown are not rooted. The viral sequences used and their corresponding GenBank accession numbers are shown in TABLES 31. The evolutionary distance between each HCV genotype and each of the HGBV viruses for alignments made within the helicase, RdRp, or complete large open reading frame are presented below in TABLES 32, 33, and 34 respectively. The distances calculated between the HCV genotypes or the HGBV viruses and the other viruses listed in TABLE 30 are not shown. The phylogenetic trees produced for amino acids alignments of the viral helicases, RdRps, or complete large open reading frames sequences are shown in FIGURES 42, 43 and 44, respectively.

Amino acid sequence alignments of the putative RdRps, encoded within the NS5B region, of HGBV-A, B and C with the RdRp of several HCV genotypes, two of the pestiviruses, several representative flaviviruses, and several positive-strand RNA plant viruses, show that they possess conserved sequence motifs associated with the RdRps of positive-strand RNA viruses (data not shown). Based on similar analyses, the HGBV-A and HGBV-B encoded helicases show significant identity with the helicases of these positive-strand RNA viruses (data not shown), with the exception of CARMV, TCV, and MNSV which presumably do not possess helicase genes [Guilley, H et al. (1985) Nucleic Acids Res. 13:6663-6677]. These results were not unexpected in view of the association of the helicase and RdRp genes of these viruses into Supergroups demonstrated by previous phylogenetic analyses [Koonin, E.V. & Dolja, V.V. (1993) Crit. Rev.

Biochem. Mol. Biol. 28, 375-430]. However, examination of the phylogenetic distances between the HGBV isolates and the HCV isolates based upon alignment of the helicase or RdRp sequences (TABLES 30 and 31) demonstrates that there is considerable distance between the members of these two groups. The distances
5 calculated demonstrate the close relationship among the HCV genotypes, where the maximum distance between any two genotypes is 0.3696 (RdRp distance). However, the distances calculated from the RdRp alignment between HGBV-A, -B, or -C and any member of the HCV group is 0.96042-1.46261. Similarly, the distances calculated from the helicase alignments for any two HCV genotype
10 ranges from 0.044555-0.19706, while distances between any member of the HCV group and HGBV-A, -B, or -C ranges from 0.69130-0.87120. In addition, alignment of the predicted amino acid sequence of the entire large open reading frames of the HCV genotype and the GB viruses demonstrates a narrow range of evolutionary distance for the HCV isolates (0.17918-0.39646) while the minimum
15 distance between any GB virus and any HCV isolate is 1.68650. Thus, the hepatitis GB viruses exhibit evolutionary distances that are clearly outside the range demonstrated for the hepatitis C virus genotypes.

The phylogenetic analysis of the HGBV and HCV sequences is attempting to answer the question, "How does the divergence of the HGBV sequences from
20 the HCV sequences compare with the divergence among the HCV sequences? In particular, might it be that the HGBV sequences are no more diverged from HCV sequences than the HCV sequences are from one another?" A reasonable condition to be met, if the HGBV sequences were no more diverged from HCV sequences than HCV sequences are from one another, would be that the HGBV-A, HGBV-
25 B, and/or HGBV-C sequences would be at least as close to one of the HCV sequences as the most distantly related pair of HCV sequences (i.e., the minimum distance from any HGBV sequence to any HCV sequence is less than or equal to the maximum observed distance among HCV sequences). This condition is not met by the present sequence data; in Table 31 (RdRp alignment), the minimum
30 HCV-HGBV distance is 2.83 times the maximum HCV-HCV distance; and in Table 32 (helicase alignment), the minimum HCV-HGBV distance is 3.51 times the maximum HCV-HCV distance. Thus, the data do not support the idea that the HGBV sequences are members of a group whose diversity is delimited by previously characterized members of the HCV group.

35 The distribution of these relative distances can be examined with a test based on the bootstrap [Efron, B. (1982) "The jackknife, the bootstrap, and other resampling plans", Society Industrial and Applied Mathematics: Philadelphia;

Efron, B. and Gong, G. (1983) "A leisurely look at the bootstrap, the jackknife, and cross-validation." Am. Stat. 37: 36-48]. The results obtained from the bootstrap sampling are shown in Table 32; which shows the comparison of the HCV-HGBV divergence (minimum of all HCV-HGBV distances) to the HCV diversity (maximum of all HCV-HCV distances) based on PAM distances as calculated using the PROTDIST program. In 1000 bootstrap resamplings of the columns in the sequence alignments, the greatest divergence among HCV sequences was never as large as the smallest of the divergences of the HGBV sequences from the HCV sequences (Table 32). Thus, in independent measurements based on alignments of coding regions from two separate genes, there was not a single instance in which the data were consistent with the HGBV sequences falling within the genetic sequence diversity of HCV genotypes. Leaning in the direction of a conservative estimate, there is less than one chance in 100,000 that the data for the HGBVs could be drawn from the same pool of sequences as the HCV sequences.

TABLE 32

(a) Distances Determined from RdRp Alignment

Out of bootstrap 1000 samples:

Average min(HCV-HGBV distance)/max(HCV-HCV distance) = 2.543645 +/- 0.367443

Minimum min(HCV-HGBV distance)/max(HCV-HCV distance) = 1.617575

(b) Distances Determined from Helicase Alignment

Out of bootstrap 1000 samples:

Average min(HCV-HGBV distance)/max(HCV-HCV distance) = 3.346040 +/- 0.511875

Minimum min(HCV-HGBV distance)/max(HCV-HCV distance) = 2.092055

Assuming that the HCV sequences utilized in this study are representative of the most divergent of the HCV genotypes, these results indicate that HGBV-A, B and C are not genotypes of HCV. In addition, it appears that HGBV-A and HGBV-C are more closely related to each other than either is to HGBV-B, which suggests that HGBV-A and HGBV-C may be representatives of a separate viral lineage. Similarly, HGBV-B may be the sole representative of its own viral lineage. The relative evolutionary distances between the viral sequences analyzed are readily apparent upon inspection of the unrooted phylogentic trees presented in

Figures 45 and 46, where the branch lengths are proportional to the evolutionary distance. The close evolutionary relationship of the HCV viruses is apparent and is consistent whether the analysis is performed using a portion of the encoded genomic sequence or the entire genome (FIGURE 44). The large degree of
5 divergence between HGBV-A, HGBV-B, and HGBV-C and other Flaviviridae members demonstrate that, while being most closely related to the hepatitis C viruses, the GB-agents cannot be considered genotypes of HCV and may actually be representatives of a new virus group, or groups, within the Flaviviridae.

The present invention thus provides reagents and methods for determining
10 the presence of HGBV-A, HGBV-B and HGBV-C in a test sample. It is contemplated and within the scope of the present invention that a polynucleotide or polypeptide (or fragment[s] thereof) specific for HGBV-A, HGBV-B and HGBV-C described herein, or antibodies produced from these polypeptides and
15 polynucleotides, can be combined with commonly used assay reagents and incorporated into current assay procedures for the detection of antibody to these viruses. Alternatively, the polynucleotides or polypeptides specific for the HGBV-A, HGBV-B and HGBV-C (or fragment[s] thereof) described herein, or
20 antibodies produced from such polypeptides and polynucleotides (or fragment[s] thereof), can be used separately for detection of the HGBV-A, HGBV-B and HGBV-C viruses.

Other uses or variations of the present invention will be apparent to those of ordinary skill of the art when considering this disclosure. Therefore, the present invention is intended to be limited only by the appended claims.

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TABLE 2

PRE INOCULATION DAYS PRE	T-1048			T-1053			T-1057			T-1061			GB Challenge
	ALT	GGT	ICD	ALT	GGT	ICD	ALT	GGT	ICD	ALT	GGT	ICD	
87	16	7		59	12		107	4		56	4		
72	16	8	9	47	10	17	32	19	9	20	7	9	
59	36	8	12	37	10	18	35	7	11	22	5	9	
45	28	5	12	37	8	17	19	4	11	23	5	12	
37	23	5	11	32	8	17	26	8	10	27	6	17	
30	31	5	11	44	10	18	18	7	10	24	6	14	
24	25	5	10	39	9	18	34	3	12	24	7	10	
17	19	4	11	49	10	18	32	7	8	26	7	11	
9	24	6	9	30	7	15	24	12	12	27	8	12	
0	31	6	16	48	4	17	21	9	8	19	2	15	
POST INOCULATION													
DAYS POST													
7	38	9	15	67	11	29	47	10	13	32	8	12	
11				172	15	53							
14	63		39	Sacrificed			198	34	90	48	7	16	
21	93	28	57				137	180	22	68	11	42	
28	138	42	71				179	197	45	69	19	34	
35	115	37	64				156	112	26	70	21	8	
42	116	42	76				139	177	54	87	23	61	
49	81	56	34				40	59	16	59	20	41	
56	56	34	42				29	26	12	59	30	45	
63	42	18	25				29	13	11	91	34	60	
77	33	7	15				35	9	12	37	22	29	
84	35	6	17				26	10	12	38	15	23	
91	41	7	19				33	7	12	17	11	14	
97	28	7	20				20	8	10	15	10	9	
105	36	11	22				46	23	14	20	8	13	
112	28	8	9				30	13	11	19	10	12	
119	35	6	18				27	7	10	24	11	15	
CO	48.1	10.7	18.7	65.1	15.5	20.7	50.3	25.2	15.5	33.7	12.1	21.9	

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TABLE 3

PRE INOCULATION DAYS PRE	T-1047			T-1042		
	ALT	GGT	ICD	ALT	GGT	ICD
87	79	12		99	6	
72	40	6	18	27	4	8
59	48	5	20	37	6	8
45	60	10	19	24	5	8
37				40	7	11
30	47	8	26	39	4	10
24				25	2	11
17	54	12	27	33	5	12
9				44	5	11
0	43	12	18	33	5	12
POST INOCULATION DAYS POST						
	ALT	GGT	ICD	ALT	GGT	ICD
7	33	10	15	30	6	9
11						
14	49	9	18	32	6	8
21	33	6	13	48	8	12
28	38	7	12	28	5	11
35	44	8	15	38	7	11
42	38	8	14	31	9	11
49	52	8	16	28	7	9
56	41	9	15	21	6	11

CO	73.7	19.1	35.3	58.6	9.7	16.1
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TABLE 4

PRE INOCULATION DAYS PRE	T-1044		T-1034		ALT	ICD	T-1044 GGT	ICD	ALT	T-1034 GGT	ICD
	ALT	GGT	ALT	GGT							
87	102	6	97		97						
72	19	5	42		42	11	6		6	12	12
59	23	6	12		12	11	11		11	12	12
45	37	6	32		32	12	6		6	10	10
37	37	6	21		21	15	6		6	22	22
30	41	7	29		29	24	6		6	23	23
24	27	5	22		22	12	8		8	15	15
17	22	6	26		26	10	10		10	12	12
9	31	4	30		30	12	4		4	11	11
0	40	4	19		19	14	3		3	17	17
POST INOCULATION DAYS POST											
7	34	6	27		27	14	8		8	13	13
11											
14	39	8	28		28	16	12		12	13	13
21	36	6	21		21	10	8		8	16	16
28	37	6	14		14	9	9		9	13	13
35	35	5	19		19	10	9		9	12	12
42	27	4	32		32	9	8		8	13	13
49	59	7	33		33	13	7		7	14	14
56	24	4	30		30	12	9		9	12	12
63	30	5	31		31	11	9		9	12	12
67	21	7	39		39	9	11		11	10	10
CO	60.3	9.0	56.6		56.6	28.5	15.9		15.9	31.9	31.9

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TABLE 5

PRE INOCULATION DAYS PRE	T-1038			T-1049			T-1051			T-1055		
	ALT	CGT	ICD	ALT	CGT	ICD	ALT	CGT	ICD	ALT	CGT	ICD
115	82	9		102	13		41	15		97	34	
100	42	4	15	23	9	9	31	6	13	30	3	9
87	30	8	13	28	7	12				41	6	11
73	45	5	16	68	10	27				44	4	12
65												
58	29	9	15	22	6	15	23	10	16	35	6	14
52												
45	48	8	17	49	9	16	23	13	13	27	8	11
37												
31	41	14	12	28	7	14	26	7	12	24	3	10
28												
16				30	9	14	29	9	13	15	5	8
0	32	16	10	24	6	15	27	9	11	23	7	10
POST INOCULATION DAYS POST												
7	30	12	10	42	5	15	27	6	18	150	11	21
11	81	18	42	79	15	33	66	13	42	161	19	50
14	178	24	77	123	21	86	78	14	35			
	sacrificed			sacrificed						sacrificed		
21				108	18	60						
28				308	53	39						
35				273	108	56						
49				84	27	34						
56				66	28	34						
63				72	28	29						
69				41	18	19						
76				28	11	13						
83				44	12	15						
90				43	7	16						
CO	66.2	20.1	21.0	94.2	13.2	34.9	38.4	18.2	18.5	65.8	11.3	17.6

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TABLE 8

HGBV CLONES

Clone	size ^a	Southern ^b	Genomic PCR ^c	Tamarin Plasma ^d						H205 ^e	Northern ^f
				Pre-inoculation		Acute Phase					
				PCR	RT-PCR	PCR	RT-PCR	PCR	RT-PCR		
2	737 bp	neg.	ND	0/1	0/1	0/1	1/1		+	ND	
4	221 bp	ND ^g	neg.	ND	0/1	0/1	1/1		+	≥7 kb	
10	307 bp	ND	neg.	ND	0/1	0/1	1/1		+	ND	
16	532 bp	neg.	neg.	0/1	0/7	0/1	4/6		+	ND	
18	306 bp	ND	neg.	ND	0/1	0/1	1/1		+	ND	
23	369 bp	ND	ND	ND	0/1	ND	1/1		+	ND	
50	337 bp	ND	neg.	ND	0/1	0/1	1/1		+	≥7 kb	

^a size of clone in base pairs (bp). ^b Southern blot analysis of tamarin, human, yeast and *E. coli* genomic DNA using GB clone sequence as a probe. Negative (neg.) indicates that clone did not hybridize with any of the genomic DNAs tested. ^c Genomic PCR was performed on tamarin, human yeast and *E. coli* DNAs with primers that amplify the cloned sequence. Neg. indicates that the clone was not amplified from the DNA sources tested. ^d Tamarin plasmids, both pre-HGBV-inoculation (pre-inoc.) and acute phase (acute) were tested for the presence of cloned sequence by PCR (to detect DNA sequences) or RT-PCR (to detect RNA and DNA sequences). The results are reported as the number of PCR-positive samples per number of samples examined. ^e H205 was tested for the presence of the clones by RT-PCR. All clones were RT-PCR positive (+) in H205 source. ^f Northern blot analysis was performed on total liver RNA from normal tamarin liver and acute phase tamarin liver using radiolabel clone sequences. The estimated size of the specific band detected in the acute phase liver RNA is given. ^g ND: not determined.

TABLE 12

Sera	Days Pre (-) or Post (+) Inoculation	CORZYME		HAVAB		HCV 2.0		HEV	
		A492	Result c/o=0.582*	A492	Result c/o=0.662**	A492	S/N c/o=0.408***	A492	S/N c/o= >6****
Control Sera									
HuN/C		1.397	-	1.295	-	0.070	-	0.038	-
HuP/C		0.036	+	0.030	+	1.352	+	1.932	+
Tamarin Sera									
T1048 pre	-44	N.D	N.D	N.D	N.D	N.D	N.D	0.007	1.47
T1048 pre	-23	0.912	-	1.834	-	0.023	-	N.D	N.D
T1048 post	+112	1.148	-	1.387	-	0.025	-	0.026	0.68
T1051 pre	-52	N.D	N.D	N.D	N.D	N.D	N.D	0.019	0.50
T1051pre	-8	0.548	+	1.465	-	0.035	-	N.D	N.D
T1051 post	+76	0.700	-	1.559	-	0.043	-	0.029	0.76
T1057 pre	-30	N.D	N.D	N.D	N.D	N.D	N.D	0.016	0.42
T1057 pre	-23	0.369	+	1.411	-	0.029	-	N.D	N.D
T1057 post	+49	N.D	N.D	N.D	N.D	N.D	N.D	0.017	0.45
T1057 post	+77	0.580	+	1.444	-	0.028	-	N.D	N.D
T1061 pre	-30	N.D	N.D	N.D	N.D	N.D	N.D	0.102	2.68
T1061 pre	-23	0.248	+	0.029	+	0.040	-	N.D	N.D
T1061 post	+112	0.240	+	0.048	+	0.030	-	0.077	2.03

*Cutoff was determined: $0.4 \times N/Cx + 0.6 \times P/Cx$ ** Cutoff was determined: $N/Cx + P/Cx / 2$ *** Cutoff was determined: $N/Cx + 25\% P/C$ **** Cutoff was determined: $S/N > 6$

TABLE 14

HGBV-A Samples

PCR product ^a	Restriction digest ^b	Reactivity with T1048 + T1051 sera	Reactivity with GB serum	Reactivity with G1-41 serum	Reactivity with G1-14 serum	Reactivity with G1-31 serum	Reactivity with 341C serum
1.2	EcoRI, PstI	-	-	-	-	-	-
1.5	EcoRI, HindIII	-	-	+	-	-	-
1.8	KpnI, PstI	-	-	-	-	-	-
1.17	KpnI, PstI	-	-	ND	ND	-	-
1.18	KpnI, PstI	-	-	ND	ND	+	+
1.19	KpnI, PstI	-	-	ND	ND	-	+
1.20	KpnI, PstI	-	-	ND	ND	-	-
1.21	XbaI, BamHI	-	-	ND	ND	-	-
1.22	KpnI, PstI	-	+	ND	ND	-	-
1.23	KpnI, PstI	-	-	ND	ND	-	-
2.17	BamHI, SphI	-	+	ND	ND	+	+
2.18	KpnI, PstI	-	-	ND	ND	-	-
4.2	EcoRI, blunt	-	-	ND	ND	-	-

^aPCR product is as indicated in Table 9, Table 10, or Example 13. ^bRestriction digests used to liberate the PCR fragment from pT7Blue T-vector or for direct digestion of 4.2 PCR product. ND = not done.

Table 16 SEROLOGIC RESULTS HGBV- B

POS/TOTAL

CATEGORY	SPECIMENS	1.4 ELISA*	4.1 ELISA*	1.7 ELISA*	TOTAL
Individuals Assumed "Low Risk" for HGBV Exposure	Volunteer Blood Donors				
	1	0/200	0/200	0/200	0/200
	2	4/200			4/200
	Interstate Blood Bank	9/760	ND**	0/760	9/760
Individuals Assumed "At Risk" for HGBV Exposure	Intravenous				
	Drug Users 1	3/112	5/112	3/112	9/112
	2	1/99	0/99	0/99	1/99
	Western Africa Hemophiliacs	91/1300	51/1300	43/1300	181/1300
		2/100	ND	1/100	2/100
Individuals with "Non A-E Hepatitis"	Clinics in Japan	0/180	7/89	2/180	9/180
	Clinics in Greece	4/73	0/67	3/73	5/73
	Clinics in U.S. (SET M)	1/72	2/72	3/72	4/72
	Clinics in U.S. (SET T)	0/64	0/64	0/64	0/64
	Clinics in U.S.	0/62	2/62	2/62	3/62
	Clinics in Egypt	9/132	1/132	9/132	11/132
	Clinics in New Zealand	2/56	1/56	1/56	4/56
	Clinics in Costa Rica	2/100	ND	1/100	2/100
	Clinics in Pakistan	2/82	ND	2/82	4/82
	Clinics in Italy	0/10	0/10	0/10	0/10
	Clinics in U.S. SET 1	0/56	ND**	0/56	0/56
	SET 2	0/20	ND**	0/20	0/20
	SET 3	3/51	ND**	1/51	3/51

TABLE 1 [†]HGBV-B Serological Results

	Repeatably Reactive 1.4, 1.7 or 4.1 ELISA	Negative In 1.4, 1.7 or 4.1 ELISA	X ² *	SIG**
Volunteer Blood Donors	0	200	-	-
IBB Ohio	9	751	-	???
Intravenous Drug Users (US)	1 9	99 103	-	NS* ???
West Africa	181	1119		???
Clinics in Japan	4	81	-	???
" in New Zealand	4	52	-	???
" in Greece	1	10	-	???
" in Egypt in U.S.	5	20	-	???
Set 1	0	56		NS*
Set 2	0	20		NS*
Set 3	3	51		???
Set M	4	68		????
Set T	0	64		NS*
Assumed Low Risk	0	200	-	-
Paid Blood Donors	9	751		???
Assumed High Risk	191	1321		•??
Non A-E Hepatitis	21	431	-	NS*

*Chi square value obtained by applying the Chi square test. **Determination of statistical significance based upon the Chi square analysis. †Not statistically significant by the Chi square test. •Statistically significant by the Chi square test, with p<0.050.

Table 18. SEROLOGIC RESULTS - TABLE A

POS/TOTAL

CATEGORY	SPECIMENS	1.18 ELISA	2.17 ELISA	1.22 ELISA	1.5 ELISA	TOTAL REACTIVE
Individuals Assumed "Low Risk" for HGBV Exposure	Volunteer Blood Donors 1	0/200	1/200	0/200	0/200	1/200
	2 Interstate Blood Bank	ND*	ND	ND	0/760	0/760
Individuals Assumed "At Risk" for HGBV Exposure	Intravenous Drug Users	1/112	1/112	0/112	0/112	2/112
	Western Africa	9/353	43/817	6/817	58/1300	91/1300
Individuals with "Non A-E Hepatitis"	Clinics in Japan	0/89	1/89	ND	4/89	3/89
	Clinica in Greece	0/67	0/67	0/67	0/67	0/67
	Clinics in (Mayo)	3/72	2/72	4/72	0/72	7/72
	Clinics in U.S. (Thiele)	0/64	0/64	0/64	0/64	1/64
	Clinics in U.S. (1/3)	1/62	2/62	2/62	0/62	3/62
	Clinics in Egypt	0/132	7/132	0/132	0/132	7/132
	Clinica in New Zealand	ND	ND	ND	0/56	ND

* Separate ELISA's were developed and cutoffs determined

** Not Done

TABLE 19 HGBV-A Serological Results

	Repeatably Reactive in 1.18, 2.17, 1.22, or 1.5 ELISA	Negative In 1.18, 2.17, 1.22, or 1.5 ELISA	χ^2 *	SIG**
Volunteer Blood Donors	1	199	-	-
IBB Ohio	0	760	-	NS*
Intravenous Drug Users (US)	2	110	-	NS*
West Africa	91	1209	-	???
Clinics in Japan	2	83	-	???
" in New Zealand	0	56	-	NS*
" in Greece	0	11	-	NS*
" in Egypt	3	22	-	???
in U.S.				
Set 1	ND	ND	-	-
Set 2	ND	ND	-	-
Set 3	ND	ND	-	-
Set M	7	65	-	???
Set T	1	63	-	???
Assumed Low Risk	1	200	-	-
Paid Blood Donors	0	760	-	NS*
Assumed High Risk	93	1319	-	???
Non A-E Hepatitis	13	300	-	????*

*Chi square value obtained by applying the Chi square test. **Determination of statistical significance based upon the Chi square analysis. †Not statistically significant by the Chi square test. *Statistically significant by the Chi square test, with $p < 0.050$.

Table 23 SEROLOGIC RESULTS HGBV-C

CATEGORY	SPECIMENS	POS/TOTAL			
		C.7 ELISA*	C.1 ELISA*	C.6 ELISA*	TOTAL
Individuals Assumed "Low Risk" for HGBV Exposure	Volunteer Blood Donors 1 2	0/200	1/200	3/200	4/200
	Interstate Blood Bank	ND**	ND**	ND**	ND**
Individuals Assumes "At Risk" for HGBV Exposure	Intravenous Drug Users	1/112	1/112	0/112	2/112
	Western Africa	5/137	12/97	3/52	20/137
Individuals with "Non A-E Hepatitis"	Clinics in Japan	ND**	0/89	ND**	0/89
	Clinics in Greece	0/67	0/67	ND**	0/67
	Clinics in U.S. (SET M)	0/72	2/72	4/72	6/72
	Clinics in U.S. (SET T)	1/64	0/64	0/64	1/64
	Clinics in U.S. (SET 1/3)	2/62	1/62	1/62	3/62
	Clinics in Egypt	3/132	0/132	15/132	18/132
	Clinics in New Zealand	ND**	ND**	ND**	ND**

TABLE 24 HGBV-C Serological Results

	Repeatably Reactive in C.1, C.6, or C.7 ELISA	Negative In C.1, C.6, or C.7 ELISA	χ^2 *	SIG**
Volunteer Blood Donors	4	196	-	-
IBB Ohio	ND	ND	-	NS*
Intravenous Drug Users (US)	2	110	-	NS*
West Africa	20	117	-	???
Clinics in Japan	0	85	-	NS*
" in New Zealand	ND	ND	-	NS*
" in Greece	0	11	-	NS*
" in Egypt	6	19	-	???
in U.S.				
Set 1/3	3	59		???
Set M	6	66		???
Set T	1	63		NS*
Assumed Low Risk	0	200	-	-
Paid Blood Donors	9	751		???
Assumed High Risk	191	1330		???
Non A-E Hepatitis	21	303	-	???

*Chi square value obtained by applying the Chi square test. **Determination of statistical significance based upon the Chi square analysis. †Not statistically significant by the Chi square test. *Statistically significant by the Chi square test, with $p < 0.050$.

TABLE 28 Amino acid sequence similarity (identity) across large ORFs (%)

genotype: isolate:	1a JK1	1b J6	2a J8	2b K3A	3a Tr	3b HGBV-A	HGBV-B
HCV-1							
HCV-JK1	91 (85)						
HCV-J6	84 (72)	83 (72)					
HCV-J8	84 (72)	83 (71)	92 (84)				
HCV-K3A	85 (74)	84 (75)	91 (84)	82 (70)			
HCV-Tr	84 (74)	84 (73)	82 (69)	81 (69)	91 (84)		
HGBV-A	49 (26)	52 (31)	49 (28)	50 (28)	48 (26)	47 (27)	
HGBV-B	52 (32)	49 (27)	52 (33)	52 (33)	50 (31)	50 (31)	
49 (27)							
HGBV-C	51 (29)	49 (27)	51 (28)	50 (28)	51 (29)	50 (28)	
66 (48)		51 (28)					

TABLE 29 . Nucleotide sequence identity across entire genomes (%)

genotype: 3b	1a	1b	2a	2b	3a	Tr
isolate:	HCV-1	JK1	J6	J8	K3A	
HGBV-A						
HCV-JK1	78.8					
HCV-J6	67.8	68.0				
HCV-J8	67.3	67.2	77.0			
HCV-K3A	68.6	69.1	65.2			
HCV-Tr	68.3	68.4	64.9	77.5		
HGBV-A	41.6	41.8	41.0	41.6	41.6	
HGBV-B	43.8	43.4	43.3	43.5	43.1	42.6
HGBV-C	42.9	42.3	42.1	41.1	41.5	53.3
						41.6

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TABLE 30 GenBank Accession numbers

Virus	GenBank Accession Number
HCV-1	M62321
HCV-JK1	X61596
HCV-J6	D00944
HCV-J8	D10988
HCV-Tr	D26556
Dengue 1	M87512
Dengue 2	M29095
BVDV, Bovine viral diarrhoea virus	M31182
HCHV, Hog cholera virus	J04358
WNV, West Nile virus	M12294
YFV, Yellow fever virus	X15062
JEV, Japanese encephalitis virus	M18370
CARMV, Carnation mottle virus	X02986
TCV, Turnip crinkle virus	M22445
MNSV, Melon necrotic spot virus	D12536
PBMSV, Pea seed-borne mosaic virus	D10930
PPV, Plum pox virus	X16415
TVMV, Tobacco vein mottling virus	X04083
TEV, Tobacco etch virus	M15239

TABLE 31 Evolutionary distances: RdRp sequences.

	HGBV-A	HGBV-C	HCV-J6	HCV-J8	HCV-1	HCV-JK1	HCV-3A
HGBV-C	0.54878						
HCV-J6	1.14632	1.43972					
HCV-J8	1.16398	1.43043	0.11550				
HCV-1	1.25705	1.36554	0.26824	0.26864			
HCV-JK1	1.23506	1.46261	0.29041	0.29207	0.11347		
HCV-3A	1.26876	1.40316	0.34880	0.36960	0.30535	0.35182	
HGBV-B	1.14880	1.31596	1.00961	0.96402	1.07379	1.04486	1.01997

TABLE 32 Evolutionary distances: helec case sequences.

	HGBV-A	HGBV-C	HCV1	HCVJK1	HCVJ6	HCVJ8	HCV3A
HGBV-C	0.42074						
HCV-1	0.86162	0.71571					
HCV-JK1	0.87120	0.71731	0.04455				
HCV-J6	0.85757	0.73261	0.14090	0.14079			
HCV-J8	0.83480	0.72594	0.14200	0.14779	0.07495		
HCV-3A	0.86537	0.77858	0.18703	0.19706	0.16267	0.17985	
HGBV-B	1.02224	0.92174	0.72260	0.71806	0.72050	0.69130	0.73171

TABLE 33 Evolutionary distances: complete large open reading frames.

	HGBV-A	HGBV-C	HCVJ6	HCVJ8	HCVI	HCVJKI	HCV3A
HGBV-C	0.92796						
HCV-J6	2.41182	2.14894					
HCV-J8	2.41162	2.16319	0.17918				
HCV-1	2.38813	2.11644	0.35897	0.36481			
HCV-JK1	2.40833	2.12664	0.36577	0.37948	0.17411		
HCV-3A	2.44255	2.15842	0.38848	0.39646	0.32500	0.32271	
HGBV-B	2.68767	2.47039	1.69983	1.68650	1.71216	1.71657	1.73779

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 720

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCACTCTCC AGCCTCTCAC CGCA

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCTGCGGT GA

12

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGCAACTGT GCTATCCGAG GGAA

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCTTCCCT CG

12

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCGACGTCG ACTATCCATG AACA

24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCTGTTCA TG

12

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCGCG GCCGCTCG

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGAGCGGCCG CGAATTCCTT

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGACACCAG ACCAACTGGT AATG

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAATTCGTG TGGGTTCGGT GGTGGTGGCG CTTTAGGCAG CCTCCACGCC CACCACCTCC 60
CAGATAGAGC GCGGGCACTG TAGGGAAGAC CEGGGACCGG TCACTACCAA GGACGCAGAC 120
CTCTTTTGA GTATCACGCC TCCGGAAGTA GTTGGGCAAG CCCACCTAYA TGTGTTGGGA 180
TGGTTGGGGT TAGCCATCCA TACCGTACTG CCTGATAGGG TCCTTGCGAG GGGATCTGGG 240
AGTCTCGTAG ACCGTAGCAC ATGCCTGTTA TTTCTACTCA AACAAGTCCT GTACCTGCRC 300
CCAGAACCGC CAAGAACAAG CAGACGCAGG CTTCATATCC TGTGTCCATT AAAACATCTG 360
TTGAAAGGGG ACAACGAGCA ARGCGCAAAG TCCAGCGCGA TGCTCGGCCT CGTAATTACA 420
AAATTGCTGG TATCCATGAT GGCTTGCGA CATTGGCTCA GGCTGCTTTR CCAGCTCATG 480
GTTGGGGACG CCAAGACCCT CGCCATAAGT CTCGCAATCT TGGAATCCTT CTGGATTACC 540
CTTTGGGGTG GATTGGTGAT GTTACAACTC ACACACCTCT AGTAGGCCCG CTGGTGGCAG 600
GAGCGGTCGT TCGACCAGTC TGCCAGATAG TACGCTTGCT GGAGGATGGA GTCAACTGGG 660
CTACTGGTTG GTTCGGTGTC CACCTTTTTG TGGTATGTCT GCTATYTTTG GCCTGTCCCT 720
GTAGTGGGGC GCGGGTCACT GACCCAGACA CAAATACCAC AATCCTGACC AATTGCTGCC 780
AGCGTAATCA GGTTATCTAY TGTCTCCTT CCACTTGCCCT ACACGAGCCT GGTGTGTGA 840
TCTGTGYGGA CGAGTGCTGG GTTCCCGCCA ATCCRTACAT CTCACACCCT TCCAATTGGA 900
CTGGCACGGA CTCCTTCTTG GCTGACCACA TTGATTTTGT TATGGGCGCT CTTGTGACCT 960
GTGACGCCCT TGACATTGGT GAGTTGTGTG GTGCGTGTGT ATTAGTCGGT GACTGGCTTG 1020
TCAGGCACTG GCTTATTCAC ATAGACCTCA ATGAACTGG TACTTGTTAC CTGGAAKTGC 1080
CTACTGGAAT AGATCCTGGG TTCCTAGGGT TTATCGGGTG GATGGCCGGC AAGGTCGAGG 1140
CTGTCATCTT CTTGACCAA CTGGCTTCAC AAGTACCATA CGCTATTGCG ACTATGTTTA 1200
GCAGTGATCA CTACCTGGCG GTTGGCGCTC TGATCTACTA YGCCTCTCGG GGCAAGTGGT 1260
ATCAGTTGCT CCTAGCGCTT AYGCTTTACA TAGAAGCGAC CTCTGGAAAC CCYATCAGGG 1320
TGCCCACTGG ATGCTCAATA GCTGAGTTTT GCTCGCCTTT GATGATACCA TGTCTTGCC 1380
ACTCTTATTT GAGTGAGAAT GTGTCAGAAG TCATTTGTTA CAGTCCAAAG TGGACCAGGC 1440
CTGTCACTCT AGAGTATAAB AACTCCATAT CTTGGTACCC CTATACAATC CCTGGTGC GA 1500
GGGGATGTAT GGTAAATTC AAAAATAACA CATGGGGTTG CTGCCGWWTC GCAATGTGCC 1560
ATCGTACTGC ACTATGGGCA CTGATGCAGT GTGGAASSAC AGTCGCAACA CTTACGAAGC 1620

ATGCGGTGTA ACACCATGGC TAACAACCGC ATGGCACAAC GGCTCAGCCC TGAAATTGGC	1680
TATATTACAA TACCCTGGGT CTAAAGAAAT GTTTAAACCT CATAATTGGA TGTCAGGCCA	1740
CTTGATTTTT GAGGGATCAG ATACCCCTAT AGTTTACTTT TATGACCCTG TGAATTCCAC	1800
TCTCCTACCA CCGGAGAGGT GGGCTAGGTT GCCCGGTACC CCACCTGTGG TACGTGGTTC	1860
TTGGTTACAG GTTCCGCAAG GTTTTACAGT GATGTGAAAG ACCTAGCCAC AGGATTGATC	1920
ACCAAAGACA AAGCCTGGAA AAATTATCAG YTCTTATATT CCGCCACGGG TGCTTTGTCT	1980
CTTACGGGAG TTACCACCAA GGCCGTGGTG CTAATTCTGT TGGGGTTGTG TGGCAGCAAG	2040
TATCTTATTT TAGCCTACCT CTGTTACTTG TCCCTTTGTT TTGGGCGCGC TTCTGGTTAC	2100
MCTTTGCGTC CTGTGCTCCC ATCCCAGTCG TATCTCCAAG CTGGCTGGGA TGTTTTGTCT	2160
AAAGCTCAAG TAGCTCMTT TGCTTTGATT TTCTTCATCT GTTGCTATCT CCGCTGCAGG	2220
CTACGTTATG CTGCCCTTTT AGGGTTTGTG CCCATGGCTG CGGGCTTGCC CCTAACTTTC	2280
TTTGTTGCAG CAGCTGCTGC CCAACCAGAT TATGACTGGT GGGTGCGACT GCTAGTGGCA	2340
GGGTTAGTTT TGTGGGCCGG CCGTGACCGT GGTACGCAT AGCTCTGCTT GTAGGTCCTT	2400
GGCCTCTGGT AGCGCTTTYT AACCTCTTG CATTTSSKA CGCCTGCTTA GCTTTTGACA	2460
CCGAGATAAT TGGAGGGCTG ACAATACCAC CTGTAGTAGC ATTAGTTGTC ATGTCTCGTT	2520
TTGGCTTCTT TGCTCACTTG TTACCTCGCT GTGCTTTAGT TAACTCCTAT CTTTGGCAAC	2580
GTTGGGAGAA TTGGTTTTGG AACGTTACAC TAAGACCGGA GAGGTTTCTC CTTGYGCTGG	2640
TTTGTTCCTT CCGTGCGACA TATGACGTGC TGGTGACWTT CTGTGTGTGT CACGTAGCTC	2700
TTCTATGTTT AACATCCAGT GCAGCAYMGT TCTTTGGGAC TGA CTCTAGG GTTAGGGCCC	2760
ATAGAATGTT GGTGCGTCTC GGAAAGTGTC ATGCTTGGTA TTCTCATTAT GTTCTTAAGT	2820
TTTTCTCTT AGTGTGTTGGT GAGAATGGTG TGTTCCTTA KAAGCACTTG CATGGTGATG	2880
TCTTGCTTAA TGATTTTGCC TCGAACTAC CATTGCAAGA GCCATTTTTC CCTTTTGAAG	2940
GCAAGGCAAG GGTCTATAGG AATGAAGGAA GACGCTTGGG KKGTTGGGAC ACGGTTGATG	3000
GTTTGSSCGT TGTBGC GCGT CTCGGCGACC TTGTTTTGCG AGGTTAGCT ATGCCGCCAG	3060
ATGGGTGGGC CATTACCGCA CCTTTTACGC TGCAGTGTCT CTCTGAACGT GGCACGCTGT	3120
CAGCGATGGC AGTGGTCATG ACTGGTATAG ACCCCGAAC TTGGACTGGA ACTATCTTCA	3180
GATTAGGATC TCTGGCCACT AGCTACATGG GATTTGTTTG TGACAACGTG TTGAATACTG	3240
CTCACCATGG CAGCAACGGG GGCCGGTTGG CTCATCCAC AGGCTCCATA CACCCAATAA	3300
CCGTTGACGC GGCTAATGAC CAGGACATCT ATCAACCACC ATGTGGAGCT GGGTCCCTTA	3360

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CTCGGTGCTC TTGCGGGGAG ACCAAGGGGT ATCTGGTAAC ACGACTGGGG TCATTGGTTG	3420
AGGTCAACAA ATCCGATGAC CCTTATTGGT GTGTGTGCGG GGCCCTTCCC ATGGCTGTTG	3480
CCAAGGGTTC TTCAGGTGCC CCGATTCTGT GCTCCTCCGG GCATGTTATT GGGATGTTCA	3540
CCGCTGCTAG AAATTCTGGC GGTTCTAGTCG GCCAGATTAG GGTTAGGCCG TTGGTGTGTG	3600
CTGGATACCA TCCCCAGTAC ACAGCACATG CCACTCTTGA TACAAAACCT ACTGTGCCTA	3660
ACGAGTATTC AGTGCAAATT TTAATTGCCC CCACTGGCAG CGGCAAGTCA ACCAAATTAC	3720
CACTTTCTTA CATGCAGGRG AAGYATGAGG TCTTGGTCCT AAATCCCAGT GTGGCTACAA	3780
CAGCATCAAT GCCAAAGTAC ATGCACGCGA CGTACGGCGT GAATCCAAAT TGCTATTTTA	3840
ATGGCAAATG TACCAACACA GGGGCTTCAC TTACGTACAG CACATATGGC ATGTACCTGA	3900
CCGGACGATG TTCCCGGAAC TATGATGTAA TCATTTGTGA CGAATGCCAT GCTACCGATC	3960
GAACCACCGT GTTGGGCATT GGAAAGGTCC TAACCGAAGC TCCATCCAAA AATGTTAGGC	4020
TAGTGGTTCT TGCCACGGCT ACCCCCCCTG GAGTAATCCC TACACCACAT GCCAACATAA	4080
CTGAGATTCA ATTAACYGAT GAAGGCACTA TCCCCTTTCA TGGAAAAAAG ATTAAGGAGG	4140
AAAATCTGAA GAAAGGGAGA CACCTTATCT TTGAGGCTAC CAAAAACAC TGTGATGAGC	4200
TTGCTAACGA GTTAGCTCGA AAGGGAATAA CAGCTGTCTC TTAATATAGG GGATGTGACA	4260
TCTCAAAAAT GCCTGAGGGC GACTGTGTAG TAGTTGCCAC TGATGCCTTG TGTACAGGGT	4320
ACACTGGTGA CTTTGATTCC GTGTATGACT GCAGCCTCAT GGTAGAAGGC ACATGCCATG	4380
TTGACCTTGA CCCTACTTTC ACCATGGGTG TTCGTGTGTG CGGGGTTTCA GCAATAGTTA	4440
AAGGCCAGCG TAGGGGCCGC ACAGGCCGTG GGAGAGCTGG CATATACTAC TATGTAGACG	4500
GGAGTTGTAC CCCTTCGGGT ATGGTTCCCTG AATGCAACAT TGTGAAGCC TTCGACGCAG	4560
CCAAGGCATG GTATGGTTTG TCATCAACAG AAGCTCAAAC TATTCTGGAC ACCTATCGCA	4620
CCCAACCTGG GTTACCTGCG ATAGGAGCAA ATTTGGACGA GTGGGCTGAT CTCTTTTCTA	4680
TGGTCAACCC CGAACCTTCA TTTGTCAATA CTGCAAAAAG AACTGCTGAC AATTATGTTT	4740
TGTTGACTGC AGCCCCACTA CAACTGTGTC ATCAGTATGG CTATGCTGCT CCAATGTACG	4800
CACCACGGTG GCAGGGAGCC CGGCTTGGA AAAAACCTTG TGGGGTTCTG TGGCGCTTGG	4860
ACGGCTGTGA CGCCTGTCCT GGCCCAGAGC CCAGCGAGGT GACCAGATAC CAAATGTGCT	4920
TCACTGAAGT CAATACTTCT GGGACAGCCG CACTCGCTGT TGGCGTTGGA GTGGCTATGG	4980
CTTATCTAGC CATTGACACT TTTGGCGCCA CTTGTGTGCG GCGTTGCTGG TCTATTACAT	5040
CAGTCCCTAC CGGTGCTACT GTCGCCCCAG TGGTTGACGA AGAGGAAATC GTGGAGGAGT	5100

GTGCATCATT CATTCCCTTG GAGGCCATGG TTGCTGCAAT TGACAAGCTG AAGAGTACAA	5160
TCACCACAAC TAGTCCTTTC ACATTGGAAA CCGCCCTTGA AAAACTTAAC ACCTTTCTTG	5220
GGCCTCATGC AGCTACAATC CTTGCTATCA TAGAGTATTG CTGTGGCTTA GTCACTTTAC	5280
CTGACAATCC CTTTGCATCA TGCCTGTTTG CTTTCATTGC GGGTATTACT ACCCCACTAC	5340
CTCACAAGAT CAAAATGTTC CTGTCATTAT TTGGAGGCGC AATTGCGTCC AAGCTTACAG	5400
ACGCTAGAGR CGCACTGGCG TTCATGATGG CCGGGGCTGY GGAACAGCT CTTGGTACAT	5460
GGACATCGGT GGGTTTTGTC TTTGACATGC TAGGCGGCTA TGCTGGCGCC TCATCCACTG	5520
CTTGCTTGAC ATTTAAATGC TTGATGGTG AGTGGCYCAC TATGGATCAG CTTGCTGGTT	5580
TAGTCTACTC CGCGTTCAAT CCGGCCGCGAG GAGTTGTGGG CGTCTTGTC GCTTGTGCAA	5640
TGTTTGCTTT GACAACAGCA GGGCCAGATC ACTGGCCCAA CAGACTTCTT ACTATGCTTG	5700
CTAGGAGCAA CACTGTATGT ARTGAGTACT TTATTGCCAC TCGTGACATC CGCAGGAAGA	5760
TACTGGGCAT TCTGGAGGCA TCTACCCCTT GGAGTRTCAT ATCAGCTTGC ATCCGTTGGC	5820
TYCACACCCC GACGGAGGAT GATTGCGGCC TCATTGCTTG GGGTCTARAG ATTTGGCAGT	5880
ATGTGTGCAA TTTCTTTGTG ATTTGCTTTA ATGTCCTTAA AGCTGGAGTT CAGAGCATGG	5940
TTAACATTCC TGGTTGTCCT TTCTACAGCT GCCAGAAGGG GTACAAGGGC CCCTGGATTG	6000
GATCAGGTAT GCTCCAAGCA CGCTGTCCAT GCGGTGCTGA ACTCATCTT TCTGTTGAGA	6060
ATGGTTTTGC AAAACTTTAC AAAGGACCCA GAACTTGTTT AAATTACTGG AGAGGGGCTG	6120
TTCCAGTCAA CGCTAGGCTG TGTGGGTCGG CTAGACCGGA CCCAACTGAT TGGACTAGTC	6180
TTGTCGTCAA TTATGGCGTT AGGGACTACT GTAAATATGA GAAATTGGGA GATCACATTT	6240
TTGTTACAGC AGTATCCTCT CCAAATGTCT GTTTCACCCA GGTGCCCCCA ACCTTGAGAG	6300
CTGCAGTGGC CGTGGACCGC GTACAGGTTT AGYGTATCT AGGTGAGCCC AAAACTCCTT	6360
GGACGACATC TGCTTGCTGT TACGGTCCTG ACGGTAAGGG TAAACTGTT AAGCTTCCCT	6420
TCCGCGTTGA CGGACACACA CCTGGTGGTC GCATGCAACT TAATTTGCGT GATCGACTTG	6480
AGGCAAATGA CTGTAATTCC ATAAACAACA CTCCTAGTGA TGAAGCCGCA GTGTCCGCTC	6540
TTGTTTTCAA ACAGGAGTTG CGGCGTACAA ACCAATTGCT TGAGGCAATT TCAGCTGGCG	6600
TTGACACCAC CAAACTGCCA GCCCCCTCCC AGATCGAAGA GGTAGTGGTA AGAAAGCGCC	6660
AGTTCCGGGC AAGAACTGGT TCGCTTACCT TGCCTCCCCC TCCGAGATCC GTCCCAGGAG	6720
TGTCATGTCC TGAAAGCCTG CAACGAAGTG ACCCGTTAGA AGGTCCTTCA AjCCTCCCTT	6780
CTTCACCACC TGTTCTRCAG TTGGCCATGC CGATGCCCCCT GTTGGGAGCA GGTGAGTGTA	6840

ACCCTTTTAC	TGCAATTGGA	TGTGCAATGA	CCGAAACARG	YGGAGKCCC1	MAKRATTTAC	6900
CCAGTTACCC	TCCCAAAAAG	GAGGTCTCTG	AATGGTCAGA	CGAAAGTTGG	TCAACGACTA	6960
CAACCGCTTC	CAGCTACGTT	ACTGGCCCCC	CGTACCCTAA	GATACGGGGC	AAGGATTCCA	7020
CTCAATCAGC	CACCGCCAAA	CGGCCTACAA	AAAAGAAGTT	GGGAAAGAGT	GAGTTTTTCGT	7080
GCAGCATGAG	CTACACTTGG	ACCGACGTGA	TTAGCTTCAA	AACTGCTTCT	AAAGTTCTGT	7140
CTGCAACTCG	GGCCATCACT	AGTGGTTTCC	TCAAACAAAG	ATCATTGGTG	TATGTGACTG	7200
AGCCGCGGGA	TGCGGAGCTT	AGAAAACAAA	AAGTCACTAT	TAATAGACAA	CCTCTGTTCC	7260
CCCCATCATA	CCACAAGCAA	GTGAGATTGG	CTAAGGAAAA	AGCTTCAAAA	GTTGTCCGGT	7320
TCATGTGGGA	CTATGATGAA	GTAGCAGCTC	ACACGCCCTC	TAAGTCTGCT	AAGTCCCACA	7380
TCACTGGCCT	TCGGGGCACT	GATGTTTCGT	CTGGAGCGGC	CCGCAAGGCT	GTTCTGGACT	7440
TGCAGAAGTG	TGTCGAGGCA	GGTGAGATAC	CGAGTCATTA	TCGGCAAAC	GTGATAGTTC	7500
CAAAGGAGGA	GGTCTTCGTG	AAGACCCCCC	AGAAACCAAC	AAAGAAACCC	CCAAGGCTTA	7560
TCTCGTACCC	CCACCTTGAA	ATGAGATGTG	TTGAGAAGAT	GTAACGCTG	CAGGTTGCTC	7620
CTGACGTAGT	TAAAGCTGTC	ATGGGAGATG	CGTACGGGTT	TGTAGATCCA	CGTACCCGTG	7680
TCAAGCGTCT	GTTGTCGATG	TGGTCACCCG	ATGCAGTCGG	AGCCACATGC	GATACAGTGT	7740
GTTTTGACAG	TACCATCACA	CCCGAGGATA	TCATGGTGGA	GACAGACATC	TACTCAGCAG	7800
CTAAACTCAG	TGACCAACAC	CGAGCTGGCA	TTACACCAT	TGCGAGGCAG	TATCACGCTG	7860
GAGGACCGAT	GATCGCTTAT	GATGGCCGAG	AGATCGGATA	TCGTAGGTGT	AGGTCTTCCG	7920
GCGTCTATAC	TACCTCAAGT	TCCAACAGTT	TGACCTGCTG	GCTGAAGGTA	AATGCTGCAG	7980
CCGAACAGGC	TGGCATGAAG	AACCCTCGCT	TCCTTATTTG	CGGCGATGAT	TGCACCGTAA	8040
TTTGGAAGAG	CGCCGGAGCA	GATGCAGACA	AACAAGCAAT	GCGTGTCTTT	GCTAGCTGGA	8100
TGAAGGTGAT	GGGTGCACCA	CAAGATTGTG	TGCCTCAACC	CAAATACAGT	TTGGAAGAAT	8160
TAACATCATG	CTCATCAAAT	GTTACCTCTG	GAATTACCAA	AAGTGGCAAG	CCTTACTACT	8220
TTCTTACAAG	AGATCCTCGT	ATCCCCCTTG	GCAGGTGCTC	TGCCGAGGGT	CTGGGATACA	8280
ACCCCAGKGC	KGCGTGGATT	GGGTATCTAA	TACATCACTA	CCCATGTTTG	TGGGTTAGCC	8340
GTGTGTTGGC	TGTCCATTTT	ATGGAGCAGA	TGCTCTTTGA	GGACAAACTT	CCCGAGACTG	8400
TGACCTTTGA	CTGGTATGGG	AAAAATTATA	CGGTGCCTGT	AGAAGATCTG	CCCAGCATCA	8460
TTGCTGGTGT	GCACGGTATT	GAGGCTTTCT	CGGTGGTGCG	CTACACCAAC	GCTGAGATCC	8520
TCAGAGTTTC	CCAATCACTA	ACAGACATGA	CCATGCCCCC	CCTGCGAGCC	TGGCGAAAGA	8580

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AAGCCAGGGC GGTCTCGCC AGCGCCAAGA GGCCTGGCGG AGCACACGAA AATTGGCTCG	8640
CTTCCTTCTC TGGCATGCTA CATCTAGACC TCTACCAGAT TTGGATAAGA CGAGCGTGGC	8700
TCGGTACACC ACTTTCAATT ATTGTGATGT TTA CTCCCSG AGRGGGATGT GTTTATTACA	8760
CCACAGAGAA GATTGCAGAA GTTTCTTG TG AAGTATTTGG CTGTCATTGT TTGTGCCCTA	8820
GGGCTCATTG CTGTTGGACT AGCCATCAGC TGAACCCCCA AATTCAAAT TAATTAACAG	8880
TTTTTTTTTT TTTTTTTTTT TTTTTTTAGG GC	8912

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTGTAACC CTTTCACTGC AATTGGATGT GCAATGACCG AAACAGGCGG AGGCCCTGAT	60
GATTTACCCA GTTACCCTCC CAAAAAGGAG GTCTCTGAAT GGTCAGACGA AAGTTGGTCA	120
ACGACTACAA CCGCTTCCAG CTACGTTACT GGCCCCCGTA CCCTAAGATA CGGGAAAGGA	180
TTCCACTCAA TTAGCCC	197

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGACACA CTTCTGCAAG TCCAGAACAG CCTTGCGGGC TGCTCCAGAA CGAACATCAG	60
TGCCCCGAAG CCAGTGATGT GGGACTTAGC AGACTTAGAG GGC GTGTGAG CTGCTACTTC	120
ATCATAGTCC CACATGACAC CGACAACTTT TGAAGCTTTT TCCTTAGCCA ATCTCACTTG	180

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CTTGTGGTAT GATGGGGGGA ACAGAGG

207

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Cys Asn Pro Phe Thr Ala Ile Gly Cys Ala Met Thr Glu Thr Xaa
 1 5 10 15
 Gly Xaa Xaa Xaa Xaa Leu Pro Ser Tyr Pro Pro Lys Lys Glu Val Ser
 20 25 30
 Glu Trp Ser Asp Glu Ser Trp Ser Thr Thr Thr Thr Ala Ser Ser Tyr
 35 40 45
 Val Thr Gly Pro Pro Tyr Pro Lys Ile Arg Gly Lys Asp Ser Thr Gln
 50 55 60
 Ser Ala Thr Ala Lys Arg Pro Thr Lys Lys Lys Leu Gly Lys Ser Glu
 65 70 75 80
 Phe Ser Cys Ser Met Ser Tyr Thr Trp Thr Asp Val Ile Ser Phe Lys
 85 90 95
 Thr Ala Ser Lys Val Leu Ser Ala Thr Arg Ala Ile Thr Ser Gly Phe
 100 105 110
 Leu Lys Gln Arg Ser Leu Val Tyr Val Thr Glu Pro Arg Asp Ala Glu
 115 120 125
 Leu Arg Lys Gln Lys Val Thr Ile Asn Arg Gln Pro Leu Phe Pro Pro
 130 135 140
 Ser Tyr His Lys Gln Val Arg Leu Ala Lys Glu Lys Ala Ser Lys Val
 145 150 155 160
 Val Gly Val Met Trp Asp Tyr Asp Glu Val Ala Ala His Thr Pro Ser
 165 170 175
 Lys Ser Ala Lys Ser His Ile Thr Gly Leu Arg Gly Thr Asp Val Arg
 180 185 190
 Ser Gly Ala Ala Arg Lys Ala Val Leu Asp L u Gln Lys Cys Val Glu
 195 200 205

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GGTTCCTGAA TGCAACATTG TTGAAGCCTT CGACGCAGCC AAGGCATGGT ATGGTTTGTC      60
ATCAACAGAA GCTCAAATA TTCTGGACAC CTATCGCACC CAACCTGGGT TACCTGCGAT      120
AGGAGCAAAT TTGGACGAGT GGGCTGATCT CTTTCTATG GTCAACCCCG AACCTTCATT      180
TGTCAATACT GCAAAAAGAA CTGCTGACAA TTATGTTTTG TTGACTGCAG      230

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Val Pro Glu Cys Asn Ile Val Glu Ala Phe Asp Ala Ala Lys Ala Trp
          5              10              15
Tyr Gly Leu Ser Ser Thr Glu Ala Gln Thr Ile Leu Asp Thr Tyr Arg
          20              25              30
Thr Gln Pro Gly Leu Pro Ala Ile Gly Ala Asn Leu Asp Glu Trp Ala
          35              40              45
Asp Leu Phe Ser Met Val Asn Pro Glu Pro Ser Phe Val Asn Thr Ala
          50              55              60
Lys Arg Thr Ala Asp Asn Tyr Val Leu Leu Thr Ala
          65              70              75

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTATGGTTCC TGAATGCAAC ATTGTTGAAG CCTTCGACGC AGCCAAGGCA TGGTATGGTT	60
TGTCATCAAC AGAAGCTCAA ACTATTCTGG ACACCTATCG CACCCAACCT GGGTTACCTG	120
CGATAGGAGC AAATTGGAC GAGTGGGCTG ATCTCTTTTC TATGGTCAAC CCCGAACCTT	180
CATTTGTCAA TACTGCAAAA AGAACTGCTG ACAATTATGT TTTGTTGACT GCAGCCCTGC	240
CACCGTGGTG CGTCATTGGG AGCAGCATAG CCATACTGAT GACACAGTTG T	291

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGCATGCAA CTTAATTTGC GTGATGCACT TGAGACAAAT GACTGTAATT CCATAAACAA	60
CACTCCTAGT GATGAAGCCG CAGTGTCCGC TCTTGTTCCTT AACAGGAGT TGCGGCGTAC	120
AAACCAATTG CTTGAGGCAA TTTCAGCTGG CGTTGACACC ACCAAACTGC CAGCCCCCTC	180
CATCGAAGAG GTAGTGGTAA GAAAGCGCCA GTTCCGGGCA AGAACTGGTT CGCTTACCTT	240
GCCTCCCCCT CCGAGATCCG TCCCAGGAGT GTCATGTCCT G	281

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Arg Met Gln Leu Asn Leu Arg Asp Ala Leu Glu Thr Asn Asp Cys Asn
1           5           10           15
Ser Ile Asn Asn Thr Pro Ser Asp Glu Ala Ala Val Ser Ala Leu Val
20           25           30
Phe Lys Gln Glu Leu Arg Arg Thr Asn Gln Leu Leu Glu Ala Ile Ser
35           40           45
Ala Gly Val Asp Thr Thr Lys Leu Pro Ala Pro Ser Ile Glu Glu Val
50           55           60
Val Val Arg Lys Arg Gln Phe Arg Ala Arg Thr Gly Ser Leu Thr Leu
65           70           75           80
Pro Pro Pro Pro Arg Ser Val Pro Gly Val Ser Cys Pro
85           90

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GCGCATGCAA CTTAATTTGC GTGATGCACT TGAGACAAAT GACTGTAATT CCATAAACAA      60
CACTCCTAGT GATGAAGCCG CAGTGTCCGC TCTTGTTTTC AAACAGGAGT TCGGGCGTAC      120
AAACCAATTG CTTGAGGCAA TTTCAGCTGG CGTTGACACC ACCAACTGC CAGCCCCCTC      180
CATCGAAGAG GTAGTGGTAA GAAAGCGCCA GTTCCGGGCA AGAACTGGTT CGCTTACCTT      240
GCCTCCCCCT CCGAGATCCG TCCCAGGAGT GTCATGTCCT G                        281

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCCATAGT GAGCCACTCA CCCATCAAGC ATTTAAATGT CAAGCAAGCA GTGGATGAGG	60
CGGCAGCATA GCCGCCTAGC ATGTCAAAGA CAAAACCCAC CGATGTCCAT GTACCAAGAG	120
CTGTTCCAC AGCCCCGGCC ATCATGAACG CCAGTGCCTC TCTAGCGTCT GTAAGCTTGG	180
ACGCAATTGC GCCTCCAAAT AATGACAGGA ACATTTTGAT C	221

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCGAAGCA CACCTCAAGC CCTAAGACGC TGTGTCGCTC CCGGGTTACC CCGCAGCTAC	60
CACCAATACC AGCGGCAGAC GACCCCTTGC GAAGTGCATC GCCACAAGCA CGGCAGCCCT	120
CACAGAGCCC AGGACATTCA GGTACGCCAC GACACACATC ACACCCAGAC AACCAGTGAA	180
CCACCACTCC TGGGCTGCCC AGCCGACCAC CGGGGCGCAC ACCAGCTCGG GAGCCAGCGC	240
GCCTCGACGA CCGGCAAGTA AGCCCCAACA TTTGACAACC AGGCCAGACC GGCAGCGAAC	300
GTTCGCAGCT TGAGCCACGC GGGCCAGATG TCACCAACGA CGGCCTGAGC ACCATCATTG	360
GCAGCACCCC AGACCGCCTG AGCCCCGGCC GTCAGGCCTG CCACCATGTA GCAACCAGCA	420
TTGTAGGTAG AGTCCGCGAC TCCGGTGGTA GAATTCGGAC AAGATGGAGT TGGAACAGTG	480
GGCGGAGTCC ACAATGGAAC ACTTTCAGTG GACTTCGTGA CAGAAGGGTG TATGATAACA	540
ATAGTGGCGG CAGATGCTCC ATTCAACCAC CACCACATTG CCAGCATAAA CAGGGGGGCA	600
ACTCTAGCCT CAGCCAACTT CATCACTACC AACAGGGCCA GGACCATGTC AGTAAGCAAC	660
CAAGCCGCGG AAGACCTTCG CTGACCACTG TAAACCTGCT GTCTGTTGCC TTAAACATGG	720
ATGAAGCCGT TGTGATC	737

(2) INFORMATION FOR SEQ ID NO:23:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCACTGTG GACGCCACTT GTTTCGACTC ATCGATTGAT GAGCACGATA TGCAGGTGGA	60
GGCCTCGGTG TTTGCGGCGG CTAGTGACAA CCCCTCAATG GTACATGCTT TGTGCAAGTA	120
CTACTCTGGT GGCCCTATGG TTTCCCCAGA TGGGGTTCCC TTGGGGTACC GCCACTGTAG	180
GTCGTCGGGC GTGTTGACAA CTAGCTCGGC GAACAGCATC ACTTGTTACA TTAAGGTCAG	240
CGCGGCCTGC AGGCGGGTGG GGATTAAGGC ACCATCATTC TTTATAGCTG GAGATGATTG	300
CTTGATC	307

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCAGGCCG CTGAGCGGCC GAGAAGGTTA CAATCTGGAG GGGTGATAGG AAGTATGACA	60
AGCATTATGA GGCTGTCGTT GAGGCTGTCC TGAAAAAGGC AGCCGCGACG AAGTCTCATG	120
GCTGGACCTA TTCCCAGGCT ATAGCTAAAG TTAGGCGCCG AGCAGCCGCT GGATACGGCA	180
GCAAGGTGAC CGCTCCACA TTGGCCACTG GTTGGCCTCA CGTGGAGGAG ATGCTGGACA	240
AAATAGCCAG GGGACAGGAA GTTCCTTTCA CTTTTGTGAC CAAGCGAGAG GTTTTCTTCT	300
CCAAACTAC CCGTAAGCCC CCAAGATTCA TAGTTTTCCC ACCTTGGAC TTCAGGATAG	360
CTGAAAAGAT GATTCTGGGT GACCCCGGCA TCGTTGCAAA GTCAATTCTG GGTGACGCTT	420
ATCTGTTCCA GTACACGCCC AATCAGAGGG TCAAAGCTCT GGTTAAGGCG TGGGAGGGGA	480

AGTTGCATCC CGCTGCGATC

500

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCACATTT TTGTTACAGC AGTATCCTCT CCAAATGTCT GTTTCACCCA GGTGCCCCCA	60
ACCTTGAGAG CTGCAGTGGC CGTGGACCGC GTACAGGTTT AGYGTATCT AGGTGAGCCC	120
AAAACCTCCTT GGACGACATC TGCTTGCTGT TACGGTCCTG ACGGTAAGGG TAAACTGTT	180
AAGCTTCCCT TCCGCGTTGA CGGACACACA CCTGGTGGTC GCATGCAACT TAATTTGCGT	240
GATCGACTTG AGGCAAATGA CTGTAATTCC ATAAACAACA CTCCTAGTGA TGAAGCCGCA	300
GTGTCCGCTC TTGTTTTCAA ACAGGAGTTG CGGCGTACAA ACCAATTGCT TGAGGCAATT	360
TCAGCTGGCG TTGACACCAC CAACTGCCA GCCCCCTCCC AGATCGAAGA GGTAGTGGTA	420
AGAAAGCGCC AGTTCCGGGC AAGAACTGGT TCGCTTACCT TGCCTCCCCC TCCGAGATC	479

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATCAACACC TCGTCACCCC GTCTCGCAAC CACAGGTTTC CCGTGGACCA ACTGTCCACA	60
GCCTAACACA CGAGCAGAGT CCCGAACAAT AGCACAATCT TCCTTGGTTA TGCTAACAGG	120
CTCAAGCGCA AAACCCCACT CTCGCAAGCG GGCAGCACCG CGCCTGCTAG TGTGACCGGC	180
GTGCTCGTAG AGGAGGACGC CCTGCTTGCG CAGGACGCCC ACCAGCCAAG AGCAGGCCAG	240
CCGCTCCTCA GCAAGAGCTA AGGAGTCCAG CACCCGCGCC AAGCGCGCGA GATTTGGTGA	300

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GTTAACCAAG AGTACTTCCA AGATGAAATC AATGACATCT AAAGTGTCTA AACAGAGTAT	360
GAAGATGACG GAAACTGTGG CAACTGTTTG GGGGAAGAAC CAAGCCACAA CCAACCAAGC	420
TTTCCAGCAC GCCTCCAACG GCCAAAAGCT CCAACCGGCG AGTTGTTTAC CCACCGGCGA	480
ACCCTCTGGT AATTGACGGC CCACCTGGCA TACCAAGTCA ATCTGGCTGA TC	532

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATCCATCTT GACAATGACA ACTTTCGCAG GACAGTAGAC ACCTTGGTGA CGAACTCATC	60
TTTGAGGAAG AAATCGTCAG GCATCACCGA ACTGCGTGGC ATCATCGTCA ACAATCTGTT	120
AACCCAATCT TGACCCACAC CCTTTTGTAC AGACCAGAGC AACAAGCCCA GAACCACACC	180
GGCCACCGAA GCGCCCGGAG AGGCCAGGCA ACTGACCAGG CACCAAGCGT CACTCGCTTG	240
TAACTTCCCC GCCAGGAGGT CGAAGGTGAG TGAGCGCGGT TCACCGCCCC CTCCCAGCCT	300
CTGATC	306

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATCACCCAC ACCCGGTTG GTTGGCACTT GCATGCCTGA AGGCAAGAAG CACCATTAGG	60
GAGCGGGTAG ACCGTGACGT CGTCACTCGC TAACCACCAC CGAGCATTGA CAGGACCGAA	120
AGCCCCACCA TAGGCCGGAC GTTGGTACCA CGGTATGTCG TGTACATCAC TCCGTTACG	180

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CAGCAGCCCA TGGAACGAGT TGTTGAAGTC CCAAGGACCA CCACGTTCCC GTGATGTTTCG 240
GACGAGTCCT TGCCTGTCAT GGAGGTCCTC ACAACCCCGA AGAATCCCTT GCCAGCTTGA 300
TGAAGCACCA CGGGAGCAGT GGGAACAAAG CCAGGCGGAA GGTCGAACCG ACTGTTTACA 360
CAACTGATC 369

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCCAATCC AGGGGCCCTC GTACCCCTCC TGGCAGCTGT AGAAAGGACA ACCAGGAATG 60
TTAACCATGC TCTGAACTCC AGCTTTAAGG ACATTAAAGC AAATCACAAA GAAATTGCAC 120
ACATACTGCC AAATCTCTAG ACCCCAAGCA ATGAGGCCGC AATCATCCTC CGTCGGGGTG 180
TGGAGCCAAC GGATGCAAGC TGATATGATA CTCCAGGGGG TAGATGCCTC CAGAATGCCC 240
AGTATCTTCT GCGGATGTCA CGAGTGCGAA TAAAGTACTC ACTACATACA GTGTTGCTCC 300
TAGCAAGCAT AGTAAGAAGT CTGTTGGGCC AGTGATC 337

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCAGGTAT GCTCCAAGCA CGCTGTCCAT GCGGTGCTGA ACTCATCTTT TCTGTTGAGA 60
ATGGTTTTGC AAAACTTTAC AAAGGACCCA GAACTTGTTT AAATTACTGG AGAGGGGCTG 120
TTCCAGTCAA CGCTAGGCTG TGTGGGTCGG CTAGACCGGA CCCAACTGAT TGGACTAGTC 180

TTGTCGTCAA TTATGGCGTT AGGGACTACT GTAAATATGA GAAATTGGGA GATC

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asp Pro Xaa Xaa Ala Thr His Pro Ser Ser Ile Xaa Met Ser Ser Lys
1 5 10 15
Gln Trp Met Arg Arg Gln His Ser Arg Leu Ala Cys Gln Arg Gln Asn
20 25 30
Pro Pro Met Ser Met Tyr Gln Glu Leu Phe Pro Gln Pro Arg Pro Ser
35 40 45
Xaa Thr Pro Val Arg Leu Xaa Arg Leu Xaa Ala Trp Thr Gln Leu Arg
50 55 60
Leu Gln Ile Met Thr Gly Thr Phe Xaa
65 70

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile His Ser Glu Pro Leu Thr His Gln Ala Phe Lys Cys Gln Ala Ser
1 5 10 15
Ser Gly Xaa Gly Gly Ser Ile Ala Ala Xaa His Val Lys Asp Lys Thr
20 25 30
His Arg Cys Pro Cys Thr Lys Ser Cys Ser His Ser Pro Gly His His
35 40 45

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Glu Arg Gln Cys Val Ser Ser Val Cys Lys Leu Gly Arg Asn Cys Ala
 50 55 60

Ser Lys Xaa Xaa Gln Glu His Phe Asp
 65 70

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ile Val Ser His Ser Pro Ile Lys His Leu Asn Val Lys Gln Ala
 1 5 10 15

Val Asp Glu Ala Ala Ala Xaa Pro Pro Ser Met Ser Lys Thr Lys Pro
 20 25 30

Thr Asp Val His Val Pro Arg Ala Val Pro Thr Ala Pro Ala Ile Met
 35 40 45

Asn Ala Ser Ala Ser Leu Ala Ser Val Ser Leu Asp Ala Ile Ala Pro
 50 55 60

Pro Asn Asn Asp Arg Asn Ile Leu Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Gln Asn Val Pro Val Ile Ile Trp Arg Arg Asn Cys Val Gln Ala
 1 5 10 15

Tyr Arg Arg Xaa Arg Arg Thr Gly Val His Asp Gly Arg Gly Cys Gly
 20 25 30

Asn Ser Ser Trp Tyr Met Asp Ile Gly Gly Phe Cys Leu Xaa His Ala
 35 40 45

196

Arg Arg Leu Cys Cys Arg Leu Ile His Cys Leu Leu Asp Ile Xaa Met
 50 55 60

Leu Asp Gly Xaa Val Ala His Tyr Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile Lys Met Phe Leu Ser Leu Phe Gly Gly Ala Ile Ala Ser Lys Leu
 1 5 10 15

Thr Asp Ala Arg Asp Ala Leu Ala Phe Met Met Ala Gly Ala Val Gly
 20 25 30

Thr Ala Leu Gly Thr Trp Thr Ser Val Gly Phe Val Phe Asp Met Leu
 35 40 45

Gly Gly Tyr Ala Ala Ala Ser Ser Thr Ala Cys Leu Thr Phe Lys Cys
 50 55 60

Leu Met Gly Glu Trp Leu Thr Met Asp
 65 70

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Lys Cys Ser Cys His Tyr Leu Glu Ala Gln Leu Arg Pro Ser Leu
 1 5 10 15

Gln Thr Leu Glu Thr His Trp Arg Ser Xaa Trp Pro Gly Leu Trp Glu
 20 25 30

Gln Leu Leu Val His Gly His Arg Trp Val Leu Ser Leu Thr Cys Xaa
 35 40 45

197

Ala Ala Met Leu Pro Pro His Pro Leu Leu Ala Xaa His Leu Asn Ala
 50 55 60

Xaa Trp Val Ser Gly Ser Leu Trp Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Arg Ser Thr Pro Gln Ala Leu Arg Arg Cys Val Ala Pro Gly Leu
 1 5 10 15

Pro Arg Ser Tyr His Gln Tyr Gln Arg Gln Thr Thr Pro Cys Glu Val
 20 25 30

His Arg His Lys His Gly Ser Pro His Arg Ala Gln Asp Ile Gln Val
 35 40 45

Arg His Asp Thr His His Thr Gln Thr Thr Ser Glu Pro Pro Leu Leu
 50 55 60

Gly Cys Pro Ala Asp His Arg Gly Ala His Gln Leu Gly Ser Gln Arg
 65 70 75 80

Ala Ser Thr Thr Gly Lys Xaa Ala Pro Thr Phe Asp Asn Gln Ala Arg
 85 90 95

Pro Ala Ala Asn Val Arg Ser Leu Ser His Ala Gly Gln Met Ser Pro
 100 105 110

Thr Thr Ala Xaa Ala Pro Ser Leu Ala Ala Pro Gln Thr Ala Xaa Ala
 115 120 125

Pro Ala Val Arg Pro Ala Thr Met Xaa Gln Pro Ala Leu Xaa Val Glu
 130 135 140

Ser Ala Thr Pro Val Val Glu Phe Gly Gln Asp Gly Val Gly Thr Val
 145 150 155 160

Gly Gly Val His Asn Gly Thr Leu Ser Val Asp Phe Val Thr Glu Gly
 165 170 175

Cys Met Ile Thr Ile Val Ala Ala Asp Ala Pro Phe Asn His His His
 180 185 190

198

Ile Ala Ser Ile Asn Arg Gly Ala Thr Leu Ala Ser Ala Asn Phe Ile
 195 200 205

Thr Thr Asn Arg Ala Arg Thr Met Ser Val Ser Asn Gln Ala Ala Glu
 210 215 220

Asp Leu Arg Xaa Pro Leu Xaa Thr Cys Cys Leu Leu Pro Leu Thr Trp
 225 230 235 240

Met Lys Pro Leu Xaa
 245

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile Glu Ala His Leu Lys Pro Xaa Asp Ala Val Ser Leu Pro Gly Tyr
 1 5 10 15

Pro Ala Ala Thr Thr Asn Thr Ser Gly Arg Arg Pro Leu Ala Lys Cys
 20 25 30

Ile Ala Thr Ser Thr Ala Ala Leu Thr Glu Pro Arg Thr Phe Arg Tyr
 35 40 45

Ala Thr Thr His Ile Thr Pro Arg Gln Pro Val Asn His His Ser Trp
 50 55 60

Ala Ala Gln Pro Thr Thr Gly Ala His Thr Ser Ser Gly Ala Ser Ala
 65 70 75 80

Pro Arg Arg Pro Ala Ser Lys Pro Gln His Leu Thr Thr Arg Pro Asp
 85 90 95

Arg Gln Arg Thr Phe Ala Ala Xaa Ala Thr Arg Ala Arg Cys His Gln
 100 105 110

Arg Arg Pro Glu His His His Trp Gln His Pro Arg Pro Pro Glu Pro
 115 120 125

Arg Pro Ser Gly Leu Pro Pro Cys Ser Asn Gln His Cys Arg Xaa Ser
 130 135 140

Pro Arg Leu Arg Trp Xaa Asn Ser Asp Lys Met Glu Leu Glu Gln Trp
 145 150 155 160

Ala Glu Ser Thr Met Glu His Phe Gln Trp Thr Ser Xaa Gln Lys Gly

199

165	170	175
Val Xaa Xaa Gln Xaa Trp Arg Gln Met Leu His Ser Thr Thr Thr Thr		
180	185	190
Leu Pro Ala Xaa Thr Gly Gly Gln Leu Xaa Pro Gln Pro Thr Ser Ser		
195	200	205
Leu Pro Thr Gly Pro Gly Pro Cys Gln Xaa Ala Thr Lys Pro Arg Lys		
210	215	220
Thr Phe Ala Asp His Cys Lys Pro Ala Val Cys Cys Leu Xaa His Gly		
225	230	235
Xaa Ser Arg Cys Asp		
245		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Lys His Thr Ser Ser Pro Lys Thr Leu Cys Arg Ser Arg Val Thr		
1	5	10
Pro Gln Leu Pro Pro Ile Pro Ala Ala Asp Asp Pro Leu Arg Ser Ala		
20	25	30
Ser Pro Gln Ala Arg Gln Pro Ser Gln Ser Pro Gly His Ser Gly Thr		
35	40	45
Pro Arg His Thr Ser His Pro Asp Asn Gln Xaa Thr Thr Thr Pro Gly		
50	55	60
Leu Pro Ser Arg Pro Pro Gly Arg Thr Pro Ala Arg Glu Pro Ala Arg		
65	70	75
Leu Asp Asp Arg Gln Val Ser Pro Asn Ile Xaa Gln Pro Gly Gln Thr		
85	90	95
Gly Ser Glu Arg Ser Gln Leu Glu Pro Arg Gly Pro Asp Val Thr Asn		
100	105	110
Asp Gly Leu Ser Thr Ile Ile Gly Ser Thr Pro Asp Arg Leu Ser Pro		
115	120	125

200

Gly Arg Gln Ala Cys His His Val Ala Thr Ser Ile Val Gly Arg Val
 130 135 140
 Arg Asp Ser Gly Gly Arg Ile Arg Thr Arg Trp Ser Trp Asn Ser Gly
 145 150 155 160
 Arg Ser Pro Gln Trp Asn Thr Phe Ser Gly Leu Arg Asp Arg Arg Val
 165 170 175
 Tyr Asp Asn Asn Ser Gly Gly Arg Cys Ser Ile Gln Pro Pro Pro His
 180 185 190
 Cys Gln His Lys Gln Gly Gly Asn Ser Ser Leu Ser Gln Leu His His
 195 200 205
 Tyr Gln Gln Gly Gln Asp His Val Ser Lys Gln Pro Ser Arg Gly Arg
 210 215 220
 Pro Ser Leu Thr Thr Val Asn Leu Leu Ser Val Ala Phe Asn Met Asp
 225 230 235 240
 Glu Ala Val Val Ile
 245

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp His Asn Gly Phe Ile His Val Lys Gly Asn Arg Gln Gln Val Tyr
 1 5 10 15
 Ser Gly Gln Arg Arg Ser Ser Ala Ala Trp Leu Leu Thr Asp Met Val
 20 25 30
 Leu Ala Leu Leu Val Val Met Lys Leu Ala Glu Ala Arg Val Ala Pro
 35 40 45
 Leu Phe Met Leu Ala Met Trp Trp Trp Leu Asn Gly Ala Ser Ala Ala
 50 55 60
 Thr Ile Val Ile Ile His Pro Ser Val Thr Lys Ser Thr Glu Ser Val
 65 70 75 80
 Pro Leu Trp Thr Pro Pro Thr Val Pro Thr Pro Ser Cys Pro Asn Ser
 85 90 95

201

Thr Thr Gly Val Ala Asp Ser Thr Tyr Asn Ala Gly Cys Tyr Met Val
 100 105 110
 Ala Gly Leu Thr Ala Gly Ala Gln Ala Val Trp Gly Ala Ala Asn Asp
 115 120 125
 Gly Ala Gln Ala Val Val Gly Asp Ile Trp Pro Ala Trp Leu Lys Leu
 130 135 140
 Arg Thr Phe Ala Ala Gly Leu Ala Trp Leu Ser Asn Val Gly Ala Tyr
 145 150 155 160
 Leu Pro Val Val Glu Ala Arg Trp Leu Pro Ser Trp Cys Ala Pro Arg
 165 170 175
 Trp Ser Ala Gly Gln Pro Arg Ser Gly Gly Ser Leu Val Val Trp Val
 180 185 190
 Xaa Cys Val Ser Trp Arg Thr Xaa Met Ser Trp Ala Leu Xaa Gly Leu
 195 200 205
 Pro Cys Leu Trp Arg Cys Thr Ser Gln Gly Val Val Cys Arg Trp Tyr
 210 215 220
 Trp Trp Xaa Leu Arg Gly Asn Pro Gly Ala Thr Gln Arg Leu Arg Ala
 225 230 235 240
 Xaa Gly Val Leu Arg
 245

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ile Thr Thr Ala Ser Ser Met Leu Lys Ala Thr Asp Ser Arg Phe Thr
 1 5 10 15
 Val Val Ser Glu Gly Leu Pro Arg Leu Gly Cys Leu Leu Thr Trp Ser
 20 25 30
 Trp Pro Cys Trp Xaa Xaa Xaa Ser Trp Leu Arg Leu Glu Leu Pro Pro
 35 40 45
 Cys Leu Cys Trp Gln Cys Gly Gly Gly Xaa Met Glu His Leu Pro Pro
 50 55 60

202

Leu Leu Leu Ser Tyr Thr Leu Leu Ser Arg Ser Pro Leu Lys Val Phe
 65 70 75 80
 His Cys Gly Leu Arg Pro Leu Phe Gln Leu His Leu Val Arg Ile Leu
 85 90 95
 Pro Pro Glu Ser Arg Thr Leu Pro Thr Met Leu Val Ala Thr Trp Trp
 100 105 110
 Gln Ala Xaa Arg Pro Gly Leu Arg Arg Ser Gly Val Leu Pro Met Met
 115 120 125
 Val Leu Arg Pro Ser Leu Val Thr Ser Gly Pro Arg Gly Ser Ser Cys
 130 135 140
 Glu Arg Ser Leu Pro Val Trp Pro Gly Cys Gln Met Leu Gly Leu Thr
 145 150 155 160
 Cys Arg Ser Ser Arg Arg Ala Gly Ser Arg Ala Gly Val Arg Pro Gly
 165 170 175
 Gly Arg Leu Gly Ser Pro Gly Val Val Val His Trp Leu Ser Gly Cys
 180 185 190
 Asp Val Cys Arg Gly Val Pro Glu Cys Pro Gly Leu Cys Glu Gly Cys
 195 200 205
 Arg Ala Cys Gly Asp Ala Leu Arg Lys Gly Ser Ser Ala Ala Gly Ile
 210 215 220
 Gly Gly Ser Cys Gly Val Thr Arg Glu Arg His Ser Val Leu Gly Leu
 225 230 235 240
 Glu Val Cys Phe Asp
 245

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Gln Arg Leu His Pro Cys Xaa Arg Gln Gln Thr Ala Gly Leu Gln
 1 5 10 15
 Trp Ser Ala Lys Val Phe Arg Gly Leu Val Ala Tyr Xaa His Gly Pro-
 20 25 30

203

Gly Pro Val Gly Ser Asp Glu Val Gly Xaa Gly Xaa Ser Cys Pro Pro
 35 40 45
 Val Tyr Ala Gly Asn Val Val Val Val Glu Trp Ser Ile Cys Arg His
 50 55 60
 Tyr Cys Tyr His Thr Pro Phe Cys His Glu Val His Xaa Lys Cys Ser
 65 70 75 80
 Ile Val Asp Ser Ala His Cys Ser Asn Ser Ile Leu Ser Glu Phe Tyr
 85 90 95
 His Arg Ser Arg Gly Leu Tyr Leu Gln Cys Trp Leu Leu His Gly Gly
 100 105 110
 Arg Pro Asp Gly Arg Gly Ser Gly Gly Leu Gly Cys Cys Gln Xaa Trp
 115 120 125
 Cys Ser Gly Arg Arg Trp Xaa His Leu Ala Arg Val Ala Gln Ala Ala
 130 135 140
 Asn Val Arg Cys Arg Ser Gly Leu Val Val Lys Cys Trp Gly Leu Leu
 145 150 155 160
 Ala Gly Arg Arg Gly Ala Leu Ala Pro Glu Leu Val Cys Ala Pro Val
 165 170 175
 Val Gly Trp Ala Ala Gln Glu Trp Trp Phe Thr Gly Cys Leu Gly Val
 180 185 190
 Met Cys Val Val Ala Tyr Leu Asn Val Leu Gly Ser Val Arg Ala Ala
 195 200 205
 Val Leu Val Ala Met His Phe Ala Arg Gly Arg Leu Pro Leu Val Leu
 210 215 220
 Val Val Ala Ala Gly Xaa Pro Gly Ser Asp Thr Ala Ser Xaa Gly Leu
 225 230 235 240
 Arg Cys Ala Ser Ile
 245

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp His Cys Gly Arg His Leu Phe Arg Leu Ile Asp Xaa Xaa Ala Arg

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

BNSDOCID: <WO_9521922A2 | >

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

BNSDOCID: <WO___9521922A2_I_>

206

Arg Arg Ala Ser Cys Gln His Ala Arg Arg Pro Thr Leu Ala Val Pro
 35 40 45

Gln Gly Asn Pro Ile Trp Gly Asn His Arg Ala Thr Arg Val Val Leu
 50 55 60

Ala Gln Ser Met Tyr His Xaa Gly Val Val Thr Ser Arg Arg Lys His
 65 70 75 80

Arg Gly Leu His Leu His Ile Val Leu Ile Asn Arg Xaa Val Glu Thr
 85 90 95

Ser Gly Val His Ser Asp
 100

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Lys Gln Ser Ser Pro Ala Ile Lys Asn Asp Gly Ala Leu Ile Pro
 1 5 10 15

Thr Arg Leu Gln Ala Ala Leu Thr Leu Met Xaa Gln Val Met Leu Phe
 20 25 30

Ala Glu Leu Val Val Asn Thr Pro Asp Asp Leu His Trp Arg Tyr Pro
 35 40 45

Lys Gly Thr Pro Ser Gly Glu Thr Ile Gly Pro Pro Glu Xaa Tyr Leu
 50 55 60

His Lys Ala Cys Thr Ile Glu Gly Leu Ser Leu Ala Ala Ala Asn Thr
 65 70 75 80

Glu Ala Ser Thr Cys Ile Ser Cys Ser Ser Ile Asp Glu Ser Lys Gln
 85 90 95

Val Ala Ser Thr Val Ile
 100

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

207

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Ser Ser Asn His Leu Gln Leu Xaa Arg Met Met Val Pro Xaa Ser Pro
1           5           10           15

Pro Ala Cys Arg Pro Arg Xaa Pro Xaa Cys Asn Lys Xaa Cys Cys Ser
          20           25           30

Pro Ser Xaa Leu Ser Thr Arg Pro Thr Thr Tyr Thr Gly Gly Thr Pro
          35           40           45

Arg Glu Pro His Leu Gly Lys Pro Xaa Gly His Gln Ser Ser Thr Cys
          50           55           60

Thr Lys His Val Pro Leu Arg Gly Cys His Xaa Pro Pro Gln Thr Pro
65           70           75           80

Arg Pro Pro Pro Ala Tyr Arg Ala His Gln Ser Met Ser Arg Asn Lys
          85           90           95

Trp Arg Pro Gln Xaa
          100

```

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Asp Gln His Leu Val Thr Pro Ser Arg Asn His Arg Phe Pro Val Asp
1           5           10           15

Gln Leu Ser Thr Ala Xaa His Thr Ser Arg Val Pro Asn Asn Ser Thr
          20           25           30

Ile Phe Leu Gly Tyr Ala Asn Arg Leu Lys Arg Lys Thr Pro Leu Ser
          35           40           45

Gln Ala Gly Ser Thr Ala Pro Ala Ser Val Thr Gly Val Leu Val Glu
          50           55           60

```

208

Asp

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ile	Asn	Thr	Ser	Ser	Pro	Arg	Leu	Ala	Thr	Thr	Gly	Phe	Pro	Trp	Thr
1				5					10					15	
Asn	Cys	Pro	Gln	Pro	Asn	Thr	Arg	Ala	Glu	Ser	Arg	Thr	Ile	Ala	Gln
			20					25					30		
Ser	Ser	Leu	Val	Met	Leu	Thr	Gly	Ser	Ser	Ala	Lys	Pro	His	Ser	Arg
		35					40					45			
Lys	Arg	Ala	Ala	Pro	Arg	Leu	Leu	Val	Xaa	Pro	Ala	Cys	Ser	Xaa	Arg
	50					55					60				
Arg	Thr	Pro	Cys	Leu	Arg	Arg	Thr	Pro	Thr	Ser	Gln	Glu	Gln	Ala	Ser
65					70					75					80
Arg	Ser	Ser	Ala	Arg	Ala	Lys	Glu	Ser	Ser	Thr	Arg	Ala	Lys	Arg	Ala
				85					90					95	
Arg	Phe	Gly	Glu	Leu	Thr	Lys	Ser	Thr	Ser	Lys	Met	Lys	Ser	Met	Thr

209

100	105	110
Ser Lys Leu Leu Lys Gln Ser Met Lys Met Thr Glu Thr Val Ala Thr		
115	120	125
Val Trp Gly Lys Asn Gln Ala Thr Thr Asn Gln Ala Phe Gln His Ala		
130	135	140
Ser Asn Gly Gln Lys Leu Gln Pro Ala Ser Cys Ser Pro Thr Gly Glu		
145	150	155
Pro Ser Gly Asn Xaa Arg Pro Thr Trp His Thr Lys Ser Ile Trp Leu		
165	170	175
Ile		

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Thr Pro Arg His Pro Val Ser Gln Pro Gln Val Ser Arg Gly Pro		
1	5	10
Thr Val His Ser Leu Thr His Glu Gln Ser Pro Glu Gln Xaa His Asn		
20	25	30
Leu Pro Trp Leu Cys Xaa Gln Ala Gln Ala Gln Asn Pro Thr Leu Ala		
35	40	45
Ser Gly Gln His Arg Ala Cys Xaa Cys Asp Arg Arg Ala Arg Arg Gly		
50	55	60
Gly Arg Pro Ala Cys Ala Gly Arg Pro Pro Ala Lys Ser Arg Pro Ala		
65	70	75
Ala Pro Gln Gln Glu Leu Arg Ser Pro Ala Pro Ala Pro Ser Ala Arg		
85	90	95
Asp Leu Val Ser Xaa Pro Arg Val Leu Pro Arg Xaa Asn Gln Xaa His		
100	105	110
Leu Asn Cys Ser Asn Arg Val Xaa Arg Xaa Arg Lys Leu Trp Gln Leu		
115	120	125
Phe Gly Gly Arg Thr Lys Pro Gln Pro Thr Lys Leu Ser Ser Thr Pro		
130	135	140

210

Pro Thr Ala Lys Ser Ser Asn Arg Arg Val Val His Pro Pro Ala Asn
 145 150 155 160

Pro Leu Val Ile Asp Gly Pro Pro Gly Ile Pro Ser Gln Ser Gly Xaa
 165 170 175

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Asp Gln Pro Asp Xaa Leu Gly Met Pro Gly Gly Pro Ser Ile Thr Arg
 1 5 10 15
 Gly Phe Ala Gly Gly Xaa Thr Thr Arg Arg Leu Glu Leu Leu Ala Val
 20 25 30
 Gly Gly Val Leu Glu Ser Leu Val Gly Cys Gly Leu Val Leu Pro Pro
 35 40 45
 Asn Ser Cys His Ser Phe Arg His Leu His Thr Leu Phe Glu Gln Phe
 50 55 60
 Arg Cys His Xaa Phe His Leu Gly Ser Thr Leu Gly Xaa Leu Thr Lys
 65 70 75 80
 Ser Arg Ala Leu Gly Ala Gly Ala Gly Leu Leu Ser Ser Cys Xaa Gly
 85 90 95
 Ala Ala Gly Leu Leu Leu Ala Gly Gly Arg Pro Ala Gln Ala Gly Arg
 100 105 110
 Pro Pro Leu Arg Ala Arg Arg Ser His Xaa Gln Ala Arg Cys Cys Pro
 115 120 125
 Leu Ala Arg Val Gly Phe Cys Ala Xaa Ala Cys Xaa His Asn Gln Gly
 130 135 140
 Arg Leu Cys Tyr Cys Ser Gly Leu Cys Ser Cys Val Arg Leu Trp Thr
 145 150 155 160
 Val Gly Pro Arg Glu Thr Cys Gly Cys Glu Thr Gly Xaa Arg Gly Val
 165 170 175
 Asp

(2) INFORMATION FOR SEQ ID NO:53:

211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Ile Ser Gln Ile Asp Leu Val Cys Gln Val Gly Arg Gln Leu Pro Glu
1           5           10           15
Gly Ser Pro Val Gly Glu Gln Leu Ala Gly Trp Ser Phe Trp Pro Leu
20           25           30
Glu Ala Cys Trp Lys Ala Trp Leu Val Val Ala Trp Phe Phe Pro Gln
35           40           45
Thr Val Ala Thr Val Ser Val Ile Phe Ile Leu Cys Leu Ser Ser Leu
50           55           60
Asp Val Ile Asp Phe Ile Leu Glu Val Leu Leu Val Asn Ser Pro Asn
65           70           75           80
Leu Ala Arg Leu Ala Arg Val Leu Asp Ser Leu Ala Leu Ala Glu Glu
85           90           95
Arg Leu Ala Cys Ser Trp Leu Val Gly Val Leu Arg Lys Gln Gly Val
100          105          110
Leu Leu Tyr Glu His Ala Gly His Thr Ser Arg Arg Gly Ala Ala Arg
115          120          125
Leu Arg Glu Trp Gly Phe Ala Leu Glu Pro Val Ser Ile Thr Lys Glu
130          135          140          145
Asp Cys Ala Ile Val Arg Asp Ser Ala Arg Val Leu Gly Cys Gly Gln
145          150          155          160
Leu Val His Gly Lys Pro Val Val Ala Arg Arg Gly Asp Glu Val Leu
165          170          175
Ile

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

212

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Ser Ala Arg Leu Thr Trp Tyr Ala Arg Trp Ala Val Asn Tyr Gln Arg
1           5           10           15
Val Arg Arg Trp Val Asn Asn Ser Pro Val Gly Ala Phe Gly Arg Trp
20           25           30
Arg Arg Ala Gly Lys Leu Gly Trp Leu Trp Leu Gly Ser Ser Pro Lys
35           40           45
Gln Leu Pro Gln Phe Pro Ser Ser Ser Tyr Ser Val Xaa Ala Val Xaa
50           55           60
Met Ser Leu Ile Ser Ser Trp Lys Tyr Ser Trp Leu Thr His Gln Ile
65           70           75           80
Ser Arg Ala Trp Arg Gly Cys Trp Thr Pro Xaa Leu Leu Leu Arg Ser
85           90           95
Gly Trp Pro Ala Leu Gly Trp Trp Ala Ser Cys Ala Ser Arg Ala Ser
100          105          110
Ser Ser Thr Ser Thr Pro Val Thr Leu Ala Gly Ala Val Leu Pro Ala
115          120          125
Cys Glu Ser Gly Val Leu Arg Leu Ser Leu Leu Ala Xaa Pro Arg Lys
130          135          140
Ile Val Leu Leu Phe Gly Thr Leu Leu Val Cys Xaa Ala Val Asp Ser
145          150          155          160
Trp Ser Thr Gly Asn Leu Trp Leu Arg Asp Gly Val Thr Arg Cys Xaa
165          170          175

```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

Asp Pro Ser Xaa Gln Xaa Gln Leu Ser Gln Asp Ser Arg His Leu Gly
1           5           10           15
Asp Glu Leu Ile Phe Glu Glu Glu Ile Val Arg His His Arg Thr Ala
20           25           30

```

213

Trp His His Arg Gln Gln Ser Val Asn Pro Ile Leu Thr His Thr Leu
 35 40 45
 Phe Asp Arg Pro Glu Gln Gln Ala Gln Asn His Thr Gly His Arg Ser
 50 55 60
 Pro Arg Arg Gly Gln Ala Thr Asp Gln Ala Pro Ser Val Thr Arg Leu
 65 70 75 80
 Xaa Leu Pro Arg Gln Glu Val Glu Gly Glu Xaa Ala Arg Phe Thr Ala
 85 90 95
 Pro Ser Gln Pro Leu Ile
 100

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ile His Leu Asp Asn Asp Asn Phe Arg Arg Thr Val Asp Thr Leu Val
 1 5 10 15
 Thr Asn Ser Ser Leu Arg Lys Lys Ser Ser Gly Ile Thr Glu Leu Arg
 20 25 30
 Gly Ile Ile Val Asn Asn Leu Leu Thr Gln Ser Xaa Pro Thr Pro Phe
 35 40 45
 Leu Thr Asp Gln Ser Asn Lys Pro Arg Thr Thr Pro Ala Thr Glu Ala
 50 55 60
 Pro Gly Glu Ala Arg Gln Leu Thr Arg His Gln Ala Ser Leu Ala Cys
 65 70 75 80
 Asn Phe Pro Ala Arg Arg Ser Lys Val Ser Glu Arg Gly Ser Pro Pro
 85 90 95
 Pro Pro Ser Leu Xaa
 100

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids

214

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

Ser Ile Leu Thr Met Thr Thr Phe Ala Gly Gln Xaa Thr Pro Trp Xaa
1           5           10           15
Arg Thr His Leu Xaa Gly Arg Asn Arg Gln Ala Ser Pro Asn Cys Val
          20           25           30
Ala Ser Ser Ser Thr Ile Cys Xaa Pro Asn Leu Asp Pro His Pro Phe
          35           40           45
Xaa Gln Thr Arg Ala Thr Ser Pro Glu Pro His Arg Pro Pro Lys Pro
          50           55           60
Pro Glu Arg Pro Gly Asn Xaa Pro Gly Thr Lys Arg His Ser Leu Val
65           70           75           80
Thr Ser Pro Pro Gly Gly Arg Arg Xaa Val Ser Ala Val His Arg Pro
          85           90           95
Leu Pro Ala Ser Asp
          100
  
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Asp Gln Arg Leu Gly Gly Gly Gly Glu Pro Arg Ser Leu Thr Phe Asp
1           5           10           15
Leu Leu Ala Gly Lys Leu Gln Ala Ser Asp Ala Trp Cys Leu Val Ser
          20           25           30
Cys Leu Ala Ser Pro Gly Ala Ser Val Ala Gly Val Val Leu Gly Leu
          35           40           45
Leu Leu Trp Ser Val Lys Lys Gly Val Gly Gln Asp Trp Val Asn Arg
          50           55           60
Leu Leu Thr Met Met Pro Arg Ser Ser Val Met Pro Asp Asp Phe Phe
  
```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

BNSDOCID: <WO___9521922A2_|_>

216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Glu Ala Gly Arg Gly Arg Xaa Thr Ala Leu Thr His Leu Arg Pro
 1 5 10 15
 Pro Gly Gly Glu Val Thr Ser Glu Xaa Arg Leu Val Pro Gly Gln Leu
 20 25 30
 Pro Gly Leu Ser Gly Gly Phe Gly Gly Arg Cys Gly Ser Gly Leu Val
 35 40 45
 Ala Leu Val Cys Gln Lys Gly Cys Gly Ser Arg Leu Gly Xaa Gln Ile
 50 55 60
 Val Asp Asp Asp Ala Thr Gln Phe Gly Asp Ala Xaa Arg Phe Leu Pro
 65 70 75 80
 Gln Arg Xaa Val Arg His Gln Gly Val Tyr Cys Pro Ala Lys Val Val
 85 90 95
 Ile Val Lys Met Asp
 100

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 61:

Asp His Pro His Pro Gly Trp Leu Ala Leu Ala Cys Leu Lys Ala Arg
 1 5 10 15
 Ser Thr Ile Arg Glu Arg Val Asp Arg Asp Val Val Thr Arg Xaa Pro
 20 25 30
 Pro Pro Ser Ile Asp Arg Thr Glu Ser Pro Thr Ile Gly Arg Thr Leu
 35 40 45
 Val Pro Arg Tyr Val Val Tyr Ile Thr Pro Phe Thr Gln Gln Pro Met
 50 55 60
 Glu Arg Val Val Glu Val Pro Arg Thr Thr Thr Phe Pro Xaa Cys Ser
 65 70 75 80
 Asp Glu Ser Leu Pro Val Met Glu Val Leu Thr Thr Pro Lys Asn Pro
 85 90 95
 Leu Pro Ala Xaa Xaa Ser Thr Thr Gly Ala Val Gly Thr Lys Pro Gly

217

100

105

110

Gly Arg Ser Asn Arg Leu Phe Thr Gln Leu Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 62:

Ile Thr His Thr Pro Val Gly Trp His Leu His Ala Xaa Arg Gln Glu
 1 5 10 15
 Ala Pro Leu Gly Ser Gly Xaa Thr Val Thr Ser Ser Leu Ala Asn His
 20 25 30
 His Arg Ala Leu Thr Gly Pro Lys Ala Pro Pro Xaa Ala Gly Arg Trp
 35 40 45
 Tyr His Gly Met Ser Cys Thr Ser Leu Arg Ser Arg Ser Ser Pro Trp
 50 55 60
 Asn Glu Leu Leu Lys Ser Gln Gly Pro Pro Arg Ser Arg Asp Val Arg
 65 70 75 80
 Thr Ser Pro Cys Leu Ser Trp Arg Ser Ser Gln Pro Arg Arg Ile Pro
 85 90 95
 Cys Gln Leu Asp Glu Ala Pro Arg Glu Gln Trp Glu Gln Ser Gln Ala
 100 105 110
 Glu Gly Arg Thr Asp Cys Ser His Asn Xaa
 115 120

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

Ser Pro Thr Pro Arg Leu Val Gly Thr Cys Met Pro Glu Gly Lys Lys
1           5           10           15
His His Xaa Gly Ala Gly Arg Pro Xaa Arg Arg His Ser Leu Thr Thr
          20           25           30
Thr Glu His Xaa Gln Asp Arg Lys Pro His His Arg Pro Asp Val Gly
          35           40           45
Thr Thr Val Cys Arg Val His His Ser Val His Ala Ala Ala His Gly
          50           55           60
Thr Ser Cys Xaa Ser Pro Lys Asp His His Val Pro Val Met Phe Gly
65           70           75           80
Arg Val Leu Ala Cys His Gly Gly Pro His Asn Pro Glu Glu Ser Leu
          85           90           95
Ala Ser Leu Met Lys His His Gly Ser Ser Gly Asn Lys Ala Arg Arg
          100          105          110
Lys Val Glu Pro Thr Val His Thr Thr Asp
          115          120

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 64:

```

Asp Gln Leu Cys Glu Gln Ser Val Arg Pro Ser Ala Trp Leu Cys Ser
1           5           10           15
His Cys Ser Arg Gly Ala Ser Ser Ser Trp Gln Gly Ile Leu Arg Gly
          20           25           30
Cys Glu Asp Leu His Asp Arg Gln Gly Leu Val Arg Thr Ser Arg Glu
          35           40           45
Arg Gly Gly Pro Trp Asp Phe Asn Asn Ser Phe His Gly Leu Leu Arg
          50           55           60
Glu Arg Ser Asp Val His Asp Ile Pro Trp Tyr Gln Arg Pro Ala Tyr
65           70           75           80

```


1

1

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1

220

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Val Val Xaa Thr Val Gly Ser Thr Phe Arg Leu Ala Leu Phe Pro
 1 5 10 15
 Leu Leu Pro Trp Cys Phe Ile Lys Leu Ala Arg Asp Ser Ser Gly Leu
 20 25 30
 Xaa Gly Pro Pro Xaa Gln Ala Arg Thr Arg Pro Asn Ile Thr Gly Thr
 35 40 45
 Trp Trp Ser Leu Gly Leu Gln Gln Leu Val Pro Trp Ala Ala Ala Xaa
 50 55 60
 Thr Glu Xaa Cys Thr Arg His Thr Val Val Pro Thr Ser Gly Leu Trp
 65 70 75 80
 Trp Gly Phe Arg Ser Cys Gln Cys Ser Val Val Val Ser Glu Xaa Arg
 85 90 95
 Arg His Gly Leu Pro Ala Pro Xaa Trp Cys Phe Leu Pro Ser Gly Met
 100 105 110
 Gln Val Pro Thr Asn Arg Gly Val Gly Asp
 115 120

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Pro Ile Gln Gly Pro Ser Tyr Pro Ser Trp Gln Leu Xaa Lys Gly
 1 5 10 15
 Gln Pro Gly Met Leu Thr Met Leu Xaa Thr Pro Ala Leu Arg Thr Leu
 20 25 30
 Lys Gln Ile Thr Lys Lys Leu His Thr Tyr Cys Gln Ile Ser Arg Pro
 35 40 45
 Gln Ala Met Arg Pro Gln Ser Ser Ser Val Gly Val Trp Ser Gln Arg--
 50 55 60

221

Met Gln Ala Asp Met Ile Leu Gln Gly Val Asp Ala Ser Arg Met Pro
 65 70 75 80

Ser Ile Phe Cys Gly Cys His Glu Trp Gln Xaa Ser Thr His Tyr Ile
 85 90 95

Gln Cys Cys Ser Xaa Gln Ala Xaa Xaa Glu Val Cys Trp Ala Ser Asp
 100 105 110

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ile Gln Ser Arg Gly Pro Arg Thr Pro Pro Gly Ser Cys Arg Lys Asp
 1 5 10 15

Asn Gln Glu Cys Xaa Pro Cys Ser Glu Leu Gln Leu Xaa Gly His Xaa
 20 25 30

Ser Lys Ser Gln Arg Asn Cys Thr His Thr Ala Lys Ser Leu Asp Pro
 35 40 45

Lys Gln Xaa Gly Arg Asn His Pro Pro Ser Gly Cys Gly Ala Asn Gly
 50 55 60

Cys Lys Leu Ile Xaa Tyr Ser Arg Gly Xaa Met Pro Pro Glu Cys Pro
 65 70 75 80

Val Ser Ser Ala Asp Val Thr Ser Gly Asn Lys Val Leu Thr Thr Tyr
 85 90 95

Ser Val Ala Pro Ser Lys His Ser Lys Lys Ser Val Gly Pro Val Ile
 100 105 110

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Ser Asn Pro Gly Ala Leu Val Pro Leu Leu Ala Ala Val Glu Arg Thr
1           5           10           15
Thr Arg Asn Val Asn His Ala Leu Asn Ser Ser Phe Lys Asp Ile Lys
          20           25           30
Ala Asn His Lys Glu Ile Ala His Ile Leu Pro Asn Leu Xaa Thr Pro
          35           40           45
Ser Asn Glu Ala Ala Ile Ile Leu Arg Arg Gly Val Glu Pro Thr Asp
          50           55           60
Ala Ser Xaa Tyr Asp Thr Pro Gly Gly Arg Cys Leu Gln Asn Ala Gln
          65           70           75           80
Tyr Leu Leu Arg Met Ser Arg Val Ala Ile Lys Tyr Ser Leu His Thr
          85           90           95
Val Leu Leu Leu Ala Ser Ile Val Arg Ser Leu Leu Gly Gln Xaa
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Asp His Trp Pro Asn Arg Leu Leu Thr Met Leu Ala Arg Ser Asn Thr
1           5           10           15
Val Cys Ser Glu Tyr Phe Ile Ala Thr Arg Asp Ile Arg Arg Arg Tyr
          20           25           30
Trp Ala Phe Trp Arg His Leu Pro Gly Val Ser Tyr Gln Leu Ala
          35           40           45
Ser Val Gly Ser Thr Pro Arg Arg Arg Met Ile Ala Ala Ser Leu Leu
          50           55           60
Gly Val Xaa Arg Phe Gly Ser Met Cys Ala Ile Ser Leu Xaa Phe Ala
          65           70           75           80

```

Leu Met Ser Leu Lys Leu Glu Phe Arg Ala Trp Leu Thr Phe Leu Val
85 90 95

Val Leu Ser Thr Ala Ala Arg Arg Gly Thr Arg Ala Pro Gly Leu Asp
100 105 110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile Thr Gly Pro Thr Asp Phe Leu Leu Cys Leu Leu Gly Ala Thr Leu
1 5 10 15

Tyr Val Val Ser Thr Leu Leu Pro Leu Val Thr Ser Ala Glu Asp Thr
20 25 30

Gly His Ser Gly Gly Ile Tyr Pro Leu Glu Tyr His Ile Ser Leu His
35 40 45

Pro Leu Ala Pro His Pro Asp Gly Gly Xaa Leu Arg Pro His Cys Leu
50 55 60

Gly Ser Arg Asp Leu Ala Val Cys Val Gln Phe Leu Cys Asp Leu Leu
65 70 75 80

Xaa Cys Pro Xaa Ser Trp Ser Ser Glu His Gly Xaa His Ser Trp Leu
85 90 95

Ser Phe Leu Gln Leu Pro Gly Gly Val Arg Gly Pro Leu Asp Trp Ile
100 105 110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:72:

224

Ser Leu Ala Gln Gln Thr Ser Tyr Tyr Ala Cys Xaa Glu Gln His Cys
 1 5 10 15
 Met Xaa Xaa Val Leu Tyr Cys His Ser Xaa His Pro Gln Lys Ile Leu
 20 25 30
 Gly Ile Leu Glu Ala Ser Thr Pro Trp Ser Ile Ile Ser Ala Cys Ile
 35 40 45
 Arg Trp Leu His Thr Pro Thr Glu Asp Asp Cys Gly Leu Ile Ala Trp
 50 55 60
 Gly Leu Glu Ile Trp Gln Tyr Val Cys Asn Phe Phe Val Ile Cys Phe
 65 70 75 80
 Asn Val Leu Lys Ala Gly Val Gln Ser Met Val Asn Ile Pro Gly Cys
 85 90 95
 Pro Phe Tyr Ser Cys Gln Glu Gly Tyr Glu Gly Pro Trp Ile Gly
 100 105 110

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GATCAGGCCG CTGAGCGGCC GAGAAGGTTA CAATCTGGAG GGGTGATAGG AAGTATGACA 60
 AGCATTATGA GGCTGTCGTT GAGGCTGTCC TGAAAAAGGC AGCCGCGACG AAGTCTCATG 120
 GCTGGACCTA TTCCCAGGCT ATAGCTAAAG TTAGGCGCCG AGCAGCCGCT GGATACGGCA 180
 GCAAGGTGAC CGCCTCCACA TTGGCCACTG GTTGGCCTCA CGTGGAGGAG ATGCTGGACA 240
 AAATAGCCAG GGGACAGGAA GTTCCTTTCA CTTTGTGAC CAAGCGAGAG GTTTTCTTCT 300
 CCAAACTAC CCGTAAGCCC CCAAGATTCA TAGTTTTCCC ACCTTTGGAC TTCAGGATAG 360
 CTGAAAAGAT GATTCTGGGT GACCCCGGCA TCGTTGCAAA GTCAATTCTG GGTGACGCTT 420
 ATCTGTTCCA GTACACGCCC AATCAGAGGG TCAAAGCTCT GGTTAAGGCG TGGGAGGGGA 480
 AGTTGCATCC CGCTGCGATC ACCGTGKACG CCACTTGTTT CGACTCATCG ATTGATGAGC 540
 ACGACATGCA GGTGGAGGCT TCGGTGTTTG CGGCGGCTAG TGACAACCCC TCAATGGTAC 600
 ATGCTTTGTG CAAGTACTAC TCTGGTGGCC CTATGGTTTC CCCAGATGGG GTTCCCTTGG 660

225

GGTACCGCCA GTGTAGGTCG TCGGGCGTGT TGACAACTAG CTCGGCGAAC AGCATCACTT 720
 GTTACATTAA GGTCAGCGCG GCCTGCAGGC GGGTGGGGAT TAAGGCACCA TCATTCTTTA 780
 TAGCTGGAGA TGATT 795

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asp Gln Ala Ala Glu Arg Pro Arg Arg Leu Gln Ser Gly Gly Val Ile
 1 5 10 15
 Gly Ser Met Thr Ser Ile Met Arg Leu Ser Leu Arg Leu Ser Xaa Lys
 20 25 30
 Arg Gln Pro Arg Arg Ser Leu Met Ala Gly Pro Ile Pro Arg Leu Xaa
 35 40 45
 Leu Lys Leu Gly Ala Glu Gln Pro Leu Asp Thr Ala Ala Arg Xaa Pro
 50 55 60
 Pro Pro His Trp Pro Leu Val Gly Leu Thr Trp Arg Arg Cys Trp Thr
 65 70 75 80
 Lys Xaa Pro Gly Asp Arg Lys Phe Leu Ser Leu Leu Xaa Pro Ser Glu
 85 90 95
 Arg Phe Ser Ser Pro Lys Leu Pro Val Ser Pro Gln Asp Ser Xaa Phe
 100 105 110
 Ser His Leu Trp Thr Ser Gly Xaa Leu Lys Arg Xaa Phe Trp Val Thr
 115 120 125
 Pro Ala Ser Leu Gln Ser Gln Phe Trp Val Thr Leu Ile Cys Ser Ser
 130 135 140
 Thr Arg Pro Ile Arg Gly Ser Lys Leu Trp Leu Arg Arg Gly Arg Gly
 145 150 155 160
 Ser Cys Ile Pro Leu Arg Ser Pro Xaa Thr Pro Leu Val Ser Thr His
 165 170 175
 Arg Leu Met Ser Thr Thr Cys Arg Trp Arg Leu Arg Cys Leu Arg Arg
 180 185 190

226

Leu Val Thr Thr Pro Gln Trp Tyr Met Leu Cys Ala Ser Thr Thr Leu
 195 200 205
 Val Ala Leu Trp Phe Pro Gln Met Gly Phe Pro Trp Gly Thr Ala Ser
 210 215 220
 Val Gly Arg Arg Ala Cys Xaa Gln Leu Ala Arg Arg Thr Ala Ser Leu
 225 230 235 240
 Val Thr Leu Arg Ser Ala Arg Pro Ala Gly Gly Trp Gly Leu Arg His
 245 250 255
 His His Ser Leu Xaa Leu Glu Met Ile
 260 265

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Arg Pro Leu Ser Gly Arg Glu Gly Tyr Asn Leu Glu Gly Xaa Xaa
 1 5 10 15
 Glu Val Xaa Gln Ala Leu Xaa Gly Cys Arg Xaa Gly Cys Pro Glu Lys
 20 25 30
 Gly Ser Arg Asp Glu Val Ser Trp Leu Asp Leu Phe Pro Gly Tyr Ser
 35 40 45
 Xaa Ser Xaa Ala Pro Ser Ser Arg Trp Ile Arg Gln Gln Gly Asp Arg
 50 55 60
 Leu His Ile Gly His Trp Leu Ala Ser Arg Gly Gly Asp Ala Gly Gln
 65 70 75 80
 Asn Ser Gln Gly Thr Gly Ser Ser Phe His Phe Cys Asp Gln Ala Arg
 85 90 95
 Gly Phe Leu Leu Gln Asn Tyr Pro Xaa Ala Pro Lys Ile His Ser Phe
 100 105 110
 Pro Thr Phe Gly Leu Gln Asp Ser Xaa Lys Asp Asp Ser Gly Xaa Pro
 115 120 125
 Arg His Arg Cys Lys Val Asn Ser Gly Xaa Arg Leu Ser Val Pro Val
 130 135 140

227

His Ala Gln Ser Glu Gly Gln Ser Ser Gly Xaa Gly Val Gly Gly Glu
 145 150 155 160
 Val Ala Ser Arg Cys Asp His Arg Xaa Arg His Leu Phe Arg Leu Ile
 165 170 175
 Asp Xaa Xaa Ala Arg His Ala Gly Gly Gly Phe Gly Val Cys Gly Gly
 180 185 190
 Xaa Xaa Gln Pro Leu Asn Gly Thr Cys Phe Val Gln Val Leu Leu Trp
 195 200 205
 Trp Pro Tyr Gly Phe Pro Arg Trp Gly Ser Leu Gly Val Pro Pro Val
 210 215 220
 Xaa Val Val Gly Arg Val Asp Asn Xaa Leu Gly Glu Gln His His Leu
 225 230 235 240
 Leu His Xaa Gly Gln Arg Gly Leu Gln Ala Gly Gly Asp Xaa Gly Thr
 245 250 255
 Ile Ile Leu Tyr Ser Trp Arg Xaa
 260

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Gly Arg Xaa Ala Ala Glu Lys Val Thr Ile Trp Arg Gly Asp Arg
 1 5 10 15
 Lys Tyr Asp Lys His Tyr Glu Ala Val Val Glu Ala Val Leu Lys Lys
 20 25 30
 Ala Ala Ala Thr Lys Ser His Gly Trp Thr Tyr Ser Gln Ala Ile Ala
 35 40 45
 Lys Val Arg Arg Arg Ala Ala Gly Tyr Gly Ser Lys Val Thr Ala
 50 55 60
 Ser Thr Leu Ala Thr Gly Trp Pro His Val Glu Glu Met Leu Asp Lys
 65 70 75 80
 Ile Ala Arg Gly Gln Glu Val Pro Phe Thr Phe Val Thr Lys Arg Glu
 85 90 95

228

Val Phe Phe Ser Lys Thr Thr Arg Lys Pro Pro Arg Phe Ile Val Phe
 100 105 110

Pro Pro Leu Asp Phe Arg Ile Ala Glu Lys Met Ile Leu Gly Asp Pro
 115 120 125

Gly Ile Val Ala Lys Ser Ile Leu Gly Asp Ala Tyr Leu Phe Gln Tyr
 130 135 140

Thr Pro Asn Gln Arg Val Lys Ala Leu Val Lys Ala Trp Glu Gly Lys
 145 150 155 160

Leu His Pro Ala Ala Ile Thr Val Xaa Ala Thr Cys Phe Asp Ser Ser
 165 170 175

Ile Asp Glu His Asp Met Gln Val Glu Ala Ser Val Phe Ala Ala Ala
 180 185 190

Ser Asp Asn Pro Ser Met Val His Ala Leu Cys Lys Tyr Tyr Ser Gly
 195 200 205

Gly Pro Met Val Ser Pro Asp Gly Val Pro Leu Gly Tyr Arg Gln Cys
 210 215 220

Arg Ser Ser Gly Val Leu Thr Thr Ser Ser Ala Asn Ser Ile Thr Cys
 225 230 235 240

Tyr Ile Lys Val Ser Ala Ala Cys Arg Arg Val Gly Ile Lys Ala Pro
 245 250 255

Ser Phe Phe Ile Ala Gly Asp Asp
 260

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn His Leu Gln Leu Xaa Arg Met Met Val Pro Xaa Ser Pro Pro Ala
 1 5 10 15

Cys Arg Pro Arg Xaa Pro Xaa Cys Asn Lys Xaa Cys Cys Ser Pro Ser
 20 25 30

Xaa Leu Ser Thr Arg Pro Thr Thr Tyr Thr Gly Gly Thr Pro Arg Glu
 35 40 45

229

Pro His Leu Gly Lys Pro Xaa Gly His Gln Ser Ser Thr Cys Thr Lys
 50 55 60
 His Val Pro Leu Arg Gly Cys His Xaa Pro Pro Gln Thr Pro Lys Pro
 65 70 75 80
 Pro Pro Ala Cys Arg Ala His Gln Ser Met Ser Arg Asn Lys Trp Arg
 85 90 95
 Xaa Arg Xaa Ser Gln Arg Asp Ala Thr Ser Pro Pro Thr Pro Xaa Pro
 100 105 110
 Glu Leu Xaa Pro Ser Asp Trp Ala Cys Thr Gly Thr Asp Lys Arg His
 115 120 125
 Pro Glu Leu Thr Leu Gln Arg Cys Arg Gly His Pro Glu Ser Ser Phe
 130 135 140
 Gln Leu Ser Xaa Ser Pro Lys Val Gly Lys Leu Xaa Ile Leu Gly Ala
 145 150 155 160
 Tyr Gly Xaa Phe Trp Arg Arg Lys Pro Leu Ala Trp Ser Gln Lys Xaa
 165 170 175
 Lys Glu Leu Pro Val Pro Trp Leu Phe Cys Pro Ala Ser Pro Pro Arg
 180 185 190
 Glu Ala Asn Gln Trp Pro Met Trp Arg Arg Ser Pro Cys Cys Arg Ile
 195 200 205
 Gln Arg Leu Leu Gly Ala Xaa Leu Xaa Leu Xaa Pro Gly Asn Arg Ser
 210 215 220
 Ser His Glu Thr Ser Ser Arg Leu Pro Phe Ser Gly Gln Pro Gln Arg
 225 230 235 240
 Gln Pro His Asn Ala Cys His Thr Ser Tyr His Pro Ser Arg Leu Xaa
 245 250 255
 Pro Ser Arg Pro Leu Ser Gly Leu Ile
 260 265

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

230

Ile Ile Ser Ser Tyr Lys Glu Xaa Trp Cys Leu Asn Pro His Pro Pro
 1 5 10 15
 Ala Gly Arg Ala Asp Leu Asn Val Thr Ser Asp Ala Val Arg Arg Ala
 20 25 30
 Ser Cys Gln His Ala Arg Arg Pro Thr Leu Ala Val Pro Gln Gly Asn
 35 40 45
 Pro Ile Trp Gly Asn His Arg Ala Thr Arg Val Val Leu Ala Gln Ser
 50 55 60
 Met Tyr His Xaa Gly Val Val Thr Ser Arg Arg Lys His Arg Ser Leu
 65 70 75 80
 His Leu His Val Val Leu Ile Asn Arg Xaa Val Glu Thr Ser Gly Val
 85 90 95
 His Gly Asp Arg Ser Gly Met Gln Leu Pro Leu Pro Arg Leu Asn Gln
 100 105 110
 Ser Phe Asp Pro Leu Ile Gly Arg Val Leu Glu Gln Ile Ser Val Thr
 115 120 125
 Gln Asn Xaa Leu Cys Asn Asp Ala Gly Val Thr Gln Asn His Leu Phe
 130 135 140
 Ser Tyr Pro Glu Val Gln Arg Trp Glu Asn Tyr Glu Ser Trp Gly Leu
 145 150 155 160
 Thr Gly Ser Phe Gly Glu Glu Asn Leu Ser Leu Gly His Lys Ser Glu
 165 170 175
 Arg Asn Phe Leu Ser Pro Gly Tyr Phe Val Gln His Leu Leu His Val
 180 185 190
 Arg Pro Thr Ser Gly Gln Cys Gly Gly Gly His Leu Ala Ala Val Ser
 195 200 205
 Ser Gly Cys Ser Ala Pro Asn Phe Ser Tyr Ser Leu Gly Ile Gly Pro
 210 215 220
 Ala Met Arg Leu Arg Arg Gly Cys Leu Phe Gln Asp Ser Leu Asn Asp
 225 230 235 240
 Ser Leu Ile Met Leu Val Ile Leu Pro Ile Thr Pro Pro Asp Cys Asn
 245 250 255
 Leu Leu Gly Arg Ser Ala Ala Xaa
 260

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

231

- (A) LENGTH: 264 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Ser Ser Pro Ala Ile Lys Asn Asp Gly Ala Leu Ile Pro Thr Arg Leu
1           5           10           15
Gln Ala Ala Leu Thr Leu Met Xaa Gln Val Met Leu Phe Ala Glu Leu
20           25           30
Val Val Asn Thr Pro Asp Asp Leu His Trp Arg Tyr Pro Lys Gly Thr
35           40           45
Pro Ser Gly Glu Thr Ile Gly Pro Pro Glu Xaa Tyr Leu His Lys Ala
50           55           60
Cys Thr Ile Glu Gly Leu Ser Leu Ala Ala Ala Asn Thr Glu Ala Ser
65           70           75           80
Thr Cys Met Ser Cys Ser Ser Ile Asp Glu Ser Lys Gln Val Ala Xaa
85           90           95
Thr Val Ile Ala Ala Gly Cys Asn Phe Pro Ser His Ala Leu Thr Arg
100          105          110
Ala Leu Thr Leu Xaa Leu Gly Val Tyr Trp Asn Arg Xaa Ala Ser Pro
115          120          125
Arg Ile Asp Phe Ala Thr Met Pro Gly Ser Pro Arg Ile Ile Phe Ser
130          135          140
Ala Ile Leu Lys Ser Lys Gly Gly Lys Thr Met Asn Leu Gly Gly Leu
145          150          155          160
Arg Val Val Leu Glu Lys Lys Thr Ser Arg Leu Val Thr Lys Val Lys
165          170          175
Gly Thr Ser Cys Pro Leu Ala Ile Leu Ser Ser Ile Ser Ser Thr Xaa
180          185          190
Gly Gln Pro Val Ala Asn Val Glu Ala Val Thr Leu Leu Pro Tyr Pro
195          200          205
Ala Ala Ala Arg Arg Leu Thr Leu Ala Ile Ala Trp Glu Xaa Val Gln
210          215          220
Pro Xaa Asp Phe Val Ala Ala Ala Phe Phe Arg Thr Ala Ser Thr Thr
225          230          235          240
Ala Ser Xaa Cys Leu Ser Tyr Phe Leu Ser Pro Leu Gln Ile Val Thr
245          250          255

```

232

Phe Ser Ala Ala Gln Arg Pro Asp
260

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGGCTCATCC CACAGGCTCC ATACACCCAA TAACCGTTGA CGCGGCTAAT GACCAGGACA	60
TCTATCAACC ACCATGTGGA GCTGGGTCCC TTACTCGGTG CTCTTGCGGG GAGACCAAGG	120
GGTATCTGGT AACACGACTG GGGTCATTGG TTGAGGTCAA CAAATCCGAT GACCCTTATT	180
GGTGTGTGTG CGGGGCCCTT CCCATGGCTG TTGCCAAGGG TTCTTCAGGT GCCCGATTG	240
TGTGCTCCTC CGGGCATGTT ATTGGGATGT TCACCGCTGC TAGAAATTCT GGCGGTTTCTAG	300
TCGGCCAGAT TAGGGTTAGG CCGTTGGTGT GTGCTGGATA CCATCCCCAG TACACAGCAC	360
ATGCCACTCT TGATACAAAA CCTACTGTGC CTAACGAGTA TTCAGTGCAA ATTTTAATTG	420
CCCCCACTGG CAGCGGCAAG TCAACCAAAT TACCACTTTC TTACATGCAG GRGAAGYATG	480
AGGTCTTGGT CCTAAATCCC AGTGTGGCTA CAACAGCATC AATGCCAAAG TACATGCACG	540
CGACGTACGG CGTGAATCCA AATTGCTATT TTAATGGCAA ATGTACCAAC ACAGGGGCTT	600
CACTTACGTA CAGCACATAT GGCATGTACC TGACCGGACG ATGTCCCCGG AACTATGATG	660
TAATCATTGG TGACGAATGC CATGCTACCG ATCGAACCAC CGTGTGGGGC ATTGGAAAGG	720
TCCTAACCGA AGCTCCATCC AAAAATGTGA GGCTAGTGGT TCTTGCCACG GCTACCCCCC	780
CTGGAGTAAT CCCTACACCA CATGCCAACA TAACTGAGAT TCAATTAACY GATGAAGGCA	840
CTATCCCCTT TCATGGAAAA AAGATTAAGG AGGAAAATCT GAAGAAAGGG AGACACCTTA	900
TCTTTGAGGC TACCAAAAAA CACTGTGATG AGCTTGCTAA CGAGTTAGCT CGAAAGGGAA	960
TAACAGCTGT CTCTTACTAT AGGGGATGTG ACATCTCAA AATGCCTGAG GGCGACTGTG	1020
TAGTAGTTGC CACTGATGCC TTGTGTACAG GGTACACTGG TGACTTTGAT TCCGTGTATG	1080
ACTGCAGCCT CATGGTAGAA GGCACATGCC ATGTTGACCT TGACCCTACT TTCACCATGG	1140

233

GTGTTTCGTGT	GTGCGGGGTT	TCAGCAATAG	TTAAAGGCCA	GCGTAGGGGC	CGCACAGGCC	1200
GTGGGAGAGC	TGGCATATAC	TACTATGTAG	ACGGGAGTTG	TACCCCTTCG	GGTATGGTTC	1260
CTGAATGCAA	CATTGTTGAA	GCCTTCGACG	CAGCCAAGGC	ATGGTATGGT	TTGTCATCAA	1320
CAGAAGCTCA	AACTATTCTG	GACACCTATC	GCACCCAACC	TGGGTTACCT	GCGATAGGAG	1380
CAAATTTGGA	CGAGTGGGCT	GATCTCTTTT	CTATGGTCAA	CCCCGAACCT	TCATTTGTCA	1440
ATACTGCAAA	AAGAACTGCT	GACAATTATG	TTTTGTTGAC	TGCAGCCCAA	CTACAACTGT	1500
GTCATCAGTA	TGGCTATGCT	GCTCCCAATG	ACGCACCACG	GTGGCAGGGA	GCCCCGGCTTG	1560
GGAAAAAACC	TTGTGGGGTT	CTGTGGCGCT	TGGACGGCTG	TGACGCCTGT	CCTGGCCCAG	1620
AGCCCAGCGA	GGTGACCAGA	TACCAAATGT	GCTTCACTGA	AGTCAATACT	TCTGGGACAG	1680
CCGCACTCGC	TGTTGGCGTT	GGAGTGGCTA	TGGCTTATCT	AGCCATTGAC	ACTTTTGGCG	1740
CCACTTGTGT	GCGGCGTTGC	TGGTCTATTA	CATCAGTCCC	TACCGGTGCT	ACTGTCGCCC	1800
CAGTGGTTGA	CGAAGAGGAA	ATCGTGGAGG	AGTGTGCATC	ATTCAATCCC	TTGGAGGCCA	1860
TGGTTGCTGC	AATTGACAAG	CTGAAGAGTA	CAATCACCAC	AACTAGTCCT	TTCACATTGG	1920
AAACCGCCCT	TGAAAACTT	AACACCTTTC	TTGGGCCTCA	TGCAGCTACA	ATCCTTGCTA	1980
TCATAGAGTA	TTGCTGTGGC	TTAGTCACTT	TACCTGACAA	TCCCTTTGCA	TCATGCGTGT	2040
TTGCTTTTAT	TGCGGGTATT	ACTACCCAC	TACCTCACAA	GATCAAAATG	TTCTGTTCAT	2100
TATTTGGAGG	CGCAATTGCG	TCCAAGCTTA	CAGACGCTAG	AGRCGCACTG	GCGTTCATGA	2160
TGGCCGGGGC	TGYGGGAACA	GCTCTTG GTA	CATGGACATC	GGTGGGTTTT	GTCTTTGACA	2220
TGCTAGGCGG	CTATGCTGGC	GCCTCATCCA	CTGCTTGCTT	GACATTTAAA	TGCTTGATGG	2280
GTGAGTGGCY	CACATATGGAT	CAGCTTGCTG	GTTTAGTCTA	CTCCGCGTTC	AATCCGGCCG	2340
CAGGAGTTGT	GGGCGTCTTG	TCAGCTTGTG	CAATGTTTGC	TTTGACAACA	GCAGGGCCAG	2400
ATCACTGGCC	CAACAGACTT	CTTACTATGC	TTGCTAGGAG	CAACACTGTA	TGTARTGAGT	2460
ACTTTATTGC	CACCTCGTGAC	ATCCGCAGGA	AGATACTGGG	CATTCTGGAG	GCATCTACCC	2520
CCTGGAGTRT	CATATCAGCT	TGCATCCGTT	GGCTYCACAC	CCCGACGGAG	GATGATTGCG	2580
GCCTCATTGC	TTGGGGTCTA	RAGATTTGGC	AGTATGTGTG	CAATTTCTTT	GTGATTGCTT	2640
TTAATGTCCT	TAAAGCTGGA	GTTTCAGAGCA	TGGTTAACAT	TCCTGGTTGT	CCTTTCTACA	2700
GCTGCCAGAA	GGGGTACAAG	GGCCCCCTGA	TTGGATCAGG	TATGCTCCAA	GCACGCTGTC	2760
CATGCGGTGC	TGAACTCATC	TTTTCTGTTG	AGAATGGTTT	TGCAAACTT	TACAAAGGAC	2820
CCAGAACTTG	TTCAAATTAC	TGGAGAGGGG	CTGTTCCAGT	CAACGCTAGG	CTGTGTGGGT	2880

CGGCTAGACC GGACCCAACT GATTGGACTA GTCTTGTCGT CAATTATGGC GTTAGGGACT	2940
ACTGTAAATA TGAGAAATTG GGAGATCACA TTTTGTGTAC AGCAGTATCC TCTCCAAATG	3000
TCTGTTTCAC CCAGGTGCCC CCAACCTTGA GAGCTGCAGT GGCCGTGGAC CGCGTACAGG	3060
TTCAGYGTTA TCTAGGTGAG CCCAAAACCTC CTTGGACGAC ATCTGCTTGC TGTTACGGTC	3120
CTGACGGTAA GGTAAAACT GTTAAGCTTC CCTTCCGCGT TGACGGACAC ACACCTGGTG	3180
GTCGCATGCA ACTTAATTTG CGTGATCGAC TTGAGGCAAA TGA CTGTAAT TCCATAAACA	3240
ACACTCCTAG TGATGAAGCC GCAGTGTCCG CTCTTGTTTT CAAACAGGAG TTGCGGCGTA	3300
CAAACCAATT GCTTGAGGCA ATTTCAAGCTG GCGTTGACAC CACCAAACCTG CCAGCCCCCT	3360
CCCAGATCGA AGAGGTAGTG GTAAGAAAGC GCCAGTTCCG GGCAAGAACT GGTTTCGCTTA	3420
CCTTGCCCTCC CCCTCCGAGA TCCGTCCCAG GAGTGTCTATG TCCTGAAAGC CTGCAACGAA	3480
GTGACCCGTT AGAAGGTCCT TCAAMCCTCC CTTCTTCACC ACCTGTTCTR CAGTTGGCCA	3540
TGCCGATGCC CCTGTTGGGA GCAGGTGAGT GTAACCCTTT CACTGCAATT GGATGTGCAA	3600
TGACCGAAAC ARGYGGAGKC CCWSAKRATT TACCCAGTTA CCCTCCCAA AAGGAGGTCT	3660
CTGAATGGTC AGACGAAAGT TGGTCAACGA CTACAACCGC TTCCAGCTAC GTTACTGGCC	3720
CCCCGTACCC TAAGATACGG GGCAAGGATT CCACTCAATC AGCCACCGCC AAACGGCCTA	3780
CAAAAAAGAA GTTGGGAAAG AGTGAGTTTT CGTGCAGCAT GAGCTACACT TGGACCGACG	3840
TGATTAGCTT CAAAACCTGCT TCTAAAGTTC TGTCTGCAAC TCGGGCCATC ACTAGTGGTT	3900
TCCTCAAACA AAGATCATTG GTGTATGTGA CTGAGCCGCG GGATGCGGAG CTTAGAAAAC	3960
AAAAAGTCAC TATTAATAGA CAACCTCTGT TCCCCCATC ATACCACAAG CAAGTGAGAT	4020
TGGCTAAGGA AAAAGCTTCA AAAGTTGTCG GTGTCATGTG GGA CTATGAT GAAGTAGCAG	4080
CTCACACGCC CTCTAAGTCT GCTAAGTCCC ACATCACTGG CCTTCGGGGC ACTGATGTTT	4140
TGGA CTTGCA GAAGTGTGTC GAGGCAGGTG AGATACCGAG TCATTATCGG CAAACTGTGA	4200
TAGTTCCAAA GGAGGAGGTC TTCGTGAAGA CCCCCAGAA ACCAACAAAG AAACCCCCAA	4260
GGCTTATC	4268

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 amino acids
- (B) TYPE: amino acid

235

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

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Trp Leu Ile Pro Gln Ala Pro Tyr Thr Gln Xaa Pro Leu Thr Arg Leu
1           5           10           15
Met Thr Arg Thr Ser Ile Asn His His Val Glu Leu Gly Pro Leu Leu
20           25           30
Gly Ala Leu Ala Gly Arg Pro Arg Gly Ile Trp Xaa His Asp Trp Gly
35           40           45
His Trp Leu Arg Ser Thr Asn Pro Met Thr Leu Ile Gly Val Cys Ala
50           55           60
Gly Pro Phe Pro Trp Leu Leu Pro Arg Val Leu Gln Val Pro Arg Phe
65           70           75           80
Cys Ala Pro Pro Gly Met Leu Leu Gly Cys Ser Pro Leu Leu Glu Ile
85           90           95
Leu Ala Val Gln Ser Ala Arg Leu Gly Leu Gly Arg Trp Cys Val Leu
100          105          110
Asp Thr Ile Pro Ser Thr Gln His Met Pro Leu Leu Ile Gln Asn Leu
115          120          125
Leu Cys Leu Thr Ser Ile Gln Cys Lys Phe Xaa Leu Pro Pro Leu Ala
130          135          140
Ala Ala Ser Gln Pro Asn Tyr His Phe Leu Thr Cys Arg Xaa Ser Met
145          150          155          160
Arg Ser Trp Ser Xaa Ile Pro Val Trp Leu Gln Gln His Gln Cys Gln
165          170          175
Ser Thr Cys Thr Arg Arg Thr Ala Xaa Ile Gln Ile Ala Ile Leu Met
180          185          190
Ala Asn Val Pro Thr Gln Gly Leu His Leu Arg Thr Ala His Met Ala
195          200          205
Cys Thr Xaa Pro Asp Asp Val Pro Gly Thr Met Met Xaa Ser Phe Val
210          215          220
Thr Asn Ala Met Leu Pro Ile Glu Pro Pro Cys Trp Ala Leu Glu Arg
225          230          235          240
Ser Xaa Pro Lys Leu His Pro Lys Met Leu Gly Xaa Trp Phe Leu Pro
245          250          255
Arg Leu Pro Pro L u Glu Xaa Ser Leu His His Met Pro Thr Xaa Leu

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260	265	270
Arg Phe Asn Xaa Xaa Met Lys Ala Leu Ser Pro Phe Met Glu Lys Arg		
275	280	285
Leu Arg Arg Lys Ile Xaa Arg Lys Gly Asp Thr Leu Ser Leu Arg Leu		
290	295	300
Pro Lys Asn Thr Val Met Ser Leu Leu Thr Ser Xaa Leu Glu Arg Glu		
305	310	315
		320
Xaa Gln Leu Ser Leu Thr Ile Gly Asp Val Thr Ser Gln Lys Cys Leu		
325	330	335
Arg Ala Thr Val Xaa Xaa Leu Pro Leu Met Pro Cys Val Gln Gly Thr		
340	345	350
Leu Val Thr Leu Ile Pro Cys Met Thr Ala Ala Ser Trp Xaa Lys Ala		
355	360	365
His Ala Met Leu Thr Leu Thr Leu Leu Ser Pro Trp Val Phe Val Cys		
370	375	380
Ala Gly Phe Gln Gln Xaa Leu Lys Ala Ser Val Gly Ala Ala Gln Ala		
385	390	395
		400
Val Gly Glu Leu Ala Tyr Thr Thr Met Xaa Thr Gly Val Val Pro Leu		
405	410	415
Arg Val Trp Phe Leu Asn Ala Thr Leu Leu Lys Pro Ser Thr Gln Pro		
420	425	430
Arg His Gly Met Val Cys His Gln Gln Lys Leu Lys Leu Phe Trp Thr		
435	440	445
Pro Ile Ala Pro Asn Leu Gly Tyr Leu Arg Xaa Glu Gln Ile Trp Thr		
450	455	460
Ser Gly Leu Ile Ser Phe Leu Trp Ser Thr Pro Asn Leu His Leu Ser		
465	470	475
		480
Ile Leu Gln Lys Glu Leu Leu Thr Ile Met Phe Cys Xaa Leu Gln Pro		
485	490	495
Asn Tyr Asn Cys Val Ile Ser Met Ala Met Leu Leu Pro Met Thr His		
500	505	510
His Gly Gly Arg Glu Pro Gly Leu Gly Lys Asn Leu Val Gly Phe Cys		
515	520	525
Gly Ala Trp Thr Ala Val Thr Pro Val Leu Ala Gln Ser Pro Ala Arg		
530	535	540
Xaa Pro Asp Thr Lys Cys Ala Ser Leu Lys Ser Ile Leu Leu Gly Gln		
545	550	555
		560
Pro His Ser Leu Leu Ala L u Glu Trp Leu Trp Leu Ile Xaa Pro Leu		

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565					570					575					
Thr	Leu	Leu	Ala	Pro	Leu	Val	Cys	Gly	Val	Ala	Gly	Leu	Leu	His	Gln
			580					585					590		
Ser	Leu	Pro	Val	Leu	Leu	Ser	Pro	Gln	Trp	Leu	Thr	Lys	Arg	Lys	Ser
			595				600					605			
Trp	Arg	Ser	Val	His	His	Ser	Phe	Pro	Trp	Arg	Pro	Trp	Leu	Leu	Gln
	610					615					620				
Leu	Thr	Ser	Xaa	Arg	Val	Gln	Ser	Pro	Gln	Leu	Val	Leu	Ser	His	Trp
	625					630					635				640
Lys	Pro	Pro	Leu	Lys	Asn	Leu	Thr	Pro	Phe	Leu	Gly	Leu	Met	Gln	Leu
				645					650					655	
Gln	Ser	Leu	Leu	Ser	Xaa	Ser	Ile	Ala	Val	Ala	Xaa	Ser	Leu	Tyr	Leu
			660					665						670	
Thr	Ile	Pro	Leu	His	His	Ala	Cys	Leu	Leu	Ser	Leu	Arg	Val	Leu	Leu
		675					680					685			
Pro	His	Tyr	Leu	Thr	Arg	Ser	Lys	Cys	Ser	Cys	His	Tyr	Leu	Glu	Ala
		690					695					700			
Gln	Leu	Arg	Pro	Ser	Leu	Gln	Thr	Leu	Glu	Xaa	His	Trp	Arg	Ser	Xaa
	705					710					715				720
Trp	Pro	Gly	Leu	Xaa	Glu	Gln	Leu	Leu	Val	His	Gly	His	Arg	Trp	Val
			725						730					735	
Leu	Ser	Leu	Thr	Cys	Xaa	Ala	Ala	Met	Leu	Ala	Pro	His	Pro	Leu	Leu
			740					745					750		
Ala	Xaa	His	Leu	Asn	Ala	Xaa	Trp	Val	Ser	Gly	Xaa	Leu	Trp	Ile	Ser
		755					760					765			
Leu	Leu	Val	Xaa	Ser	Thr	Pro	Arg	Ser	Ile	Arg	Pro	Gln	Glu	Leu	Trp
		770				775					780				
Ala	Ser	Cys	Gln	Leu	Val	Gln	Cys	Leu	Leu	Xaa	Gln	Gln	Gln	Gly	Gln
	785					790					795				800
Ile	Thr	Gly	Pro	Thr	Asp	Phe	Leu	Leu	Cys	Leu	Leu	Gly	Ala	Thr	Leu
			805						810					815	
Tyr	Val	Xaa	Ser	Thr	Leu	Leu	Pro	Leu	Val	Thr	Ser	Ala	Gly	Arg	Tyr
			820				825						830		
Trp	Ala	Phe	Trp	Arg	His	Leu	Pro	Pro	Gly	Val	Ser	Tyr	Gln	Leu	Ala
		835					840					845			
Ser	Val	Gly	Xaa	Thr	Pro	Arg	Arg	Arg	Met	Ile	Ala	Ala	Ser	Leu	Leu
		850				855					860				
Gly	Val	Xaa	Arg	Phe	Gly	Ser	M t	Cys	Ala	Il	Ser	Leu	Xaa	Phe	Ala

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865 870 875 880
 Leu Met Ser Leu Lys Leu Glu Phe Arg Ala Trp Leu Thr Phe Leu Val
 885 890 895
 Val Leu Ser Thr Ala Ala Arg Arg Gly Thr Arg Ala Pro Gly Leu Asp
 900 905 910
 Gln Val Cys Ser Lys His Ala Val His Ala Val Leu Asn Ser Ser Phe
 915 920 925
 Leu Leu Arg Met Val Leu Gln Asn Phe Thr Lys Asp Pro Glu Leu Val
 930 935 940
 Gln Ile Thr Gly Glu Gly Leu Phe Gln Ser Thr Leu Gly Cys Val Gly
 945 950 955 960
 Arg Leu Asp Arg Thr Gln Leu Ile Gly Leu Val Leu Ser Ser Ile Met
 965 970 975
 Ala Leu Gly Thr Thr Val Asn Met Arg Asn Trp Glu Ile Thr Phe Leu
 980 985 990
 Leu Gln Gln Tyr Pro Leu Gln Met Ser Val Ser Pro Arg Cys Pro Gln
 995 1000 1005
 Pro Xaa Glu Leu Gln Trp Pro Trp Thr Ala Tyr Arg Phe Ser Val Ile
 1010 1015 1020
 Xaa Val Ser Pro Lys Leu Leu Gly Arg His Leu Leu Ala Val Thr Val
 1025 1030 1035 1040
 Leu Thr Val Arg Val Lys Leu Leu Ser Phe Pro Ser Ala Leu Thr Asp
 1045 1050 1055
 Thr His Leu Val Val Ala Cys Asn Leu Ile Cys Val Ile Asp Leu Arg
 1060 1065 1070
 Gln Met Thr Val Ile Pro Xaa Thr Thr Leu Leu Val Met Lys Pro Gln
 1075 1080 1085
 Cys Pro Leu Leu Phe Ser Asn Arg Ser Cys Gly Val Gln Thr Asn Cys
 1090 1095 1100
 Leu Arg Gln Phe Gln Leu Ala Leu Thr Pro Pro Asn Cys Gln Pro Pro
 1105 1110 1115 1120
 Pro Arg Ser Lys Arg Xaa Trp Xaa Glu Ser Ala Ser Ser Gly Gln Glu
 1125 1130 1135
 Leu Val Arg Leu Pro Cys Leu Pro Leu Arg Asp Pro Ser Gln Glu Cys
 1140 1145 1150
 His Val Leu Lys Ala Cys Asn Glu Val Thr Arg Xaa Lys Val Leu Gln
 1155 1160 1165
 Xaa Ser Leu Leu His His Leu Phe Xaa Ser Trp Pro Cys Arg Cys Pro

239

1170	1175	1180
Cys Trp Glu Gln Val Ser Val Thr Leu Ser Leu Gln Leu Asp Val Gln 1185	1190	1195 1200
Xaa Pro Lys Gln Xaa Glu Xaa Xaa Xaa Ile Tyr Pro Val Thr Leu Pro 1205	1210	1215
Lys Arg Arg Ser Leu Asn Gly Gln Thr Lys Val Gly Gln Arg Leu Gln 1220	1225	1230
Pro Leu Pro Ala Thr Leu Leu Ala Pro Arg Thr Leu Arg Tyr Gly Ala 1235	1240	1245
Arg Ile Pro Leu Asn Gln Pro Pro Pro Asn Gly Leu Gln Lys Arg Ser 1250	1255	1260
Trp Glu Arg Val Ser Phe Arg Ala Ala Xaa Ala Thr Leu Gly Pro Thr 1265	1270	1275 1280
Xaa Leu Ala Ser Lys Leu Leu Leu Lys Phe Cys Leu Gln Leu Gly Pro 1285	1290	1295
Ser Leu Val Val Ser Ser Asn Lys Asp His Trp Cys Met Xaa Leu Ser 1300	1305	1310
Arg Gly Met Arg Ser Leu Glu Asn Lys Lys Ser Leu Leu Ile Asp Asn 1315	1320	1325
Leu Cys Ser Pro His His Thr Thr Ser Lys Xaa Asp Trp Leu Arg Lys 1330	1335	1340
Lys Leu Gln Lys Leu Ser Val Ser Cys Gly Thr Met Met Lys Xaa Gln 1345	1350	1355 1360
Leu Thr Arg Pro Leu Ser Leu Leu Ser Pro Thr Ser Leu Ala Phe Gly 1365	1370	1375
Ala Leu Met Phe Trp Thr Cys Arg Ser Val Ser Arg Gln Val Arg Tyr 1380	1385	1390
Arg Val Ile Ile Gly Lys Leu Xaa Xaa Phe Gln Arg Arg Arg Ser Ser 1395	1400	1405
Xaa Arg Pro Pro Arg Asn Gln Gln Arg Asn Pro Gln Gly Leu 1410	1415	1420

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

240

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Ser Ser His Arg Leu His Thr Pro Asn Asn Arg Xaa Arg Gly Xaa
 1 5 10 15
 Xaa Pro Gly His Leu Ser Thr Thr Met Trp Ser Trp Val Pro Tyr Ser
 20 25 30
 Val Leu Leu Arg Gly Asp Gln Gly Val Ser Gly Asn Thr Thr Gly Val
 35 40 45
 Ile Gly Xaa Gly Gln Gln Ile Arg Xaa Pro Leu Leu Val Cys Val Arg
 50 55 60
 Gly Pro Ser His Gly Cys Cys Gln Gly Phe Phe Arg Cys Pro Asp Ser
 65 70 75 80
 Val Leu Leu Arg Ala Cys Tyr Trp Asp Val His Arg Cys Xaa Lys Phe
 85 90 95
 Trp Arg Phe Ser Arg Pro Asp Xaa Gly Xaa Ala Val Gly Val Cys Trp
 100 105 110
 Ile Pro Ser Pro Val His Ser Thr Cys His Ser Xaa Tyr Lys Thr Tyr
 115 120 125
 Cys Ala Xaa Arg Val Phe Ser Ala Asn Phe Asn Cys Pro His Trp Gln
 130 135 140
 Arg Gln Val Asn Gln Ile Thr Thr Phe Leu His Ala Gly Glu Xaa Xaa
 145 150 155 160
 Gly Leu Gly Pro Lys Ser Gln Cys Gly Tyr Asn Ser Ile Asn Ala Lys
 165 170 175
 Val His Ala Arg Asp Val Arg Arg Glu Ser Lys Leu Leu Phe Xaa Trp
 180 185 190
 Gln Met Tyr Gln His Arg Gly Phe Thr Tyr Val Gln His Ile Trp His
 195 200 205
 Val Pro Asp Arg Thr Met Phe Pro Glu Leu Xaa Cys Asn His Leu Xaa
 210 215 220
 Arg Met Pro Cys Tyr Arg Ser Asn His Arg Val Gly His Trp Lys Gly
 225 230 235 240
 Pro Asn Arg Ser Ser Ile Gln Lys Cys Xaa Ala Ser Gly Ser Cys His
 245 250 255
 Gly Tyr Pro Pro Trp Ser Asn Pro Tyr Thr Thr Cys Gln His Asn Xaa
 260 265 270
 Asp Ser Ile Asn Xaa Xaa Arg His Tyr Pro Leu Ser Trp Lys Lys Asp

241

275					280					285				
Xaa Gly Gly Lys Ser Glu	Glu Arg Glu Thr Pro Tyr	Leu Xaa Gly Tyr	290	295	300									
Gln Lys Thr Leu Xaa Xaa Ala Cys Xaa Arg Val Ser Ser Lys Gly Asn			305	310	315							320		
Asn Ser Cys Leu Leu Leu Xaa Gly Met Xaa His Leu Lys Asn Ala Xaa			325		330							335		
Gly Arg Leu Cys Ser Ser Cys His Xaa Cys Leu Val Tyr Arg Val His			340		345							350		
Trp Xaa Leu Xaa Phe Arg Val Xaa Leu Gln Pro His Gly Arg Arg His			355		360							365		
Met Pro Cys Xaa Pro Xaa Pro Tyr Phe His His Gly Cys Ser Cys Val			370		375							380		
Arg Gly Phe Ser Asn Ser Xaa Arg Pro Ala Xaa Gly Pro His Arg Pro			385		390							400		
Trp Glu Ser Trp His Ile Leu Leu Cys Arg Arg Glu Leu Tyr Pro Phe			405		410							415		
Gly Tyr Gly Ser Xaa Met Gln His Cys Xaa Ser Leu Arg Arg Ser Gln			420		425							430		
Gly Met Val Trp Phe Val Ile Asn Arg Ser Ser Asn Tyr Ser Gly His			435		440							445		
Leu Ser His Pro Thr Trp Val Thr Cys Asp Arg Ser Lys Phe Gly Arg			450		455							460		
Val Gly Xaa Ser Leu Phe Tyr Gly Gln Pro Arg Thr Phe Ile Cys Gln			465		470							480		
Tyr Cys Lys Lys Asn Cys Xaa Gln Leu Cys Phe Val Asp Cys Ser Pro			485		490							495		
Thr Thr Thr Val Ser Ser Val Trp Leu Cys Cys Ser Gln Xaa Arg Thr			500		505							510		
Thr Val Ala Gly Ser Pro Ala Trp Glu Lys Thr Leu Trp Gly Ser Val			515		520							525		
Ala Leu Gly Arg Leu Xaa Arg Leu Ser Trp Pro Arg Ala Gln Arg Gly			530		535							540		
Asp Gln Ile Pro Asn Val Leu His Xaa Ser Gln Tyr Phe Trp Asp Ser			545		550							560		
Arg Thr Arg Cys Trp Arg Trp Ser Gly Tyr Gly Leu Ser Ser His Xaa			565		570							575		
His Phe Trp Arg His Leu Cys Ala Ala Leu Leu Val Tyr Tyr Ile Ser														

580

585

590

Pro Tyr Arg Cys Tyr Cys Arg Pro Ser Gly Xaa Arg Arg Gly Asn Arg
595 600 605

Gly Gly Val Cys Ile Ile His Ser Leu Gly Gly His Gly Cys Cys Asn
610 615 620

Xaa Gln Ala Glu Glu Tyr Asn His His Asn Xaa Ser Phe His Ile Gly
625 630 635 640

Asn Arg Pro Xaa Lys Thr Xaa His Leu Ser Trp Ala Ser Cys Ser Tyr
645 650 655

Asn Pro Cys Tyr His Arg Val Leu Leu Trp Leu Ser His Phe Thr Xaa
660 665 670

Gln Ser Leu Cys Ile Met Arg Val Cys Phe His Cys Gly Tyr Tyr Tyr
675 680 685

Pro Thr Thr Ser Gln Asp Gln Asn Val Pro Val Ile Ile Trp Arg Arg
690 695 700

Asn Cys Val Gln Ala Tyr Arg Arg Xaa Arg Arg Thr Gly Val His Asp
705 710 715 720

Gly Arg Gly Cys Gly Asn Ser Ser Trp Tyr Met Asp Ile Gly Gly Phe
725 730 735

Cys Leu Xaa His Ala Arg Arg Leu Cys Trp Arg Leu Ile His Cys Leu
740 745 750

Leu Asp Ile Xaa Met Leu Asp Gly Xaa Val Ala His Tyr Gly Ser Ala
755 760 765

Cys Trp Phe Ser Leu Leu Arg Val Gln Ser Gly Arg Arg Ser Cys Gly
770 775 780

Arg Leu Val Ser Leu Cys Asn Val Cys Phe Asp Asn Ser Arg Ala Arg
785 790 795 800

Ser Leu Ala Gln Gln Thr Ser Tyr Tyr Ala Cys Xaa Glu Gln His Cys
805 810 815

Met Xaa Xaa Val Leu Tyr Cys His Ser Xaa His Pro Gln Glu Asp Thr
820 825 830

Gly His Ser Gly Gly Ile Tyr Pro Leu Glu Xaa His Ile Ser Leu His
835 840 845

Pro Leu Ala Xaa His Pro Asp Gly Gly Xaa Leu Arg Pro His Cys Leu
850 855 860

Gly Ser Xaa Asp Leu Ala Val Cys Val Gln Phe Leu Cys Asp Leu Leu
865 870 875 880

Xaa Cys Pro Xaa Ser Trp Ser Ser Glu His Gly Xaa His Ser Trp Leu

243

885										890										895													
Ser	Phe	Leu	Gln	Leu	Pro	Glu	Gly	Val	Gln	Gly	Pro	Leu	Asp	Trp	Ile																		
			900					905					910																				
Arg	Tyr	Ala	Pro	Ser	Thr	Leu	Ser	Met	Arg	Cys	Xaa	Thr	His	Leu	Phe																		
		915						920				925																					
Cys	Xaa	Glu	Trp	Phe	Cys	Lys	Thr	Leu	Gln	Arg	Thr	Gln	Asn	Leu	Phe																		
		930				935						940																					
Lys	Leu	Leu	Glu	Arg	Gly	Cys	Ser	Ser	Gln	Arg	Xaa	Ala	Val	Trp	Val																		
		945				950				955				960																			
Gly	Xaa	Thr	Gly	Pro	Asn	Xaa	Leu	Asp	Xaa	Ser	Cys	Arg	Gln	Leu	Trp																		
				965				970					975																				
Arg	Xaa	Gly	Leu	Leu	Xaa	Ile	Xaa	Glu	Ile	Gly	Arg	Ser	His	Phe	Cys																		
			980					985					990																				
Tyr	Ser	Ser	Ile	Leu	Ser	Lys	Cys	Leu	Phe	His	Pro	Gly	Ala	Pro	Asn																		
		995					1000					1005																					
Leu	Glu	Ser	Cys	Ser	Gly	Arg	Gly	Pro	Arg	Thr	Gly	Ser	Xaa	Leu	Ser																		
		1010				1015					1020																						
Arg	Xaa	Ala	Gln	Asn	Ser	Leu	Asp	Asp	Ile	Cys	Leu	Leu	Leu	Arg	Ser																		
		1025			1030					1035				1040																			
Xaa	Arg	Xaa	Gly	Xaa	Asn	Cys	Xaa	Ala	Ser	Leu	Pro	Arg	Xaa	Arg	Thr																		
			1045					1050					1055																				
His	Thr	Trp	Trp	Ser	His	Ala	Thr	Xaa	Phe	Ala	Xaa	Ser	Thr	Xaa	Gly																		
			1060					1065					1070																				
Lys	Xaa	Leu	Xaa	Phe	His	Lys	Gln	His	Ser	Xaa	Xaa	Xaa	Ser	Arg	Ser																		
		1075					1080					1085																					
Val	Arg	Ser	Cys	Phe	Gln	Thr	Gly	Val	Ala	Ala	Tyr	Lys	Pro	Ile	Ala																		
		1090				1095						1100																					
Xaa	Gly	Asn	Phe	Ser	Trp	Arg	Xaa	His	His	Gln	Thr	Ala	Ser	Pro	Leu																		
		1105				1110				1115			1120																				
Pro	Asp	Arg	Arg	Gly	Ser	Gly	Lys	Lys	Ala	Pro	Val	Pro	Gly	Lys	Asn																		
				1125				1130					1135																				
Trp	Phe	Ala	Tyr	Leu	Ala	Ser	Pro	Ser	Glu	Ile	Arg	Pro	Arg	Ser	Val																		
			1140					1145					1150																				
Met	Ser	Xaa	Lys	Pro	Ala	Thr	Lys	Xaa	Pro	Val	Arg	Arg	Ser	Phe	Xaa																		
		1155					1160					1165																					
Pro	Pro	Phe	Phe	Thr	Thr	Cys	Ser	Xaa	Val	Gly	His	Ala	Asp	Ala	Pro																		
		1170				1175					1180																						
Val	Gly	Ser	Arg	Xaa	Val	Xaa	Pro	Phe	His	Cys	Asn	Trp	Met	Cys	Asn																		

244

1185	1190	1195	1200
Asp Arg Asn Xaa Xaa Xaa Pro Xaa Xaa Phe Thr Gln Leu Pro Ser Gln	1205	1210	1215
Lys Gly Gly Leu Xaa Met Val Arg Arg Lys Leu Val Asn Asp Tyr Asn	1220	1225	1230
Arg Phe Gln Leu Arg Tyr Trp Pro Pro Val Pro Xaa Asp Thr Gly Gln	1235	1240	1245
Gly Phe His Ser Ile Ser His Arg Gln Thr Ala Tyr Lys Lys Glu Val	1250	1255	1260
Gly Lys Glu Xaa Val Phe Val Gln His Glu Leu His Leu Asp Arg Arg	1265	1270	1275
Asp Xaa Leu Gln Asn Cys Phe Xaa Ser Ser Val Cys Asn Ser Gly His	1285	1290	1295
His Xaa Trp Phe Pro Gln Thr Lys Ile Ile Gly Val Cys Asp Xaa Ala	1300	1305	1310
Ala Gly Cys Gly Ala Xaa Lys Thr Lys Ser His Tyr Xaa Xaa Thr Thr	1315	1320	1325
Ser Val Pro Pro Ile Ile Pro Gln Ala Ser Glu Ile Gly Xaa Gly Lys	1330	1335	1340
Ser Phe Lys Ser Cys Arg Cys His Val Gly Leu Xaa Xaa Ser Ser Ser	1345	1350	1355
Ser His Ala Leu Xaa Val Cys Xaa Val Pro His His Trp Pro Ser Gly	1365	1370	1375
His Xaa Cys Ser Gly Leu Ala Glu Val Cys Arg Gly Arg Xaa Asp Thr	1380	1385	1390
Glu Ser Leu Ser Ala Asn Cys Asp Ser Ser Lys Gly Gly Gly Leu Arg	1395	1400	1405
Glu Asp Pro Pro Glu Thr Asn Lys Glu Thr Pro Lys Ala Tyr	1410	1415	1420

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Ala His Pro Thr Gly Ser Ile His Pro Ile Thr Val Asp Ala Ala Asn
 1 5 10 15
 Asp Gln Asp Ile Tyr Gln Pro Pro Cys Gly Ala Gly Ser Leu Thr Arg
 20 25 30
 Cys Ser Cys Gly Glu Thr Lys Gly Tyr Leu Val Thr Arg Leu Gly Ser
 35 40 45
 Leu Val Glu Val Asn Lys Ser Asp Asp Pro Tyr Trp Cys Val Cys Gly
 50 55 60
 Ala Leu Pro Met Ala Val Ala Lys Gly Ser Ser Gly Ala Pro Ile Leu
 65 70 75 80
 Cys Ser Ser Gly His Val Ile Gly Met Phe Thr Ala Ala Arg Asn Ser
 85 90 95
 Gly Gly Ser Val Gly Gln Ile Arg Val Arg Pro Leu Val Cys Ala Gly
 100 105 110
 Tyr His Pro Gln Tyr Thr Ala His Ala Thr Leu Asp Thr Lys Pro Thr
 115 120 125
 Val Pro Asn Glu Tyr Ser Val Gln Ile Leu Ile Ala Pro Thr Gly Ser
 130 135 140
 Gly Lys Ser Thr Lys Leu Pro Leu Ser Tyr Met Gln Xaa Lys Xaa Glu
 145 150 155 160
 Val Leu Val Leu Asn Pro Ser Val Ala Thr Thr Ala Ser Met Pro Lys
 165 170 175
 Tyr Met His Ala Thr Tyr Gly Val Asn Pro Asn Cys Tyr Phe Asn Gly
 180 185 190
 Lys Cys Thr Asn Thr Gly Ala Ser Leu Thr Tyr Ser Thr Tyr Gly Met
 195 200 205
 Tyr Leu Thr Gly Arg Cys Ser Arg Asn Tyr Asp Val Ile Ile Cys Asp
 210 215 220
 Glu Cys His Ala Thr Asp Arg Thr Thr Val Leu Gly Ile Gly Lys Val
 225 230 235 240
 Leu Thr Glu Ala Pro Ser Lys Asn Val Arg Leu Val Val Leu Ala Thr
 245 250 255
 Ala Thr Pro Pro Gly Val Ile Pro Thr Pro His Ala Asn Ile Thr Glu
 260 265 270
 Ile Gln Leu Thr Asp Glu Gly Thr Ile Pro Phe His Gly Lys Lys Ile
 275 280 285

246

Lys Glu Glu Asn Leu Lys Lys Gly Arg His Leu Ile Phe Glu Ala Thr
 290 295 300
 Lys Lys His Cys Asp Glu Leu Ala Asn Glu Leu Ala Arg Lys Gly Ile
 305 310 315 320
 Thr Ala Val Ser Tyr Tyr Arg Gly Cys Asp Ile Ser Lys Met Pro Glu
 325 330 335
 Gly Asp Cys Val Val Val Ala Thr Asp Ala Leu Cys Thr Gly Tyr Thr
 340 345 350
 Gly Asp Phe Asp Ser Val Tyr Asp Cys Ser Leu Met Val Glu Gly Thr
 355 360 365
 Cys His Val Asp Leu Asp Pro Thr Phe Thr Met Gly Val Arg Val Cys
 370 375 380
 Gly Val Ser Ala Ile Val Lys Gly Gln Arg Arg Gly Arg Thr Gly Arg
 385 390 395 400
 Gly Arg Ala Gly Ile Tyr Tyr Tyr Val Asp Gly Ser Cys Thr Pro Ser
 405 410 415
 Gly Met Val Pro Glu Cys Asn Ile Val Glu Ala Phe Asp Ala Ala Lys
 420 425 430
 Ala Trp Tyr Gly Leu Ser Ser Thr Glu Ala Gln Thr Ile Leu Asp Thr
 435 440 445
 Tyr Arg Thr Gln Pro Gly Leu Pro Ala Ile Gly Ala Asn Leu Asp Glu
 450 455 460
 Trp Ala Asp Leu Phe Ser Met Val Asn Pro Glu Pro Ser Phe Val Asn
 465 470 475 480
 Thr Ala Lys Arg Thr Ala Asp Asn Tyr Val Leu Leu Thr Ala Ala Gln
 485 490 495
 Leu Gln Leu Cys His Gln Tyr Gly Tyr Ala Ala Pro Asn Asp Ala Pro
 500 505 510
 Arg Trp Gln Gly Ala Arg Leu Gly Lys Lys Pro Cys Gly Val Leu Trp
 515 520 525
 Arg Leu Asp Gly Cys Asp Ala Cys Pro Gly Pro Glu Pro Ser Glu Val
 530 535 540
 Thr Arg Tyr Gln Met Cys Phe Thr Glu Val Asn Thr Ser Gly Thr Ala
 545 550 555 560
 Ala Leu Ala Val Gly Val Gly Val Ala Met Ala Tyr Leu Ala Ile Asp
 565 570 575
 Thr Phe Gly Ala Thr Cys Val Arg Arg Cys Trp Ser Ile Thr Ser Val
 580 585 590

247

Pro Thr Gly Ala Thr Val Ala Pro Val Val Asp Glu Glu Glu Ile Val
 595 600 605
 Glu Glu Cys Ala Ser Phe Ile Pro Leu Glu Ala Met Val Ala Ala Ile
 610 615 620
 Asp Lys Leu Lys Ser Thr Ile Thr Thr Thr Ser Pro Phe Thr Leu Glu
 625 630 635 640
 Thr Ala Leu Glu Lys Leu Asn Thr Phe Leu Gly Pro His Ala Ala Thr
 645 650 655
 Ile Leu Ala Ile Ile Glu Tyr Cys Cys Gly Leu Val Thr Leu Pro Asp
 660 665 670
 Asn Pro Phe Ala Ser Cys Val Phe Ala Phe Ile Ala Gly Ile Thr Thr
 675 680 685
 Pro Leu Pro His Lys Ile Lys Met Phe Leu Ser Leu Phe Gly Gly Ala
 690 695 700
 Ile Ala Ser Lys Leu Thr Asp Ala Arg Xaa Ala Leu Ala Phe Met Met
 705 710 715 720
 Ala Gly Ala Xaa Gly Thr Ala Leu Gly Thr Trp Thr Ser Val Gly Phe
 725 730 735
 Val Phe Asp Met Leu Gly Gly Tyr Ala Gly Ala Ser Ser Thr Ala Cys
 740 745 750
 Leu Thr Phe Lys Cys Leu Met Gly Glu Trp Xaa Thr Met Asp Gln Leu
 755 760 765
 Ala Gly Leu Val Tyr Ser Ala Phe Asn Pro Ala Ala Gly Val Val Gly
 770 775 780
 Val Leu Ser Ala Cys Ala Met Phe Ala Leu Thr Thr Ala Gly Pro Asp
 785 790 795 800
 His Trp Pro Asn Arg Leu Leu Thr Met Leu Ala Arg Ser Asn Thr Val
 805 810 815
 Cys Xaa Glu Tyr Phe Ile Ala Thr Arg Asp Ile Arg Arg Lys Ile Leu
 820 825 830
 Gly Ile Leu Glu Ala Ser Thr Pro Trp Ser Xaa Ile Ser Ala Cys Ile
 835 840 845
 Arg Trp Leu His Thr Pro Thr Glu Asp Asp Cys Gly Leu Ile Ala Trp
 850 855 860
 Gly Leu Xaa Ile Trp Gln Tyr Val Cys Asn Phe Phe Val Ile Cys Phe
 865 870 875 880
 Asn Val Leu Lys Ala Gly Val Gln Ser Met Val Asn Ile Pro Gly Cys
 885 890 895

248

Pro Phe Tyr Ser Cys Gln Lys Gly Tyr Lys Gly Pro Trp Ile Gly Ser
 900 905 910

Gly Met Leu Gln Ala Arg Cys Pro Cys Gly Ala Glu Leu Ile Phe Ser
 915 920 925

Val Glu Asn Gly Phe Ala Lys Leu Tyr Lys Gly Pro Arg Thr Cys Ser
 930 935 940

Asn Tyr Trp Arg Gly Ala Val Pro Val Asn Ala Arg Leu Cys Gly Ser
 945 950 955 960

Ala Arg Pro Asp Pro Thr Asp Trp Thr Ser Leu Val Val Asn Tyr Gly
 965 970 975

Val Arg Asp Tyr Cys Lys Tyr Glu Lys Leu Gly Asp His Ile Phe Val
 980 985 990

Thr Ala Val Ser Ser Pro Asn Val Cys Phe Thr Gln Val Pro Pro Thr
 995 1000 1005

Leu Arg Ala Ala Val Ala Val Asp Arg Val Gln Val Gln Xaa Tyr Leu
 1010 1015 1020

Gly Glu Pro Lys Thr Pro Trp Thr Thr Ser Ala Cys Cys Tyr Gly Pro
 1025 1030 1035 1040

Asp Gly Lys Gly Lys Thr Val Lys Leu Pro Phe Arg Val Asp Gly His
 1045 1050 1055

Thr Pro Gly Gly Arg Met Gln Leu Asn Leu Arg Asp Arg Leu Glu Ala
 1060 1065 1070

Asn Asp Cys Asn Ser Ile Asn Asn Thr Pro Ser Asp Glu Ala Ala Val
 1075 1080 1085

Ser Ala Leu Val Phe Lys Gln Glu Leu Arg Arg Thr Asn Gln Leu Leu
 1090 1095 1100

Glu Ala Ile Ser Ala Gly Val Asp Thr Thr Lys Leu Pro Ala Pro Ser
 1105 1110 1115 1120

Gln Ile Glu Glu Val Val Val Arg Lys Arg Gln Phe Arg Ala Arg Thr
 1125 1130 1135

Gly Ser Leu Thr Leu Pro Pro Pro Pro Arg Ser Val Pro Gly Val Ser
 1140 1145 1150

Cys Pro Glu Ser Leu Gln Arg Ser Asp Pro Leu Glu Gly Pro Ser Xaa
 1155 1160 1165

Leu Pro Ser Ser Pro Pro Val Leu Gln Leu Ala Met Pro Met Pro Leu
 1170 1175 1180

Leu Gly Ala Gly Glu Cys Asn Pro Phe Thr Ala Ile Gly Cys Ala Met
 1185 1190 1195 1200

249

Thr Glu Thr Xaa Gly Xaa Pro Xaa Xaa Leu Pro Ser Tyr Pro Pro Lys
 1205 1210 1215
 Lys Glu Val Ser Glu Trp Ser Asp Glu Ser Trp Ser Thr Thr Thr Thr
 1220 1225 1230
 Ala Ser Ser Tyr Val Thr Gly Pro Pro Tyr Pro Lys Ile Arg Gly Lys
 1235 1240 1245
 Asp Ser Thr Gln Ser Ala Thr Ala Lys Arg Pro Thr Lys Lys Lys Leu
 1250 1255 1260
 Gly Lys Ser Glu Phe Ser Cys Ser Met Ser Tyr Thr Trp Thr Asp Val
 1265 1270 1275 1280
 Ile Ser Phe Lys Thr Ala Ser Lys Val Leu Ser Ala Thr Arg Ala Ile
 1285 1290 1295
 Thr Ser Gly Phe Leu Lys Gln Arg Ser Leu Val Tyr Val Thr Glu Pro
 1300 1305 1310
 Arg Asp Ala Glu Leu Arg Lys Gln Lys Val Thr Ile Asn Arg Gln Pro
 1315 1320 1325
 Leu Phe Pro Pro Ser Tyr His Lys Gln Val Arg Leu Ala Lys Glu Lys
 1330 1335 1340
 Ala Ser Lys Val Val Gly Val Met Trp Asp Tyr Asp Glu Val Ala Ala
 1345 1350 1355 1360
 His Thr Pro Ser Lys Ser Ala Lys Ser His Ile Thr Gly Leu Arg Gly
 1365 1370 1375
 Thr Asp Val Leu Asp Leu Gln Lys Cys Val Glu Ala Gly Glu Ile Pro
 1380 1385 1390
 Ser His Tyr Arg Gln Thr Val Ile Val Pro Lys Glu Glu Val Phe Val
 1395 1400 1405
 Lys Thr Pro Gln Lys Pro Thr Lys Lys Pro Pro Arg Leu Ile
 1410 1415 1420

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

250

Asp Lys Pro Trp Gly Phe Leu Cys Trp Phe Leu Gly Gly Leu His Glu
 1 5 10 15
 Asp Leu Leu Leu Trp Asn Tyr His Ser Leu Pro Ile Met Thr Arg Tyr
 20 25 30
 Leu Thr Cys Leu Asp Thr Leu Leu Gln Val Gln Asn Ile Ser Ala Pro
 35 40 45
 Lys Ala Ser Asp Val Gly Leu Ser Arg Leu Arg Gly Arg Val Ser Cys
 50 55 60
 Tyr Phe Ile Ile Val Pro His Asp Thr Asp Asn Phe Xaa Ser Phe Phe
 65 70 75 80
 Leu Ser Gln Ser His Leu Leu Val Val Xaa Trp Gly Glu Gln Arg Leu
 85 90 95
 Ser Ile Asn Ser Asp Phe Leu Phe Ser Lys Leu Arg Ile Pro Arg Leu
 100 105 110
 Ser His Ile His Gln Xaa Ser Leu Phe Glu Glu Thr Thr Ser Asp Gly
 115 120 125
 Pro Ser Cys Arg Gln Asn Phe Arg Ser Ser Phe Glu Ala Asn His Val
 130 135 140
 Gly Pro Ser Val Ala His Ala Ala Arg Lys Leu Thr Leu Ser Gln Leu
 145 150 155 160
 Leu Phe Cys Arg Pro Phe Gly Gly Gly Xaa Leu Ser Gly Ile Leu Ala
 165 170 175
 Pro Tyr Leu Arg Val Arg Gly Ala Ser Asn Val Ala Gly Ser Gly Cys
 180 185 190
 Ser Arg Xaa Pro Thr Phe Val Xaa Pro Phe Arg Asp Leu Leu Phe Gly
 195 200 205
 Arg Val Thr Gly Xaa Ile Xaa Xaa Xaa Ser Xaa Cys Phe Gly His Cys
 210 215 220
 Thr Ser Asn Cys Ser Glu Arg Val Thr Leu Thr Cys Ser Gln Gln Gly
 225 230 235 240
 His Arg His Gly Gln Leu Xaa Asn Arg Trp Xaa Arg Arg Glu Xaa Xaa
 245 250 255
 Arg Thr Phe Xaa Arg Val Thr Ser Leu Gln Ala Phe Arg Thr Xaa His
 260 265 270
 Ser Trp Asp Gly Ser Arg Arg Gly Arg Gln Gly Lys Arg Thr Ser Ser
 275 280 285
 Cys Pro Glu Leu Ala Leu Ser Tyr His Tyr Leu Phe Asp Leu Gly Gly
 290 295 300

251

Gly Trp Gln Phe Gly Gly Val Asn Ala Ser Xaa Asn Cys Leu Lys Gln
 305 310 315 320
 Leu Val Cys Thr Pro Gln Leu Leu Phe Glu Asn Lys Ser Gly His Cys
 325 330 335
 Gly Phe Ile Thr Arg Ser Val Val Tyr Gly Ile Thr Val Ile Cys Leu
 340 345 350
 Lys Ser Ile Thr Gln Ile Lys Leu His Ala Thr Thr Arg Cys Val Ser
 355 360 365
 Val Asn Ala Glu Gly Lys Leu Asn Ser Phe Thr Leu Thr Val Arg Thr
 370 375 380
 Val Thr Ala Ser Arg Cys Arg Pro Arg Ser Phe Gly Leu Thr Xaa Ile
 385 390 395 400
 Thr Leu Asn Leu Tyr Ala Val His Gly His Cys Ser Ser Gln Gly Trp
 405 410 415
 Gly His Leu Gly Glu Thr Asp Ile Trp Arg Gly Tyr Cys Cys Asn Lys
 420 425 430
 Asn Val Ile Ser Gln Phe Leu Ile Phe Thr Val Val Pro Asn Ala Ile
 435 440 445
 Ile Asp Asp Lys Thr Ser Pro Ile Ser Trp Val Arg Ser Ser Arg Pro
 450 455 460
 Thr Gln Pro Ser Val Asp Trp Asn Ser Pro Ser Pro Val Ile Xaa Thr
 465 470 475 480
 Ser Ser Gly Ser Phe Val Lys Phe Cys Lys Thr Ile Leu Asn Arg Lys
 485 490 495
 Asp Glu Phe Ser Thr Ala Trp Thr Ala Cys Leu Glu His Thr Xaa Ser
 500 505 510
 Asn Pro Gly Ala Leu Val Pro Leu Leu Ala Ala Val Glu Arg Thr Thr
 515 520 525
 Arg Asn Val Asn His Ala Leu Asn Ser Ser Phe Lys Asp Ile Lys Ala
 530 535 540
 Asn His Lys Glu Ile Ala His Ile Leu Pro Asn Leu Xaa Thr Pro Ser
 545 550 555 560
 Asn Glu Ala Ala Ile Ile Leu Arg Arg Gly Val Xaa Pro Thr Asp Ala
 565 570 575
 Ser Xaa Tyr Asp Thr Pro Gly Gly Arg Cys Leu Gln Asn Ala Gln Tyr
 580 585 590
 Leu Pro Ala Asp Val Thr Ser Gly Asn Lys Val Leu Xaa Thr Tyr Ser
 595 600 605

252

Val Ala Pro S r Lys His Ser Lys Lys Ser Val Gly Pro Val Ile Trp
 610 615 620

Pro Cys Cys Cys Gln Ser Lys His Cys Thr Ser Xaa Gln Asp Ala His
 625 630 635 640

Asn Ser Cys Gly Arg Ile Glu Arg Gly Val Asp Xaa Thr Ser Lys Leu
 645 650 655

Ile His Ser Xaa Pro Leu Thr His Gln Ala Phe Lys Cys Gln Ala Ser
 660 665 670

Ser Gly Xaa Gly Ala Ser Ile Ala Ala Xaa His Val Lys Asp Lys Thr
 675 680 685

His Arg Cys Pro Cys Thr Lys Ser Cys Ser Xaa Ser Pro Gly His His
 690 695 700

Glu Arg Gln Cys Xaa Ser Ser Val Cys Lys Leu Gly Arg Asn Cys Ala
 705 710 715 720

Ser Lys Xaa Xaa Gln Glu His Phe Asp Leu Val Arg Xaa Trp Gly Ser
 725 730 735

Asn Thr Arg Asn Glu Ser Lys His Ala Xaa Cys Lys Gly Ile Val Arg
 740 745 750

Xaa Ser Asp Xaa Ala Thr Ala Ile Leu Tyr Asp Ser Lys Asp Cys Ser
 755 760 765

Cys Met Arg Pro Lys Lys Gly Val Lys Phe Phe Lys Gly Gly Phe Gln
 770 775 780

Cys Glu Arg Thr Ser Cys Gly Asp Cys Thr Leu Gln Leu Val Asn Cys
 785 790 795 800

Ser Asn His Gly Leu Gln Gly Asn Glu Xaa Cys Thr Leu Leu His Asp
 805 810 815

Phe Leu Phe Val Asn His Trp Gly Asp Ser Ser Thr Gly Arg Asp Xaa
 820 825 830

Cys Asn Arg Pro Ala Thr Pro His Thr Ser Gly Ala Lys Ser Val Asn
 835 840 845

Gly Xaa Ile Ser His Ser His Ser Asn Ala Asn Ser Glu Cys Gly Cys
 850 855 860

Pro Arg Ser Ile Asp Phe Ser Glu Ala His Leu Val Ser Gly His Leu
 865 870 875 880

Ala Gly Leu Trp Ala Arg Thr Gly Val Thr Ala Val Gln Ala Pro Gln
 885 890 895

Asn Pro Thr Arg Phe Phe Pro Lys Pro Gly Ser Leu Pro Pro Trp Cys
 900 905 910

253

Val Ile Gly Ser Ser Ile Ala Ile Leu Met Thr Gln Leu Xaa Leu Gly
 915 920 925

Cys Ser Gln Gln Asn Ile Ile Val Ser Ser Ser Phe Cys Ser Ile Asp
 930 935 940

Lys Xaa Arg Phe Gly Val Asp His Arg Lys Glu Ile Ser Pro Leu Val
 945 950 955 960

Gln Ile Cys Ser Tyr Arg Arg Xaa Pro Arg Leu Gly Ala Ile Gly Val
 965 970 975

Gln Asn Ser Leu Ser Phe Cys Xaa Xaa Gln Thr Ile Pro Cys Leu Gly
 980 985 990

Cys Val Glu Gly Phe Asn Asn Val Ala Phe Arg Asn His Thr Arg Arg
 995 1000 1005

Gly Thr Thr Pro Val Tyr Ile Val Val Tyr Ala Ser Ser Pro Thr Ala
 1010 1015 1020

Cys Ala Ala Pro Thr Leu Ala Phe Asn Tyr Cys Xaa Asn Pro Ala His
 1025 1030 1035 1040

Thr Asn Thr His Gly Glu Ser Arg Val Lys Val Asn Met Ala Cys Ala
 1045 1050 1055

Phe Tyr His Glu Ala Ala Val Ile His Gly Ile Lys Val Thr Ser Val
 1060 1065 1070

Pro Cys Thr Gln Gly Ile Ser Gly Asn Tyr Tyr Thr Val Ala Leu Arg
 1075 1080 1085

His Phe Xaa Asp Val Thr Ser Pro Ile Val Arg Asp Ser Cys Tyr Ser
 1090 1095 1100

Leu Ser Ser Xaa Leu Val Ser Lys Leu Ile Thr Val Phe Phe Gly Ser
 1105 1110 1115 1120

Leu Lys Asp Lys Val Ser Pro Phe Leu Gln Ile Phe Leu Leu Asn Leu
 1125 1130 1135

Phe Ser Met Lys Gly Asp Ser Ala Phe Ile Xaa Xaa Leu Asn Leu Ser
 1140 1145 1150

Tyr Val Gly Met Trp Cys Arg Asp Tyr Ser Arg Gly Gly Ser Arg Gly
 1155 1160 1165

Lys Asn His Xaa Pro Asn Ile Phe Gly Trp Ser Phe Gly Xaa Asp Leu
 1170 1175 1180

Ser Asn Ala Gln His Gly Gly Ser Ile Gly Ser Met Ala Phe Val Thr
 1185 1190 1195 1200

Asn Asp Tyr Ile Ile Val Pro Gly Thr Ser Ser Gly Gln Val His Ala
 1205 1210 1215

254

Ile Cys Ala Val Arg Lys Xaa Ser Pro Cys Val Gly Thr Phe Ala Ile
 1220 1225 1230
 Lys Ile Ala Ile Trp Ile His Ala Val Arg Arg Val His Val Leu Trp
 1235 1240 1245
 His Xaa Cys Cys Cys Ser His Thr Gly Ile Xaa Asp Gln Asp Leu Xaa
 1250 1255 1260
 Leu Xaa Leu His Val Arg Lys Trp Xaa Phe Gly Xaa Leu Ala Ala Ala
 1265 1270 1275 1280
 Ser Gly Gly Asn Xaa Asn Leu His Xaa Ile Leu Val Arg His Ser Arg
 1285 1290 1295
 Phe Cys Ile Lys Ser Gly Met Cys Cys Val Leu Gly Met Val Ser Ser
 1300 1305 1310
 Thr His Gln Arg Pro Asn Pro Asn Leu Ala Asp Xaa Thr Ala Arg Ile
 1315 1320 1325
 Ser Ser Ser Gly Glu His Pro Asn Asn Met Pro Gly Gly Ala Gln Asn
 1330 1335 1340
 Arg Gly Thr Xaa Arg Thr Leu Gly Asn Ser His Gly Lys Gly Pro Ala
 1345 1350 1355 1360
 His Thr Pro Ile Arg Val Ile Gly Phe Val Asp Leu Asn Gln Xaa Pro
 1365 1370 1375
 Gln Ser Cys Tyr Gln Ile Pro Leu Gly Leu Pro Ala Arg Ala Pro Ser
 1380 1385 1390
 Lys Gly Pro Ser Ser Thr Trp Trp Leu Ile Asp Val Leu Val Ile Ser
 1395 1400 1405
 Arg Val Asn Gly Tyr Trp Val Tyr Gly Ala Cys Gly Met Ser
 1410 1415 1420

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ile Ser L u Gly Gly Phe Phe Val Gly Phe Trp Gly Val Phe Thr Lys
 1 5 10 15

255

Thr Ser Ser Phe Gly Thr Ile Thr Val Cys Arg Xaa Xaa Leu Gly Ile
 20 25 30
 Ser Pro Ala Ser Thr His Phe Cys Lys Ser Arg Thr Ser Val Pro Arg
 35 40 45
 Arg Pro Val Met Trp Asp Leu Ala Asp Leu Glu Gly Val Xaa Ala Ala
 50 55 60
 Thr Ser Ser Xaa Ser His Met Thr Pro Thr Thr Phe Glu Ala Phe Ser
 65 70 75 80
 Leu Ala Asn Leu Thr Cys Leu Trp Tyr Asp Gly Gly Asn Arg Gly Cys
 85 90 95
 Leu Leu Ile Val Thr Phe Cys Phe Leu Ser Ser Ala Ser Arg Gly Ser
 100 105 110
 Val Thr Tyr Thr Asn Asp Leu Cys Leu Arg Lys Pro Leu Val Met Ala
 115 120 125
 Arg Val Ala Asp Arg Thr Leu Glu Ala Val Leu Lys Leu Ile Thr Ser
 130 135 140
 Val Gln Val Xaa Leu Met Leu His Glu Asn Ser Leu Phe Pro Asn Phe
 145 150 155 160
 Phe Phe Val Gly Arg Leu Ala Val Ala Asp Xaa Val Glu Ser Leu Pro
 165 170 175
 Arg Ile Leu Gly Tyr Gly Gly Pro Val Thr Xaa Leu Glu Ala Val Val
 180 185 190
 Val Val Asp Gln Leu Ser Ser Asp His Ser Glu Thr Ser Phe Leu Gly
 195 200 205
 Gly Xaa Leu Gly Lys Xaa Xaa Gly Xaa Pro Xaa Val Ser Val Ile Ala
 210 215 220
 His Pro Ile Ala Val Lys Gly Leu His Ser Pro Ala Pro Asn Arg Gly
 225 230 235 240
 Ile Gly Met Ala Asn Cys Arg Thr Gly Gly Glu Glu Gly Arg Xaa Glu
 245 250 255
 Gly Pro Ser Asn Gly Ser Leu Arg Cys Arg Leu Ser Gly His Asp Thr
 260 265 270
 Pro Gly Thr Asp Leu Gly Gly Gly Gly Lys Val Ser Glu Pro Val Leu
 275 280 285
 Ala Arg Asn Trp Arg Phe Leu Thr Thr Thr Ser Ser Ile Trp Glu Gly
 290 295 300
 Ala Gly Ser Leu Val Val Ser Thr Pro Ala Glu Ile Ala Ser Ser Asn
 305 310 315 320

256

Trp Phe Val Arg Arg Asn Ser Cys Leu Lys Thr Arg Ala Asp Thr Ala
 325 330 335
 Ala Ser Ser Leu Gly Val Leu Phe Met Glu Leu Gln Ser Phe Ala Ser
 340 345 350
 Ser Arg Ser Arg Lys Leu Ser Cys Met Arg Pro Pro Gly Val Cys Pro
 355 360 365
 Ser Thr Arg Lys Gly Ser Leu Thr Val Leu Pro Leu Pro Ser Gly Pro
 370 375 380
 Xaa Gln Gln Ala Asp Val Val Gln Gly Val Leu Gly Ser Pro Arg Xaa
 385 390 395 400
 Xaa Xaa Thr Cys Thr Arg Ser Thr Ala Thr Ala Ala Leu Lys Val Gly
 405 410 415
 Gly Thr Trp Val Lys Gln Thr Phe Gly Glu Asp Thr Ala Val Thr Lys
 420 425 430
 Met Xaa Ser Pro Asn Phe Ser Tyr Leu Gln Xaa Ser Leu Thr Pro Xaa
 435 440 445
 Leu Thr Thr Arg Leu Val Gln Ser Val Gly Ser Gly Leu Ala Asp Pro
 450 455 460
 His Ser Leu Ala Leu Thr Gly Thr Ala Pro Leu Gln Xaa Phe Glu Gln
 465 470 475 480
 Val Leu Gly Pro Leu Xaa Ser Phe Ala Lys Pro Phe Ser Thr Glu Lys
 485 490 495
 Met Ser Ser Ala Pro His Gly Gln Arg Ala Trp Ser Ile Pro Asp Pro
 500 505 510
 Ile Gln Gly Pro Leu Tyr Pro Phe Trp Gln Leu Xaa Lys Gly Gln Pro
 515 520 525
 Gly Met Leu Thr Met Leu Xaa Thr Pro Ala Leu Arg Thr Leu Lys Gln
 530 535 540
 Ile Thr Lys Lys Leu His Thr Tyr Cys Gln Ile Xaa Arg Pro Gln Ala
 545 550 555 560
 Met Arg Pro Gln Ser Ser Ser Val Gly Val Xaa Ser Gln Arg Met Gln
 565 570 575
 Ala Asp Met Xaa Leu Gln Gly Val Asp Ala Ser Arg Met Pro Ser Ile
 580 585 590
 Phe Leu Arg Met Ser Arg Val Ala Ile Lys Tyr Ser Xaa His Thr Val
 595 600 605
 Leu Leu Leu Ala Ser Ile Val Arg Ser Leu Leu Gly Gln Xaa Ser Gly
 610 615 620

257

Pro Ala Val Val Lys Ala Asn Ile Ala Gln Ala Asp Lys Thr Pro Thr
 625 630 635 640
 Thr Pro Ala Ala Gly Leu Asn Ala Glu Xaa Thr Lys Pro Ala Ser Xaa
 645 650 655
 Ser Ile Val Xaa His Ser Pro Ile Lys His Leu Asn Val Lys Gln Ala
 660 665 670
 Val Asp Glu Ala Pro Ala Xaa Pro Pro Ser Met Ser Lys Thr Lys Pro
 675 680 685
 Thr Asp Val His Val Pro Arg Ala Val Pro Xaa Ala Pro Ala Ile Met
 690 695 700
 Asn Ala Ser Ala Xaa Leu Ala Ser Val Ser Leu Asp Ala Ile Ala Pro
 705 710 715 720
 Pro Asn Asn Asp Arg Asn Ile Leu Ile Leu Xaa Gly Ser Gly Val Val
 725 730 735
 Ile Pro Ala Met Lys Ala Asn Thr His Asp Ala Lys Gly Leu Ser Gly
 740 745 750
 Lys Val Thr Lys Pro Gln Gln Tyr Ser Met Ile Ala Arg Ile Val Ala
 755 760 765
 Ala Xaa Gly Pro Arg Lys Val Leu Ser Phe Ser Arg Ala Val Ser Asn
 770 775 780
 Val Lys Gly Leu Val Val Val Ile Val Leu Phe Ser Leu Ser Ile Ala
 785 790 795 800
 Ala Thr Met Ala Ser Lys Gly Met Asn Asp Ala His Ser Ser Thr Ile
 805 810 815
 Ser Ser Ser Ser Thr Thr Gly Ala Thr Val Ala Pro Val Gly Thr Asp
 820 825 830
 Val Ile Asp Gln Gln Arg Arg Thr Gln Val Ala Pro Lys Val Ser Met
 835 840 845
 Ala Arg Xaa Ala Ile Ala Thr Pro Thr Pro Thr Ala Ser Ala Ala Val
 850 855 860
 Pro Glu Val Leu Thr Ser Val Lys His Ile Trp Tyr Leu Val Thr Ser
 865 870 875 880
 Leu Gly Ser Gly Pro Gly Gln Ala Ser Gln Pro Ser Lys Arg His Arg
 885 890 895
 Thr Pro Gln Gly Phe Phe Pro Ser Arg Ala Pro Cys His Arg Gly Ala
 900 905 910
 Ser Leu Gly Ala Ala Xaa Pro Tyr Xaa Xaa His Ser Cys Ser Trp Ala
 915 920 925

258

Ala Val Asn Lys Thr Xaa Leu Ser Ala Val Leu Phe Ala Val Leu Thr
 930 935 940
 Asn Glu Gly Ser Gly Leu Thr Ile Glu Lys Arg Ser Ala His Ser Ser
 945 950 955 960
 Lys Phe Ala Pro Ile Ala Gly Asn Pro Gly Trp Val Arg Xaa Val Ser
 965 970 975
 Arg Ile Val Xaa Ala Ser Val Asp Asp Lys Pro Tyr His Ala Leu Ala
 980 985 990
 Ala Ser Lys Ala Ser Thr Met Leu His Ser Gly Thr Ile Pro Glu Gly
 995 1000 1005
 Val Gln Leu Pro Ser Thr Xaa Xaa Tyr Met Pro Ala Leu Pro Arg Pro
 1010 1015 1020
 Val Arg Pro Leu Arg Trp Pro Leu Thr Ile Ala Glu Thr Pro His Thr
 1025 1030 1035 1040
 Arg Thr Pro Met Val Lys Val Gly Ser Arg Ser Thr Trp His Val Pro
 1045 1050 1055
 Ser Thr Met Arg Leu Gln Ser Tyr Thr Glu Ser Lys Ser Pro Val Tyr
 1060 1065 1070
 Pro Val His Lys Ala Ser Val Ala Thr Thr Thr Gln Ser Pro Ser Gly
 1075 1080 1085
 Ile Phe Glu Met Ser His Pro Leu Xaa Xaa Glu Thr Ala Val Ile Pro
 1090 1095 1100
 Phe Arg Ala Asn Ser Leu Ala Ser Ser Ser Gln Cys Phe Leu Val Ala
 1105 1110 1115 1120
 Ser Lys Ile Arg Cys Leu Pro Phe Phe Arg Phe Ser Ser Leu Ile Phe
 1125 1130 1135
 Phe Pro Xaa Lys Gly Ile Val Pro Ser Ser Val Asn Xaa Ile Ser Val
 1140 1145 1150
 Met Leu Ala Cys Gly Val Gly Ile Thr Pro Gly Gly Val Ala Val Ala
 1155 1160 1165
 Arg Thr Thr Ser Leu Thr Phe Leu Asp Gly Ala Ser Val Arg Thr Phe
 1170 1175 1180
 Pro Met Pro Asn Thr Val Val Arg Ser Val Ala Trp His Ser Ser Gln
 1185 1190 1195 1200
 Met Ile Thr Ser Xaa Phe Arg Glu His Arg Pro Val Arg Tyr Met Pro
 1205 1210 1215
 Tyr Val Leu Tyr Val Ser Glu Ala Pro Val Leu Val His L u Pro Leu
 1220 1225 1230

259

Lys Xaa Gln Phe Gly Phe Thr Pro Tyr Val Ala Cys Met Tyr Phe Gly
 1235 1240 1245
 Ile Asp Ala Val Val Ala Thr Leu Gly Phe Arg Thr Lys Thr Ser Xaa
 1250 1255 1260
 Phe Xaa Cys Met Xaa Glu Ser Gly Asn Leu Val Asp Leu Pro Leu Pro
 1265 1270 1275 1280
 Val Gly Ala Ile Lys Ile Cys Thr Glu Tyr Ser Leu Gly Thr Val Gly
 1285 1290 1295
 Phe Val Ser Arg Val Ala Cys Ala Val Tyr Trp Gly Trp Tyr Pro Ala
 1300 1305 1310
 His Thr Asn Gly Leu Thr Leu Ile Trp Pro Thr Glu Pro Pro Glu Phe
 1315 1320 1325
 Leu Ala Ala Val Asn Ile Pro Ile Thr Cys Pro Glu Glu His Arg Ile
 1330 1335 1340
 Gly Ala Pro Glu Glu Pro Leu Ala Thr Ala Met Gly Arg Ala Pro His
 1345 1350 1355 1360
 Thr His Gln Xaa Gly Ser Ser Asp Leu Leu Thr Ser Thr Asn Asp Pro
 1365 1370 1375
 Ser Arg Val Thr Arg Tyr Pro Leu Val Ser Pro Gln Glu His Arg Val
 1380 1385 1390
 Arg Asp Pro Ala Pro His Gly Gly Xaa Xaa Met Ser Trp Ser Leu Ala
 1395 1400 1405
 Ala Ser Thr Val Ile Gly Cys Met Glu Pro Val Gly Xaa Ala
 1410 1415 1420

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Xaa Ala Leu Gly Val Ser Leu Leu Val Ser Gly Gly Ser Ser Arg Arg
 1 5 10 15
 Pro Pro Pro Leu Glu Leu Ser Gln Phe Ala Asp Asn Asp Ser Val Ser
 20 25 30

260

His Leu Pro Arg His Thr Ser Ala Ser Pro Glu His Gln Cys Pro Glu
35 40 45

Gly Gln Xaa Cys Gly Thr Xaa Gln Thr Xaa Arg Ala Cys Glu Leu Leu
50 55 60

Leu His His Ser Pro Thr Xaa His Arg Gln Leu Leu Lys Leu Phe Pro
65 70 75 80

Xaa Pro Ile Ser Leu Ala Cys Gly Met Met Gly Gly Thr Glu Val Val
85 90 95

Tyr Xaa Xaa Xaa Leu Phe Val Phe Xaa Ala Pro His Pro Ala Ala Gln
100 105 110

Ser His Thr Pro Met Ile Phe Val Xaa Gly Asn His Xaa Xaa Trp Pro
115 120 125

Glu Leu Gln Thr Glu Leu Xaa Lys Gln Phe Xaa Ser Xaa Ser Arg Arg
130 135 140

Ser Lys Cys Ser Ser Cys Cys Thr Lys Thr His Ser Phe Pro Thr Ser
145 150 155 160

Phe Leu Xaa Ala Val Trp Arg Trp Leu Ile Glu Trp Asn Pro Cys Pro
165 170 175

Val Ser Xaa Gly Thr Gly Gly Gln Xaa Arg Ser Trp Lys Arg Leu Xaa
180 185 190

Ser Leu Thr Asn Phe Arg Leu Thr Ile Gln Arg Pro Pro Phe Trp Glu
195 200 205

Gly Asn Trp Val Asn Xaa Xaa Gly Leu Xaa Xaa Phe Arg Ser Leu His
210 215 220

Ile Gln Leu Gln Xaa Lys Gly Tyr Thr His Leu Leu Pro Thr Gly Ala
225 230 235 240

Ser Ala Trp Pro Thr Xaa Glu Gln Val Val Lys Lys Gly Gly Leu Lys
245 250 255

Asp Leu Leu Thr Gly His Phe Val Ala Gly Phe Gln Asp Met Thr Leu
260 265 270

Leu Gly Arg Ile Ser Glu Gly Glu Ala Arg Xaa Ala Asn Gln Phe Leu
275 280 285

Pro Gly Thr Gly Ala Phe Leu Pro Leu Pro Leu Arg Ser Gly Arg Gly
290 295 300

Leu Ala Val Trp Trp Cys Gln Arg Gln Leu Lys Leu Pro Gln Ala Ile
305 310 315 320

Gly Leu Tyr Ala Ala Thr Pro Val Xaa Lys Gln Glu Arg Thr Leu Arg
325 330 335

261

Leu His His Xaa Glu Cys Cys Leu Trp Asn Tyr Ser His Leu Pro Gln
 340 345 350

Val Asp His Ala Asn Xaa Val Ala Cys Asp His Gln Val Cys Val Arg
 355 360 365

Gln Arg Gly Arg Glu Ala Xaa Gln Phe Tyr Pro Tyr Arg Gln Asp Arg
 370 375 380

Asn Ser Lys Gln Met Ser Ser Lys Glu Phe Trp Ala His Leu Asp Asn
 385 390 395 400

Xaa Glu Pro Val Arg Gly Pro Arg Pro Leu Gln Leu Ser Arg Leu Gly
 405 410 415

Ala Pro Gly Xaa Asn Arg His Leu Glu Arg Ile Leu Leu Xaa Gln Lys
 420 425 430

Cys Asp Leu Pro Ile Ser His Ile Tyr Ser Ser Pro Xaa Arg His Asn
 435 440 445

Xaa Arg Gln Asp Xaa Ser Asn Gln Leu Gly Pro Val Xaa Pro Thr His
 450 455 460

Thr Ala Xaa Arg Xaa Leu Glu Gln Pro Leu Ser Ser Asn Leu Asn Lys
 465 470 475 480

Phe Trp Val Leu Cys Lys Val Leu Gln Asn His Ser Gln Gln Lys Arg
 485 490 495

Xaa Val Gln His Arg Met Asp Ser Val Leu Gly Ala Tyr Leu Ile Gln
 500 505 510

Ser Arg Gly Pro Cys Thr Pro Ser Gly Ser Cys Arg Lys Asp Asn Gln
 515 520 525

Glu Cys Xaa Pro Cys Ser Glu Leu Gln Leu Xaa Gly His Xaa Ser Lys
 530 535 540

Ser Gln Arg Asn Cys Thr His Thr Ala Lys Ser Xaa Asp Pro Lys Gln
 545 550 555 560

Xaa Gly Arg Asn His Pro Pro Ser Gly Cys Xaa Ala Asn Gly Cys Lys
 565 570 575

Leu Ile Xaa Xaa Ser Arg Gly Xaa Met Pro Pro Glu Cys Pro Val Ser
 580 585 590

Ser Cys Gly Cys His Glu Trp Gln Xaa Ser Thr His Tyr Ile Gln Cys
 595 600 605

Cys Ser Xaa Gln Ala Xaa Xaa Glu Val Cys Trp Ala Ser Asp Leu Ala
 610 615 620

Leu Leu Leu Ser Lys Gln Thr L u His Lys Leu Thr Arg Arg Pro Gln
 625 630 635 640

262

Leu Leu Arg Pro Asp Xaa Thr Arg Ser Arg Leu Asn Gln Gln Ala Asp
 645 650 655
 Pro Xaa Xaa Ala Thr His Pro Ser Ser Ile Xaa Met Ser Ser Lys Gln
 660 665 670
 Trp Met Arg Arg Gln His Ser Arg Leu Ala Cys Gln Arg Gln Asn Pro
 675 680 685
 Pro Met Ser Met Tyr Gln Glu Leu Phe Pro Gln Pro Arg Pro Ser Xaa
 690 695 700
 Thr Pro Val Arg Leu Xaa Arg Leu Xaa Ala Trp Thr Gln Leu Arg Leu
 705 710 715 720
 Gln Ile Met Thr Gly Thr Phe Xaa Ser Cys Glu Val Val Gly Xaa Xaa
 725 730 735
 Tyr Pro Gln Xaa Lys Gln Thr Arg Met Met Gln Arg Asp Cys Gln Val
 740 745 750
 Lys Xaa Leu Ser His Ser Asn Thr Leu Xaa Xaa Gln Gly Leu Xaa Leu
 755 760 765
 His Glu Ala Gln Glu Arg Cys Xaa Val Phe Gln Gly Arg Phe Pro Met
 770 775 780
 Xaa Lys Asp Xaa Leu Trp Xaa Leu Tyr Ser Ser Ala Cys Gln Leu Gln
 785 790 795 800
 Gln Pro Trp Pro Pro Arg Glu Xaa Met Met His Thr Pro Pro Arg Phe
 805 810 815
 Pro Leu Arg Gln Pro Leu Gly Arg Gln Xaa His Arg Xaa Gly Leu Met
 820 825 830
 Xaa Xaa Thr Ser Asn Ala Ala His Lys Trp Arg Gln Lys Cys Gln Trp
 835 840 845
 Leu Asp Lys Pro Xaa Pro Leu Gln Arg Gln Gln Arg Val Arg Leu Ser
 850 855 860
 Gln Lys Tyr Xaa Leu Gln Xaa Ser Thr Phe Gly Ile Trp Ser Pro Arg
 865 870 875 880
 Trp Ala Leu Gly Gln Asp Arg Arg His Ser Arg Pro Ser Ala Thr Glu
 885 890 895
 Pro His Lys Val Phe Ser Gln Ala Gly Leu Pro Ala Thr Val Val Arg
 900 905 910
 His Trp Glu Gln His Ser His Thr Asp Asp Thr Val Val Val Gly Leu
 915 920 925
 Gln Ser Thr Lys His Asn Cys Gln Gln Phe Phe Leu Gln Tyr Xaa Gln
 930 935 940

263

Met	Lys	Val	Arg	Gly	Xaa	Pro	Xaa	Lys	Arg	Asp	Gln	Pro	Thr	Arg	Pro	945	950	955	960
Asn	Leu	Leu	Leu	Ser	Gln	Val	Thr	Gln	Val	Gly	Cys	Asp	Arg	Cys	Pro	965	970	975	
Glu	Xaa	Phe	Glu	Leu	Leu	Leu	Met	Thr	Asn	His	Thr	Met	Pro	Trp	Leu	980	985	990	
Arg	Arg	Arg	Leu	Gln	Gln	Cys	Cys	Ile	Gln	Glu	Pro	Tyr	Pro	Lys	Gly	995	1000	1005	
Tyr	Asn	Ser	Arg	Leu	His	Ser	Ser	Ile	Cys	Gln	Leu	Ser	His	Gly	Leu	1010	1015	1020	
Cys	Gly	Pro	Tyr	Ala	Gly	Leu	Xaa	Leu	Leu	Leu	Lys	Pro	Arg	Thr	His	1025	1030	1035	1040
Glu	His	Pro	Trp	Xaa	Lys	Xaa	Gly	Gln	Gly	Gln	His	Gly	Met	Cys	Leu	1045	1050	1055	
Leu	Pro	Xaa	Gly	Cys	Ser	His	Thr	Arg	Asn	Gln	Ser	His	Gln	Cys	Thr	1060	1065	1070	
Leu	Tyr	Thr	Arg	His	Gln	Trp	Gln	Leu	Leu	His	Ser	Arg	Pro	Gln	Ala	1075	1080	1085	
Phe	Leu	Arg	Cys	His	Ile	Pro	Tyr	Ser	Lys	Arg	Gln	Leu	Leu	Phe	Pro	1090	1095	1100	
Phe	Glu	Leu	Thr	Arg	Xaa	Gln	Ala	His	His	Ser	Val	Phe	Trp	Xaa	Pro	1105	1110	1115	1120
Gln	Arg	Xaa	Gly	Val	Ser	Leu	Ser	Ser	Asp	Phe	Pro	Pro	Xaa	Ser	Phe	1125	1130	1135	
Phe	His	Glu	Arg	Gly	Xaa	Cys	Leu	His	Xaa	Leu	Ile	Glu	Ser	Gln	Leu	1140	1145	1150	
Cys	Trp	His	Val	Val	Xaa	Gly	Leu	Leu	Gln	Gly	Gly	Xaa	Pro	Trp	Gln	1155	1160	1165	
Glu	Pro	Leu	Ala	Xaa	His	Phe	Trp	Met	Glu	Leu	Arg	Leu	Gly	Pro	Phe	1170	1175	1180	
Gln	Cys	Pro	Thr	Arg	Trp	Phe	Asp	Arg	Xaa	His	Gly	Ile	Arg	His	Lys	1185	1190	1195	1200
Xaa	Leu	His	His	Ser	Ser	Gly	Asn	Ile	Val	Arg	Ser	Gly	Thr	Cys	His	1205	1210	1215	
Met	Cys	Cys	Thr	Xaa	Val	Lys	Pro	Leu	Cys	Trp	Tyr	Ile	Cys	His	Xaa	1220	1225	1230	
Asn	Ser	Asn	Leu	Asp	Ser	Arg	Arg	Thr	Ser	Arg	Ala	Cys	Thr	Leu	Ala	1235	1240	1245	

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Leu Met Leu Leu Xaa Pro His Trp Asp Leu Gly Pro Arg Pro His Xaa
 1250 1255 1260
 Ser Pro Ala Cys Lys Lys Val Val Ile Trp Leu Thr Cys Arg Cys Gln
 1265 1270 1275 1280
 Trp Gly Gln Leu Lys Phe Ala Leu Asn Thr Arg Xaa Ala Gln Xaa Val
 1285 1290 1295
 Leu Tyr Gln Glu Trp His Val Leu Cys Thr Gly Asp Gly Ile Gln His
 1300 1305 1310
 Thr Pro Thr Ala Xaa Pro Xaa Ser Gly Arg Leu Asn Arg Gln Asn Phe
 1315 1320 1325
 Xaa Gln Arg Xaa Thr Ser Gln Xaa His Ala Arg Arg Ser Thr Glu Ser
 1330 1335 1340
 Gly His Leu Lys Asn Pro Trp Gln Gln Pro Trp Glu Gly Pro Arg Thr
 1345 1350 1355 1360
 His Thr Asn Lys Gly His Arg Ile Cys Xaa Pro Gln Pro Met Thr Pro
 1365 1370 1375
 Val Val Leu Pro Asp Thr Pro Trp Ser Pro Arg Lys Ser Thr Glu Xaa
 1380 1385 1390
 Gly Thr Gln Leu His Met Val Val Asp Arg Cys Pro Gly His Xaa Pro
 1395 1400 1405
 Arg Gln Arg Leu Leu Gly Val Trp Ser Leu Trp Asp Glu Pro
 1410 1415 1420

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTACCACCAA TACCAGCGGC

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

265

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACATGGTCC TGGCCCTGTT GG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATCCATAGT GAGCCACTCA C

21

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAAAATGTTC CTGTCATTAT TTG

23

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

266

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAATCATCTC CAGCTATAAA G

21

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGTGGACGC CACTTGTTTC

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAATAGCACA ATCTTCCTTG G

21

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAAAGCTTGG TTGGTTGTGG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATCTTGACA ATGACAACTT TC

22

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CCTCACTCAC CTTGACCTC

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

268

GGTTGGCACT TGCATGCCTG

20

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CCTGGCTTTG TTCCCACTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTCGTACCCC TCCTGGCAGC

20

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCTAGGAGCA ACACTGTATG

20

269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGCCATAATT GACGACAAGA CTAGTCC

27

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTATTCCCAG GCTATAGCTA AAG

23

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CAGGTACATG CCATATGTGC TGTACG

26

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

270

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTTGGACGCA ATTGCGCCTC

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTCAC TAGGT AACTGATGTT G

21

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATGGTGGTT GATAGATGTC C

21

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTGTCAAAG CTAAGCAGGC

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AGATACCCCT TGGTCTCCC

19

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CAGGATCTAT TCCAGTAGGC

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTATAGGGGT ACCAAGATAT GG

22

272

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTCTGCTAAG TCCCACATCA CTGGC

25

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAAGAAC CCTCGCTTCC

20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CACCCAACCC GAGGACTCCA G

21

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid

273

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CACTTCAGCG CATGCCAATA GC

22

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTACTAAACC CATCCATTGC CAC

23

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCGAATGAG TACGTCAAGG

20

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

274

GTAGGTGTGG CCGTGGGAAA G

21

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTGCCGAAC T GAGGGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGTTACCGTT CCCATTGACA ACCC

24

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGACGGGGTC TCTGGTTGTA GTG

23

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:

275

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GTGAACCGCG CTCACTCACC TTCG

24

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCTCTAGAGC GGCCTGAGCA G

21

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGATTAAGGC ACCATCATTC

20

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GCACGATTGG ATGCCGGGGA TAC

23

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNC CGGT

34

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAGTTCAAGC TTGTCCAGGA ATTC

24

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCCTCAGCCA ACTTCATCAC

20

277

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNG CGCT

34

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCGCTGAGCC TGTTAGCATA AC

22

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CAGGCGGTGG TATTGTCAGC

20

(2) INFORMATION FOR SEQ ID NO:131:

278

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CACTTTGGAC TGTAACAAAT GAC

23

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CATCCACCCG ATAAACCCTA G

21

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTGCAAG TGTGTCGAGG CAGG

24

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

279

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TAATGCTGCA GCCGACAGCT G

21

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNG GCCT

34

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTTTCTCGGT GGTGCGCTAC

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

280

CAACGCTGAG ATCCTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CCGTGAGAGG CGACTGGTGA G

21

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CGCAGGACAG TAGACACCTT GGTG

24

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CAGGCATCAC CGAACTGCGT GGC

23

(2) INFORMATION FOR SEQ ID NO:141:

281

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CGAGTGACGC TTGGTGCCTG GTC

23

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CACCTTGCTG CCGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CCAATCGGCA GTGCTTTAGG GACC

24

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

282

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GTATCCCCGG CATCCAATCG TGC

23

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAACCATCCC AACACATGTA GG

22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGGCTTGCCC AACTACTTCC

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

283

GGAGGCGTGA TACTCAAAAA G

21

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CCGTGAGAGG CGACTGGTGA G

21

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CACCCAACCC GAGGACTCCA G

21

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CAGCAACCAC ACAGCCAAGC C

21

(2) INFORMATION FOR SEQ ID NO:151:

284

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGGCTTGCCC AACTACTTCC

20

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TAATGCTGCA GCCGACAGCT G

21

- (2) INFORMATION FOR SEQ ID NO:153:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GGAGGCGTGA TACTCAAAA G

21

- (2) INFORMATION FOR SEQ ID NO:154:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CATGAAGAAC CCTCGCTTCC

20

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CCAAGTCAAG CTTGGCGCTT GTCATCAC

28

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CAACGCTGAG ATCCTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GATCCATAGT GAGCCACTCA C

21

(2) INFORMATION FOR SEQ ID NO:158:

286

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```
GATCCATAGT GAGCCACTCA CCCATCAAGC ATTTAAATGT CAAGCAAGCA GTGGATGAGG      60
CGGCAGCATA GCCGCCTAGC ATGTCAAAGA CAAAACCCAC CGATGTCCAT GTACCAAGAG      120
CTGTTCCAC  AGCCCCGGCC ATCATGAACG CCAGTGCCTC TCTAGCGTCT GTAAGCTTGG      180
ACGCAATTGC GCCTCCAAAT AATGACAGGA ACATTTTGAT C                          221
```

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
GATCCAATCC AGGGGCCCTC GTACCCCTCC TGGCAGCTGT AGAAAGGACA ACCAGGAATG      60
TTAACCATGC TCTGAACTCC AGCTTTAAGG ACATTAAAGC AAATCACAAA GAAATTGCAC      120
ACATACTGCC AAATCTCTAG ACCCCAAGCA ATGAGGCCGC AATCATCCTC CGTCGGGGTG      180
TGGAGCCAAC GGATGCAAGC TGATATGATA CTCCAGGGGG TAGATGCCTC CAGAATGCCC      240
AGTATCTTCT GCGGATGTCA CGAGTGGCAA TAAAGTACTC ACTACATACA GTGTTGCTCC      300
TAGCAAGCAT AGTAAGAAGT CTGTTGGGCC AGTGATC                               337
```

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CCTCACTCAC CTTCGACCTC

20

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GATCCATCTT GACAATGACA ACTTTTCGCAG GACAGTAGAC ACCTTGGTGA CGAACTCATC 60
TTTGAGGAAG AAATCGTCAG GCATCACCGA ACTGCGTGGC ATCATCGTCA ACAATCTGTT 120
AACCCAATCT TGACCCACAC CCTTTTTTGAC AGACCAGAGC AACAAGCCCA GAACCACACC 180
GGCCACCGAA GCCCCCGGAG AGGCCAGGCA ACTGACCAGG CACCAAGCGT CACTCGCTTG 240
TAACTTCCCC GCCAGGAGGT CGAAGGTGAG TGAGCGCGGT TCACCGCCCC CTCCCAGCCT 300
CTGATC

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTGTCAAAAG CTAAGCAGGC

20

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

288

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CGTGGGAGTC CGGGGCCCCG GACCTCCCAC CGAGGTGGGG GGAAAGGGGC CCTGGACCGG	60
CCGGGTGGAA GGCCCGGAAC CGGTCCATCT TCCTCAAGGT TGAGGAAGGG GTACGTCTAT	120
CGGTCCGGTC GGTCCGAAAG GCGTCTGGAT GCCTAGTGTT AGGGTTCGTA GGTGGTAAAT	180
CCCAGCTAGG CGTGAAAGCG CTATAGGATA GGCTTATCCC GGTGACCGCT GCCCCGGAAC	240
CAGCCCCGCG GKTCTTTGGA CACGGTCCAC AGGTTGGGGG TACCGGTGTG AATAACCCCC	300
CGACTGAAGC GTCAGTCGTT AAACGGAGAC GGTCTCCTGA GATCGCAACG ACGCCCCACG	360
TACGGGAACG CCGCCAAAAC CTTCGGGACA GCTATGCGGG TTGACAATCC CAGTGGGGGG	420
CCGGGGACCA GCTGATTACT TGTCCTGCGA GTTCCTCTTG AGACTGGCCG AAAGGCAGCC	480
ACGGGGCCAC CAAGGCGGCG CAGCGCTGCA TCGGGCAAGG GGAAAAATCC TTCGGGTGAC	540
CCCTGGTGGC AATCCCTTCC CTTAGGAGCA TGAGTGTGGT CGACACATTC ACCATGGCTT	600
GGCTGTGGTT GCTGGTTTGC TTCCCCCTCG CGGGGGGGGT GCTCTTCAAC TCGCGGCACC	660
AGTGCTTCAA TGGGGACCAT TATGTGCTTT CCAATTGTTG TTCCCGAGAC GAGGTTTACT	720
TCTGTTTCGG GGACGGATGT CTGGTGGCTT ATGGCTGTAC TGTTTGACA CAGTCTTGCT	780
GGAAGCTCTA CCGGCCTGGG GTGGCTACTC GGCCCGGGTC CGAACCAGGT GAGCTGCTGG	840
GGAGATTGGG GAGTGTAATT GGTCCGGTGT CGGCTTCGGC TTACACCGCT GGAGTCCTCG	900
GGTTGGGTGA ACCTTACAGT TTGGCCTTCT TGGGGACGTT CCTCACCAGT CGCCTCTCAC	960
GGATTCCCAA CGTCACCTGC GTGAAGGCTT GTGACCTTGA GTTTACCTAC CCAGGCTTGT	1020
CCATCGATTT TGA CTGGGCG TTTACCAAGA TCTTGCA GTT GCCGGCCAAG CTGTGGCGAG	1080
GCCTAACGGC RGCWCCGGTC TTGAGCCTCC TCGTGATCCT CATGCTGGTC CTCGAGCAGC	1140
GCCTCCTGAT AGCCTTCCTA CTGCTTTTGG TAGTGGGCGA GGCTCAGAGG GGGATGTTCTG	1200
ACAACTGCGT GTGTGGTTAC TGGGGGGGCA AGAGGCCCCC GTCGGTGACC CCGCTGTACC	1260
GTGGCAACGG TACTGTGGTG TGTGACTGTG ATTTTGGA AATGCATTGG GCCCCCCCCT	1320
TGTGTTCCGG YCTGGTGTGG CGGGACGGTC ATAGGAGGGG CACCGTGCGC GACCTCCCCC	1380
CGGTTTGCCC CCGGGAGGTT CTCGGCACGG TGACAGTCAT GTGTCAGTGG GGTTCGCT	1440
ACTGGATTG GAGATTGGG GACTGGGTTG CATTGTACGA CGAGCTACCA CGATCAGCTC	1500
TCTGTACTTT CTCTCAGGT CATGGTCCAC AACCTAAAGA TCTCTCAGTC TTGAATCCAT	1560

CCGGGGCACC TTGTGCTTCT TGCCTCGTTG ACCAGAGGCC GCTGAAATGT GGTTCCTGCG 1620
TCCGCGACTG CTGGGAGACG GGGGGTCTTG GGTTCGATGA GTGCGGTGTC GGTACTCGGA 1680
TGACGAAGCA CCTCAGAGCC GTCCTGGTTG ATGGAGGTGT GGAGTCCAAG GTGACAACGC 1740
CCAAGGGTGA GCGCCCCAAA TACATAGGTC AGCACGGTGT GGGAACTTAC TACGGCGCTG 1800
TCCGTAGCCT CAACATCAGT TACCTAGTGA CTGAGGTGGG GGGCTATTGG CATGCGCTGA 1860
AGTGCCCGTG CGACTTTGTG CCCCAGAGTC TCCCAGAAAAG AATTCCAGGT AGGCCTGTGA 1920
ATGCATGTCT AGCTGGGAAG TCTCCGCACC CGTTCGCAAG TTGGGCTCCC GGTGGGTTTT 1980
ACGCCCCCGT GTTCACCAAG TGCAACTGGC CGAAGACCTC CGGAGTGGAT GTGTGTCCTG 2040
GGTTTGCTTT CGATTCCCT GGTGATCACA ACGGCTTCAT CCATGTTAAA GGCAACAGAC 2100
AGCAGGTTTTA CAGTGGTCAG CGAAGGTCTT CGCCGGCTTG GTTGCTTACT GACATGGTCC 2160
TGGCCCTGTT GGTGGTGATG AAGTTGGCTG AGGCTAGAGT TGTCCCCCTG TTTATGCTGG 2220
CAATGTGGTG GTGGTTGAAT GGAGCATCTG CTGCCACTAT TGTCATCATA CACCCTACTG 2280
TCACGAAGTC CACTGAAAGT GTTCCATTGT GGAATCCGCC CACTGTTCCA ACTCCATCTT 2340
GCCCCAATTC TACCACCGGA GTCGCGGACT CTACCTACAA TGCTGGTTGC TACATGGTGG 2400
CAGGCCTGGC GGCCGGGGCT CAGGCGGTCT GGGGTGCTGC CAATGATGGT GCTCAGGCCG 2460
TCGTTGGTGG CATCTGGCCC GCGTGGCTCA AGCTGCGAAG CTTGCTGCC GGTCTGGCCT 2520
GGTTGTCAA TGTGGGGCT TACTTGCCGG TCGTCGAGGC CGCVCTGGCT CCCGAGCTGG 2580
TGTGCACCCC GGTGGTCGGC TGGGCAGCCC AGGAGTGGTG GTTCACTGGT TGTCTGGGTG 2640
TGATGTGTGT CGTGGCGTAC CTGAATGTCC TGGGCTCTGT RAGGGCTGCC GTGCTTGTGG 2700
CGATGCACTT CGCAAGGGGT GCTCTGCCGC TGGTATTGGT GGTAGCTGCC GGGGTRACCC 2760
GGGAGCGGCA CAGCGTCTTA GGGCTTGAGG TGTGCTTCGA TCTGGATGGT GGAGACTGGC 2820
CRGACGCCAG TTGGTCTTGG GGTTTAGCAG GCGTGGTGAG CTGGGCCCTC CTGGTGGGGG 2880
GTCTGATGAC CCACGGTGGC CGATCAGCCA GAYTGACTTG GTAYGCCAGG TGGGCCGTCA 2940
ATTAYCAGAG GGTTCGYCGG TGGGTGAACA ACTCACCGGT TGGAGCYTTT GGYCGTTGGM 3000
GGCGYGCCTG GAAAGCYTGG TTRGTKGTGG CTTGGTTCTT CCCCCAGACA GTTGCCACAG 3060
TYTCCGTCAT CTTCACTC TGTTTGAGCA GTTTAGATGT CATTGATTTC ATCTTGARG 3120
TACTCTTGGT TAACTACCA AATCTCGCGC GCTTGGCGCG RGTGCTGGAC TCCTTAGCTC 3180
THGCTGAGGA GCGGCTGGCC TGCTCTTGGC TGGTGGGCGT CCGGCGCAAG CGGGGCGTCC 3240
TCCTCTACGA GCACGCGGT CACACTAGCA GGCGCGGTGC TGGGCTTGG CGAGAGTGGG 3300

GYTTTGCCT	YGAGCCKGTT	AGYATAACCA	AGGAAGATTG	YGCYATTGTT	CGGGACTCTG	3360
CTCGTGTGTT	GGGCTGTGGA	CAATTGGTCC	ATGGGAAACC	AGTGGTCGCG	AGGCGAGGCG	3420
ACGAGGTGTT	GATCGGCTGT	GTGAACAGTC	GGTTCGACCT	TCCGCCTGGC	TTTGTTCCTCA	3480
CTGCTCCCGT	GGTSCCTTCAT	CARGCWGGCA	ARGGRTTYTT	YGGGGTTGTG	AAGACMTCCA	3540
TGACAGGCAA	GGACCCGTCC	GAACACCACG	GRAACGTGGT	GGTCCTWGGG	ACTTCAACAA	3600
CKCGTTCCAT	GGGCTGCTGC	GTGAACGAG	TAGTGACAC	RACATACCAT	GGYACCAACG	3660
CCCGRCCKAT	GGCGGGGCK	TTTGKKCCY	TCAAYGCTCG	GTGGTGGTCW	GCGAGYGACG	3720
ACGTCACGGT	YTACCCGCTC	CCWAATGGYG	CTTCTTGCT	YCARGCWTGY	AAGTGCCAAC	3780
CAACTGGGGT	GTGGGTGATC	CGGAATGACG	GAGCTCTTTG	CCATGGAACT	CTCGGCAAGG	3840
TGGTGGATTT	AGATATGCCC	GCTGAGTTGT	CAGACTTTTCG	CGGGTCTTCT	GGATCACCAA	3900
TCTTGTCGA	TGAGGGTCAT	GCTGTTGGCA	TGCTGATTTTC	GGTGCTTCAT	AGGGGGAGTA	3960
GGGTTTCCTC	GGTGCGGTAT	ACCAAACCTT	GGGAACTCT	CCCTCGGGAG	ATTGAGGCTC	4020
GATCGGAGGC	CCCCCTGTG	CCAGGAACCA	CTGGATACAG	GGAGGCGCCA	CTGTTCTGTC	4080
CCACCGGAGC	TGGCAAGTCG	ACGCGCGTGC	CGAATGAGTA	CGTCAAGGCT	GGACACAARG	4140
TGCTTGTA	AAACCCATCC	ATTGCCACAG	TGAGGGCCAT	GGGCCCTTAC	ATGGAAAAGT	4200
TAACCGGCAA	ACATCCGTCG	GTGTACTGTG	GCCATGACAC	TACTGCATAT	TCCAGGACTA	4260
CTGACTCATC	TTTGACCTAC	TGTACATACG	GCAGGTTTAT	GGCCAATCCC	AGGAAATACT	4320
TGCGGGGGAA	CGACGTCGTA	ATTTGCGACG	AGTTGCACGT	CACCGACCCG	ACCTCAATTT	4380
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TGGGCAGTGA	GGGGGAGGTC	CCCTTCTATT	GCCAATTCCT	CCCACTGAGT	AGGTATGCTA	4560
CTGGGAGACA	CCTGCTGTTT	TGTCATTCCA	AGGTAGARTG	CACTAGGTTA	TCCTCAGCTT	4620
TGGCCAGCTT	TGGTGTCAAC	ACCGTTGTGT	ACTTCAGAGG	CAAAGAACT	GACATTCCAA	4680
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ACACCGTAAC	AGACTGTGGT	TTAATGGTTG	AGGAGGTAGT	GGAAGTGACC	CTGGACCCGA	4800
CCATCACTAT	CGGTGTGAAG	ACCGTCCCGG	CCCCTGCCGA	ACTGAGGGCT	CAGAGGCGTG	4860
GTAGGTGTGG	CCGTGGGAAA	GCGGGCACTT	ACTATCAGGC	ATTGATGTCT	TCGGCGCCGG	4920
CGGGAACSGT	TCGGTCTGGG	GCTCTCTGGG	CAGCTGTTGA	GGCTGGHGTG	TCGTGGTATG	4980
GCCTAGAGCC	CGATGCTATT	GGAGACCTGC	TTAGGGCCTA	CGACTCGTGT	CCTTATACTG	5040

CTGCCATCAG TGCGTCCATC GGAGAGGCCA TTGCCTTTTT TACTGGYCTA GTGCCAATGA 5100
GGAATTATCC TCAGGTGGTT TGGGCCAAGC AGAAGGGRC AACTGGCCA CTCTTGGTGG 5160
GTGTGCAGAG GCACATGTGT GAGGACGCGG GCTGTGGTCC KCCCGCTAAT GGTCCCGAAT 5220
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GGTTCACAGC TGCTTACGGC GCTCGGCGGA ACCCACCCTG GGGCGTCGGA GCCTCTTTCT 5880
TGCTGGGCAT GTCATCGAGC CACYTRACTC ACGTCAGACT TGCTGCTGCG TTGCTCCTCG 5940
GCGTCGGGGG TACCGTCCTA GGCACGCCTG CTACTGGGCT TGCTATGGCG GGTGCCTACT 6000
TCGCKGGGGG CAGCGTTACC GCTAACTGGC TGAGTATCAT TGTGGCTCTA ATCGGAGGCT 6060
GGGAGGGGGC RGTKAACGCA GCCTCACTCA CCTTCGAYCT CCTGGCKGGG AAGTTACAAG 6120
CKAGYGAYGC TTGGTGCCTR GTCAGYTGCY TGGCCTCTCC GGGGGCTTCG GTGGCYGGTG 6180
TGGCDCTVGG YCTDYGCTV TGGTCTGTCA ARAAGGGTGT GGGWCARGAY TGGGTTAACA 6240
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GAATCAGGAC TTACCAAATT GGGACTTCTG ACTGGTTTGA GGCTGTGGTC GTGCATGGGA 6780

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CGCCTGCGCT CGTTTACAGG CTAGGCCAGG GCATCAAAAT CGATGGAGCG CGCCGACTGT	6960
TGCCCTGTGA CTTAGCACAG GGAGCGCGCC ACCCCCCGGT ATCTGGCAGT GTTGCCGGTA	7020
GTGGTTGGAC AGATGAGGAC GAGAGGGACT TGGTGAAAC CAAGGCTGCC GCCATCGAGG	7080
CCATTGGGGC GGCCTTGCAC CTCCCTTCAC CGGAGGCTGC TCAGGCCGCT CTAGAGGCTT	7140
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CCATTGAGCC CACGGTCGGA GACGTGGAGG CACTCAAGCT GCGGGCTGCA GACCTGACCG	7320
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TTCACTGTGA CCAAATTGAG GAAACTCCAA CATCTTACTC TTACATCTGG TCAGGGGCGC	7800
CCTTGGGTAC TGGGAGAAGT GTCCCCAAC CCATGACGCG CCCTATAGGG ACCCATCTGA	7860
CTTGTGACAC TACCAAAGTT TATGTTACTG ACCCTGATCG GGCCGCTGAG CGGGCCGAGA	7920
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CTGTCTGAA AAAGGCAGCC GCGACGAAGT CTCATGGCTG GACCTATTCC CAGGCTATAG	8040
CTAAAGTTAG GCGCCGAGCA GCCGCTGGAT ACGGCAGCAA GGTGACCGCC TCCACATTGG	8100
CCACTGGTTG GCCTCACGTG GAGGAGATGC TGGACAAAAT AGCCAGGGGA CAGGAAGTTC	8160
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GATTCATAGT TTTCCACCT TTGGACTTCA GGATAGCTGA AAAGATGATT CTGGGTGACC	8280
CCGGCATCGT TGCAAAGTCA ATTCTGGGTG ACGCTTATCT GTTCCAGTAC ACGCCCAATC	8340
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TGGACGCCAC TTGTTTCGAC TCATCGATTG ATGAGCACGA CATGCAGGTG GAGGCTTCGG	8460
TGTTTGCGGC GGCTAGTGAC AACCCTCAA TGGTACATGC TTTGTGCAAG TACTACTCTG	8520

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GTGGCCCTAT GGTTCCTCCA GATGGGGTTC CCTTGGGGTA CCGCCAGTGT AGGTCGTCGG      8580
GCGTGTTAAC AACTAGCTCG GCGAACAGCA TCACTTGTTA CATTAAGGTC AGCGCGGCCT      8640
GCAGGCGGGT GGGGATTAAG GCACCATCAT TCTTTATAGC TGGAGATGAT TGCTTGATCA      8700
TCTATGAAAA TGATGGAAC TATCCCTGCC CTGCTCTTAA GGCTGCCCTG GCCAACTATG      8760
GATACAGGTG TGAACCAACA AAGCATGCTT CACTGGACAC AGCTGAGTGT TGCTCGGCCT      8820
ACTTGGCTGA GTGCGTAGCT GGGGGTGCCA AGCGCTGGTG GTTGAGCACG GACATGAGGA      8880
AGCCGCTCGC AAGGGCGTCT TCCGAATATT CGGACCCAAT CGGCAGTGCT TTAGGGACCA      8940
TCTTGATGTA TCCCCGGCAT CCAATCGTGC GGTATGTTCT AATACCACAC GTACTAATAA      9000
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GCCTACAAGT CACCACGGAC AGTACGAAGA CTAGGATGGA GGCAGGCTCA GCSTTGCGGG      9180
ATTTAGGAAT GAAATCCCTA GCCTGGCACC GCCGACGTGC CGGAAATGTG CGCACTCGCC      9240
TCCTGAGGGG AGGCAAGGAG TGGGGGCACC TGGCCAGAGC CCTCCTCTGG CAYCCAGGKT      9300
TGAAGGAGCA YCCCCRCCC ATAAATTCAC TTCCAGGTTT TCAGCTGGCG ACGCCTTACG      9360
AACACCATGA AGAGGTCTTG ATCTCGATCA AGAGTCGACC ACCTTGATA AGGTGGATTC      9420
TTGGTGCTTG TCTCTCGTTG CTGGCCGCCT TGCTGTGAAT TCGCTCCAGG CAGTAGGACC      9480
TTCGGGTCGG GGG                                         9493

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(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

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CGT GGG AGT CCG GGG CCC CGG ACC TCC CAC CGA GGT GGG GGG AAA GGG      48
Arg Gly Ser Pro Gly Pro Arg Thr Ser His Arg Gly Gly Gly Lys Gly
  1                      5                      10                      15

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GCC CTG GAC CGG CCG GGT GGA AGG CCC GGA ACC GGT CCA TCT TCC TCA Ala Leu Asp Arg Pro Gly Gly Arg Pro Gly Thr Gly Pro Ser Ser Ser	96
20 25 30	
AGG TTG AGG AAG GGG TAC GTC TAT CGG TCC GGT CGG TCC GAA AGG CGT Arg Leu Arg Lys Gly Tyr Val Tyr Arg Ser Gly Arg Ser Glu Arg Arg	144
35 40 45	
CTG GAT GCC TAG TGT TAG GGT TCG TAG GTG GTA AAT CCC AGC TAG GCG Leu Asp Ala * Cys * Gly Ser * Val Val Asn Pro Ser * Ala	192
50 55 60	
TGA AAG CGC TAT AGG ATA GGC TTA TCC CGG TGA CCG CTG CCC CGG AAC * Lys Arg Tyr Arg Ile Gly Leu Ser Arg * Pro Leu Pro Arg Asn	240
65 70 75 80	
CAG CCC CGC GGC TCT TTG GAC ACG GTC CAC AGG TTG GGG GTA CCG GTG Gln Pro Arg Xaa Ser Leu Asp Thr Val His Arg Leu Gly Val Pro Val	288
85 90 95	
TGA ATA ACC CCC CGA CTG AAG CGT CAG TCG TTA AAC GGA GAC GGT CTC * Ile Thr Pro Arg Leu Lys Arg Gln Ser Leu Asn Gly Asp Gly Leu	336
100 105 110	
CTG AGA TCG CAA CGA CGC CCC ACG TAC GGG AAC GCC GCC AAA ACC TTC Leu Arg Ser Gln Arg Arg Pro Thr Tyr Gly Asn Ala Ala Lys Thr Phe	384
115 120 125	
GGG ACA GCT ATG CGG GTT GAC AAT CCC AGT GGG GGG CCG GGG ACC AGC Gly Thr Ala Met Arg Val Asp Asn Pro Ser Gly Gly Pro Gly Thr Ser	432
130 135 140	
TGA TTA CTT GTC CTG CGA GTT CCT CTT GAG ACT GGC CGA AAG GCA GCC * Leu Leu Val Leu Arg Val Pro Leu Glu Thr Gly Arg Lys Ala Ala	480
145 150 155 160	
ACG GGG CCA CCA AGG CGG CGC AGC GCT GCA TGC GGC AAG GGG AAA AAT Thr Gly Pro Pro Arg Arg Arg Ser Ala Ala Cys Gly Lys Gly Lys Asn	528
165 170 175	
CCT TCG GGT GAC CCC TGG TGG CAA TCC CTT CCC TTA GGA GCA TGA GTG Pro Ser Gly Asp Pro Trp Trp Gln Ser Leu Pro Leu Gly Ala * Val	576
180 185 190	
TGG TCG ACA CAT TCA CCA TGG CTT GGC TGT GGT TGC TGG TTT GCT TCC Trp Ser Thr His Ser Pro Trp Leu Gly Cys Gly Cys Trp Phe Ala Ser	624
195 200 205	
CCC TCG CGG GGG GGG TGC TCT TCA ACT CGC GGC ACC AGT GCT TCA ATG Pro Ser Arg Gly Gly Cys Ser Ser Thr Arg Gly Thr Ser Ala Ser Met	672
210 215 220	
GGG ACC ATT ATG TGC TTT CCA ATT GTT GTT CCC GAG ACG AGG TTT ACT Gly Thr Ile Met Cys Phe Pro Ile Val Val Pro Glu Thr Arg Phe Thr	720
225 230 235 240	
TCT GTT TCG GGG ACG GAT GTC TGG TGG CTT ATG GCT GTA CTG TTT GCA	768

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Ser Val Ser Gly Thr Asp Val Trp Trp Leu Met Ala Val Leu Phe Ala	
245 250 255	
CAC AGT CTT GCT GGA AGC TCT ACC GGC CTG GGG TGG CTA CTC GGC CCG	816
His Ser Leu Ala Gly Ser Ser Thr Gly Leu Gly Trp Leu Leu Gly Pro	
260 265 270	
GGT CCG AAC CAG GTG AGC TGC TGG GGA GAT TTG GGA GTG TAA TTG GTC	864
Gly Pro Asn Gln Val Ser Cys Trp Gly Asp Leu Gly Val * Leu Val	
275 280 285	
CGG TGT CGG CTT CGG CTT ACA CCG CTG GAG TCC TCG GGT TGG GTG AAC	912
Arg Cys Arg Leu Arg Leu Thr Pro Leu Glu Ser Ser Gly Trp Val Asn	
290 295 300	
CTT ACA GTT TGG CCT TCT TGG GGA CGT TCC TCA CCA GTC GCC TCT CAC	960
Leu Thr Val Trp Pro Ser Trp Gly Arg Ser Ser Pro Val Ala Ser His	
305 310 315 320	
GGA TTC CCA ACG TCA CCT GCG TGA AGG CTT GTG ACC TTG AGT TTA CCT	1008
Gly Phe Pro Thr Ser Pro Ala * Arg Leu Val Thr Leu Ser Leu Pro	
325 330 335	
ACC CAG GCT TGT CCA TCG ATT TTG ACT GGG CGT TTA CCA AGA TCT TGC	1056
Thr Gln Ala Cys Pro Ser Ile Leu Thr Gly Arg Leu Pro Arg Ser Cys	
340 345 350	
AGT TGC CGG CCA AGC TGT GGC GAG GCC TAA CGG CRG CWC CGG TCT TGA	1104
Ser Cys Arg Pro Ser Cys Gly Glu Ala * Arg Xaa Xaa Arg Ser *	
355 360 365	
GCC TCC TCG TGA TCC TCA TGC TGG TCC TCG AGC AGC GCC TCC TGA TAG	1152
Ala Ser Ser * Ser Ser Cys Trp Ser Ser Ser Ser Ala Ser * *	
370 375 380	
CCT TCC TAC TGC TTT TGG TAG TGG GCG AGG CTC AGA GGG GGA TGT TCG	1200
Pro Ser Tyr Cys Phe Trp * Trp Ala Arg Leu Arg Gly Gly Cys Ser	
385 390 395 400	
ACA ACT GCG TGT GTG GTT ACT GGG GGG GCA AGA GGC CCC CGT CGG TGA	1248
Thr Thr Ala Cys Val Val Thr Gly Gly Ala Arg Gly Pro Arg Arg *	
405 410 415	
CCC CGC TGT ACC GTG GCA ACG GTA CTG TGG TGT GTG ACT GTG ATT TTG	1296
Pro Arg Cys Thr Val Ala Thr Val Leu Trp Cys Val Thr Val Ile Leu	
420 425 430	
GAA AAA TGC ATT GGG CCC CCC CCT TGT GTT CCG GYC TGG TGT GGC GGG	1344
Glu Lys Cys Ile Gly Pro Pro Cys Val Pro Xaa Trp Cys Gly Gly	
435 440 445	
ACG GTC ATA GGA GGG GCA CCG TGC GCG ACC TCC CCC CGG TTT GCC CCC	1392
Thr Val Ile Gly Gly Ala Pro Cys Ala Thr Ser Pro Arg Phe Ala Pro	
450 455 460	
GGG AGG TTC TCG GCA CGG TGA CAG TCA TGT GTC AGT GGG GTT CTG CCT	1440
Gly Arg Phe Ser Ala Arg * Gln Ser Cys Val Ser Gly Val Leu Pro	
465 470 475 480	

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ACT GGA TTT GGA GAT TTG GGG ACT GGG TTG CAT TGT ACG ACG AGC TAC Thr Gly Phe Gly Asp Leu Gly Thr Gly Leu His Cys Thr Thr Ser Tyr 485 490 495	1488
CAC GAT CAG CTC TCT GTA CTT TCT TCT CAG GTC ATG GTC CAC AAC CTA His Asp Gln Leu Ser Val Leu Ser Ser Gln Val Met Val His Asn Leu 500 505 510	1536
AAG ATC TCT CAG TCT TGA ATC CAT CCG GGG CAC CTT GTG CTT CTT GCG Lys Ile Ser Gln Ser * Ile His Pro Gly His Leu Val Leu Leu Ala 515 520 525	1584
TCG TTG ACC AGA GGC CGC TGA AAT GTG GTT CCT GCG TCC GCG ACT GCT Ser Leu Thr Arg Gly Arg * Asn Val Val Pro Ala Ser Ala Thr Ala 530 535 540	1632
GGG AGA CGG GGG GTC CTG GGT TCG ATG AGT GCG GTG TCG GTA CTC GGA Gly Arg Arg Gly Val Leu Gly Ser Met Ser Ala Val Ser Val Leu Gly 545 550 555 560	1680
TGA CGA AGC ACC TCG AGG CCG TCC TGG TTG ATG GAG GTG TGG AGT CCA * Arg Ser Thr Ser Arg Pro Ser Trp Leu Met Glu Val Trp Ser Pro 565 570 575	1728
AGG TGA CAA CGC CCA AGG GTG AGC GCC CCA AAT ACA TAG GTC AGC ACG Arg * Gln Arg Pro Arg Val Ser Ala Pro Asn Thr * Val Ser Thr 580 585 590	1776
GTG TGG GAA CCT ACT ACG GCG CTG TCC GTA GCC TCA ACA TCA GTT ACC Val Trp Glu Pro Thr Thr Ala Leu Ser Val Ala Ser Thr Ser Val Thr 595 600 605	1824
TAG TGA CTG AGG TGG GGG GCT ATT GGC ATG CGC TGA AGT GCC CGT GCG * * Leu Arg Trp Gly Ala Ile Gly Met Arg * Ser Ala Arg Ala 610 615 620	1872
ACT TTG TGC CCC GAG TGC TCC CAG AAA GAA TTC CAG GTA GGC CTG TGA Thr Leu Cys Pro Glu Cys Ser Gln Lys Glu Phe Gln Val Gly Leu * 625 630 635 640	1920
ATG CAT GTC TAG CTG GGA AGT CTC CGC ACC CGT TCG CAA GTT GGG CTC Met His Val * Leu Gly Ser Leu Arg Thr Arg Ser Gln Val Gly Leu 645 650 655	1968
CCG GTG GGT TTT ACG CCC CCG TGT TCA CCA AGT GCA ACT GGC CGA AGA Pro Val Gly Phe Thr Pro Pro Cys Ser Pro Ser Ala Thr Gly Arg Arg 660 665 670	2016
CCT CCG GAG TGG ATG TGT GTC CTG GGT TTG CTT TCG ATT TCC CTG GTG Pro Pro Glu Trp Met Cys Val Leu Gly Leu Leu Ser Ile Ser Leu Val 675 680 685	2064
ATC ACA ACG GCT TCA TCC ATG TTA AAG GCA ACA GAC AGC AGG TTT ACA Ile Thr Thr Ala Ser Ser Met Leu Lys Ala Thr Asp Ser Arg Phe Thr 690 695 700	2112
GTG GTC AGC GAA GGT CTT CGC CGG CTT GGT TGC TTA CTG ACA TGG TCC Val Val Ser Glu Gly Leu Arg Arg Leu Gly Cys Leu Leu Thr Trp Ser	2160

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705	710	715	720	
TGG CCC TGT TGG TGG TGA TGA AGT TGG CTG AGG CTA GAG TTG TCC CCC				2208
Trp Pro Cys Trp Trp * * Ser Trp Leu Arg Leu Glu Leu Ser Pro				
725		730	735	
TGT TTA TGC TGG CAA TGT GGT GGT GGT TGA ATG GAG CAT CTG CTG CCA				2256
Cys Leu Cys Trp Gln Cys Gly Gly Gly * Met Glu His Leu Leu Pro				
740		745	750	
CTA TTG TCA TCA TAC ACC CTA CTG TCA CGA AGT CCA CTG AAA GTG TTC				2304
Leu Leu Ser Ser Tyr Thr Leu Leu Ser Arg Ser Pro Leu Lys Val Phe				
755		760	765	
CAT TGT GGA CTC CGC CCA CTG TTC CAA CTC CAT CTT GCC CGA ATT CTA				2352
His Cys Gly Leu Arg Pro Leu Phe Gln Leu His Leu Ala Arg Ile Leu				
770	775		780	
CCA CCG GAG TCG CGG ACT CTA CCT ACA ATG CTG GTT GCT ACA TGG TGG				2400
Pro Pro Glu Ser Arg Thr Leu Pro Thr Met Leu Val Ala Thr Trp Trp				
785	790		795	800
CAG GCC TGG CGG CCG GGG CTC AGG CGG TCT GGG GTG CTG CCA ATG ATG				2448
Gln Ala Trp Arg Pro Gly Leu Arg Arg Ser Gly Val Leu Pro Met Met				
805		810		815
GTG CTC AGG CCG TCG TTG GTG GCA TCT GGC CCG CGT GGC TCA AGC TGC				2496
Val Leu Arg Pro Ser Leu Val Ala Ser Gly Pro Arg Gly Ser Ser Cys				
820		825		830
GAA GCT TCG CTG CCG GTC TGG CCT GGT TGT CAA ATG TTG GGG CTT ACT				2544
Glu Ala Ser Leu Pro Val Trp Pro Gly Cys Gln Met Leu Gly Leu Thr				
835	840		845	
TGC CGG TCG TCG AGG CCG CVC TGG CTC CCG AGC TGG TGT GCA CCC CGG				2592
Cys Arg Ser Ser Arg Pro Xaa Trp Leu Pro Ser Trp Cys Ala Pro Arg				
850	855		860	
TGG TCG GCT GGG CAG CCC AGG AGT GGT GGT TCA CTG GTT GTC TGG GTG				2640
Trp Ser Ala Gly Gln Pro Arg Ser Gly Gly Ser Leu Val Val Trp Val				
865	870		875	880
TGA TGT GTG TCG TGG CGT ACC TGA ATG TCC TGG GCT CTG TRA GGG CTG				2688
* Cys Val Ser Trp Arg Thr * Met Ser Trp Ala Leu Xaa Gly Leu				
885		890		895
CCG TGC TTG TGG CGA TGC ACT TCG CAA GGG GTG CTC TGC CGC TGG TAT				2736
Pro Cys Leu Trp Arg Cys Thr Ser Gln Gly Val Leu Cys Arg Trp Tyr				
900		905		910
TGG TGG TAG CTG CCG GGG TRA CCC GGG AGC GGC ACA GCG TCT TAG GGC				2784
Trp Trp * Leu Pro Gly Xaa Pro Gly Ser Gly Thr Ala Ser * Gly				
915		920		925
TTG AGG TGT GCT TCG ATC TGG ATG GTG GAG ACT GGC CRG ACG CCA GTT				2832
Leu Arg Cys Ala Ser Ile Trp Met Val Glu Thr Gly Xaa Thr Pro Val				
930	935		940	

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GGT CTT GGG GTT TAG CAG GCG TGG TGA GCT GGG CCC TCC TGG TGG GGG Gly Leu Gly Val * Gln Ala Trp * Ala Gly Pro Ser Trp Trp Gly 945 950 955 960	2880
GTC TGA TGA CCC ACG GTG GCC GAT CAG CCA GAY TGA CTT GGT AYG CCA Val * * Pro Thr Val Ala Asp Gln Pro Xaa * Leu Gly Xaa Pro 965 970 975	2928
GGT GGG CCG TCA ATT AYC AGA GGG TTC GYC GGT GGG TGA ACA ACT CAC Gly Gly Pro Ser Ile Xaa Arg Gly Phe Xaa Gly Gly * Thr Thr His 980 985 990	2976
CGG TTG GAG CYT TTG GYC GTT GGM GGC GYG CCT GGA AAG CYT GGT TRG Arg Leu Glu Xaa Leu Xaa Val Xaa Gly Xaa Pro Gly Lys Xaa Gly Xaa 995 1000 1005	3024
TKG TGG CTT GGT TCT TCC CCC AGA CAG TTG CCA CAG TYT CCG TCA TCT Xaa Trp Leu Gly Ser Ser Pro Arg Gln Leu Pro Gln Xaa Pro Ser Ser 1010 1015 1020	3072
TCA TAC TCT GTT TGA GCA GTT TAG ATG TCA TTG ATT TCA TCT TGG ARG Ser Tyr Ser Val * Ala Val * Met Ser Leu Ile Ser Ser Trp Xaa 1025 1030 1035 1040	3120
TAC TCT TGG TTA ACT CAC CAA ATC TCG CGC GCT TGG CGC GRG TGC TGG Tyr Ser Trp Leu Thr His Gln Ile Ser Arg Ala Trp Arg Xaa Cys Trp 1045 1050 1055	3168
ACT CCT TAG CTC THG CTG AGG AGC GGC TGG CCT GCT CTT GGC TGG TGG Thr Pro * Leu Xaa Leu Arg Ser Gly Trp Pro Ala Leu Gly Trp Trp 1060 1065 1070	3216
GCG TCC TGC GCA AGC GGG GCG TCC TCC TCT ACG AGC ACG CYG GTC ACA Ala Ser Cys Ala Ser Gly Ala Ser Ser Ser Thr Ser Thr Xaa Val Thr 1075 1080 1085	3264
CTA GCA GGC GCG GTG CTG CCC GCT TGC GAG AGT GGG GYT TTG CGC TYG Leu Ala Gly Ala Val Leu Pro Ala Cys Glu Ser Gly Xaa Leu Arg Xaa 1090 1095 1100	3312
AGC CKG TTA GYA TAA CCA AGG AAG ATT GYG CYA TTG TTC GGG ACT CTG Ser Xaa Leu Xaa * Pro Arg Lys Ile Xaa Xaa Leu Phe Gly Thr Leu 1105 1110 1115 1120	3360
CTC GTG TGT TGG GCT GTG GAC AAT TGG TCC ATG GGA AAC CAG TGG TCG Leu Val Cys Trp Ala Val Asp Asn Trp Ser Met Gly Asn Gln Trp Ser 1125 1130 1135	3408
CGA GGC GAG GCG ACG AGG TGT TGA TCG GCT GTG TGA ACA GTC GGT TCG Arg Gly Glu Ala Thr Arg Cys * Ser Ala Val * Thr Val Gly Ser 1140 1145 1150	3456
ACC TTC CGC CTG GCT TTG TTC CCA CTG CTC CCG TGG TSC TTC ATC ARG Thr Phe Arg Leu Ala Leu Phe Pro Leu Leu Pro Trp Xaa Phe Ile Xaa 1155 1160 1165	3504
CWG GCA ARG GRI TYT TYG GGG TTG TGA AGA CMT CCA TGA CAG GCA AGG Xaa Ala Xaa Xaa Xaa Xaa Gly Leu * Arg Xaa Pro * Gln Ala Arg	3552

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1170	1175	1180	
ACC CGT CCG AAC ACC ACG GRA ACG TGG TGG TCC TWG GGA CTT CAA CAA Thr Arg Pro Asn Thr Thr Xaa Thr Trp Trp Ser Xaa Gly Leu Gln Gln 1185 1190 1195 1200			3600
CKC GTT CCA TGG GCT GCT GCG TGA ACG GAG TAG TGT ACA CRA CAT ACC Xaa Val Pro Trp Ala Ala Ala * Thr Glu * Cys Thr Xaa His Thr 1205 1210 1215			3648
ATG GYA CCA ACG CCC GRC CKA TGG CGG GGC CKT TTG GKC CYG TCA AYG Met Xaa Pro Thr Pro Xaa Xaa Trp Arg Gly Xaa Leu Xaa Xaa Ser Xaa 1220 1225 1230			3696
CTC GGT GGT GGT CWG CGA GYG ACG ACG TCA CGG TYT ACC CGC TCC CWA Leu Gly Gly Gly Xaa Arg Xaa Thr Thr Ser Arg Xaa Thr Arg Ser Xaa 1235 1240 1245			3744
ATG GYG CTT CTT GCC TYC ARG CWT GYA AGT GCC AAC CAA CTG GGG TGT Met Xaa Leu Leu Ala Xaa Xaa Xaa Ser Ala Asn Gln Leu Gly Cys 1250 1255 1260			3792
GGG TGA TCC GGA ATG ACG GAG CTC TTT GCC ATG GAA CTC TCG GCA AGG Gly * Ser Gly Met Thr Glu Leu Phe Ala Met Glu Leu Ser Ala Arg 1265 1270 1275 1280			3840
TGG TGG ATT TAG ATA TGC CCG CTG AGT TGT CAG ACT TTC GCG GGT CTT Trp Trp Ile * Ile Cys Pro Leu Ser Cys Gln Thr Phe Ala Gly Leu 1285 1290 1295			3888
CTG GAT CAC CAA TCT TGT GCG ATG AGG GTC ATG CTG TTG GCA TGC TGA Leu Asp His Gln Ser Cys Ala Met Arg Val Met Leu Leu Ala Cys * 1300 1305 1310			3936
TTT CGG TGC TTC ATA GGG GGA GTA GGG TTT CCT CGG TGC GGT ATA CCA Phe Arg Cys Phe Ile Gly Gly Val Gly Phe Pro Arg Cys Gly Ile Pro 1315 1320 1325			3984
AAC CTT GGG AAA CTC TCC CTC GGG AGA TTG AGG CTC GAT CGG AGG CCC Asn Leu Gly Lys Leu Ser Leu Gly Arg Leu Arg Leu Asp Arg Arg Pro 1330 1335 1340			4032
CCC CTG TGC CAG GAA CCA CTG GAT ACA GGG AGG CGC CAC TGT TCC TGC Pro Leu Cys Gln Glu Pro Leu Asp Thr Gly Arg Arg His Cys Ser Cys 1345 1350 1355 1360			4080
CCA CCG GAG CTG GCA AGT CGA CGC GCG TGC CGA ATG AGT ACG TCA AGG Pro Pro Glu Leu Ala Ser Arg Arg Ala Cys Arg Met Ser Thr Ser Arg 1365 1370 1375			4128
CTG GAC ACA ARG TGC TTG TAC TAA ACC CAT CCA TTG CCA CAG TGA GGG Leu Asp Thr Xaa Cys Leu Tyr * Thr His Pro Leu Pro Gln * Gly 1380 1385 1390			4176
CCA TGG GCC CTT ACA TGG AAA AGT TAA CCG GCA AAC ATC CGT CGG TGT Pro Trp Ala Leu Thr Trp Lys Ser * Pro Ala Asn Ile Arg Arg Cys 1395 1400 1405			4224

300

ACT GTG GCC ATG ACA CTA CTG CAT ATT CCA GGA CTA CTG ACT CAT CTT Thr Val Ala Met Thr Leu Leu His Ile Pro Gly Leu Leu Thr His Leu 1410 1415 1420	4272
TGA CCT ACT GTA CAT ACG GCA GGT TTA TGG CCA ATC CCA GGA AAT ACT * Pro Thr Val His Thr Ala Gly Leu Trp Pro Ile Pro Gly Asn Thr 1425 1430 1435 1440	4320
TGC GGG GGA ACG ACG TCG TAA TTT GCG ACG AGT TGC ACG TCA CCG ACC Cys Gly Gly Thr Thr Ser * Phe Ala Thr Ser Cys Thr Ser Pro Thr 1445 1450 1455	4368
CGA CCT CAA TTT TGG GGA TGG GTC GGG CGA GGT TAC TCG CTC GCG AGT Arg Pro Gln Phe Trp Gly Trp Val Gly Arg Gly Tyr Ser Leu Ala Ser 1460 1465 1470	4416
GCG GCG TAC GCC TCC TGC TTT TCG CTA CGG CGA CCC CAC CGG TCT CTC Ala Ala Tyr Ala Ser Cys Phe Ser Leu Arg Arg Pro His Arg Ser Leu 1475 1480 1485	4464
CGA TGG CGA AGC ATG AAT CTA TTC ATG AGG AGA TGT TGG GCA GTG AGG Arg Trp Arg Ser Met Asn Leu Phe Met Arg Arg Cys Trp Ala Val Arg 1490 1495 1500	4512
GGG AGG TCC CCT TCT ATT GCC AAT TCC TCC CAC TGA GTA GGT ATG CTA Gly Arg Ser Pro Ser Ile Ala Asn Ser Ser His * Val Gly Met Leu 1505 1510 1515 1520	4560
CTG GGA GAC ACC TGC TGT TTT GTC ATT CCA AGG TAG ART GCA CTA GGT Leu Gly Asp Thr Cys Cys Phe Val Ile Pro Arg * Xaa Ala Leu Gly 1525 1530 1535	4608
TAT CCT CAG CTT TGG CCA GCT TTG GTG TCA ACA CCG TTG TGT ACT TCA Tyr Pro Gln Leu Trp Pro Ala Leu Val Ser Thr Pro Leu Cys Thr Ser 1540 1545 1550	4656
GAG GCA AAG AAA CTG ACA TTC CAA CTG GTG ACG TGT GCG TTT GCG CCA Glu Ala Lys Lys Leu Thr Phe Gln Leu Val Thr Cys Ala Phe Ala Pro 1555 1560 1565	4704
CAG ACG CAC TTT CCA CTG GTT ACA CTG GCA ATT TTG ACA CCG TAA CAG Gln Thr His Phe Pro Leu Val Thr Leu Ala Ile Leu Thr Pro * Gln 1570 1575 1580	4752
ACT GTG GTT TAA TGG TTG AGG AGG TAG TGG AAG TGA CCC TGG ACC CGA Thr Val Val * Trp Leu Arg Arg * Trp Lys * Pro Trp Thr Arg 1585 1590 1595 1600	4800
CCA TCA CTA TCG GTG TGA AGA CCG TCC CGG CCC CTG CCG AAC TGA GGG Pro Ser Leu Ser Val * Arg Pro Ser Arg Pro Leu Pro Asn * Gly 1605 1610 1615	4848
CTC AGA GGC GTG GTA GGT GTG GCC GTG GGA AAG CGG GCA CTT ACT ATC Leu Arg Gly Val Val Gly Val Ala Val Gly Lys Arg Ala Leu Thr Ile 1620 1625 1630	4896
AGG CAT TGA TGT CTT CGG CGC CGG CGG GAA CSG TTC GGT CTG GGG CTC	4944

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Arg His * Cys Leu Arg Arg Arg Arg Glu Xaa Phe Gly Leu Gly Leu	
1635 1640 1645	
TCT GGG CAG CTG TTG AGG CTG GHG TCT CGT GGT ATG GCC TAG AGC CCG	4992
Ser Gly Gln Leu Leu Arg Leu Xaa Ser Arg Gly Met Ala * Ser Pro	
1650 1655 1660	
ATG CTA TTG GAG ACC TGC TTA GGG CCT ACG ACT CGT GTC CTT ATA CTG	5040
Met Leu Leu Glu Thr Cys Leu Gly Pro Thr Thr Arg Val Leu Ile Leu	
1665 1670 1675 1680	
CTG CCA TCA GTG CGT CCA TCG GAG AGG CCA TTG CCT TTT TTA CTG GYC	5088
Leu Pro Ser Val Arg Pro Ser Glu Arg Pro Leu Pro Phe Leu Leu Xaa	
1685 1690 1695	
TAG TGC CAA TGA GGA ATT ATC CTC AGG TGG TTT GGG CCA AGC AGA AGG	5136
* Cys Gln * Gly Ile Ile Leu Arg Trp Phe Gly Pro Ser Arg Arg	
1700 1705 1710	
GRC ACA ACT GGC CAC TCT TGG TGG GTG TGC AGA GGC ACA TGT GTG AGG	5184
Xaa Thr Thr Gly His Ser Trp Trp Val Cys Arg Gly Thr Cys Val Arg	
1715 1720 1725	
ACG CGG GCT GTG GTC CKC CCG CTA ATG GTC CCG AAT GGA GCG GCA TCA	5232
Thr Arg Ala Val Val Xaa Pro Leu Met Val Pro Asn Gly Ala Ala Ser	
1730 1735 1740	
GGG GAA AAG GGC CTG TTC CCC TGT TGT GCC GAT GGG GTG GTG ACT TGC	5280
Gly Glu Lys Gly Leu Phe Pro Cys Cys Ala Asp Gly Val Val Thr Cys	
1745 1750 1755 1760	
CTG AGT CGG TGG CTC CGC ATC ACT GGG TTG ATG ACC TAC AGG CCC GGC	5328
Leu Ser Arg Trp Leu Arg Ile Thr Gly Leu Met Thr Tyr Arg Pro Gly	
1765 1770 1775	
TCG GTG TGG CCG AGG GTT ACA CTC CCT GCA TTG CTG GAC CGG TGC TTT	5376
Ser Val Trp Pro Arg Val Thr Leu Pro Ala Leu Leu Asp Arg Cys Phe	
1780 1785 1790	
TGG TCG GTT TGG CGA TGG CGG GGG GGG CTA TCC TGG CAC ACT GGA CGG	5424
Trp Ser Val Trp Arg Trp Arg Gly Gly Leu Ser Trp His Thr Gly Arg	
1795 1800 1805	
GGT CTC TGG TTG TAG TGA CCA GTT GGG TTG TCA ATG GGA ACG GTA ACC	5472
Gly Leu Trp Leu * * Pro Val Gly Leu Ser Met Gly Thr Val Thr	
1810 1815 1820	
CGC TGA TAC AAA GCG CCT CTA GGG GCG TGG CKA CYA GCG GTC CAT ACC	5520
Arg * Tyr Lys Ala Pro Leu Gly Ala Trp Xaa Xaa Ala Val His Thr	
1825 1830 1835 1840	
CAG TAC CCC CAG ATG GTG GTG AAC GGT ACC CAT CAG ACA TCA AGC CAA	5568
Gln Tyr Pro Gln Met Val Val Asn Gly Thr His Gln Thr Ser Ser Gln	
1845 1850 1855	
TYA CTG AGG CTG TGA CCA CCC TTG AGA CTG CGT GCG GYT GGG GCC CAG	5616
Xaa Leu Arg Leu * Pro Pro Leu Arg Leu Arg Ala Xaa Gly Ala Gln	
1860 1865 1870	

302

CCG CGG CBA GTC TGG CTT ATG TGA AGG CCT GTG AAA CTG GAA CCA TGT Pro Arg Xaa Val Trp Leu Met * Arg Pro Val Lys Leu Glu Pro Cys 1875 1880 1885	5664
TGG CTG ACA ARG CGA GTG CTG CGT GGC AGG CTT GGG CTG CAA ACA ACT Trp Leu Thr Xaa Arg Val Leu Arg Gly Arg Leu Gly Leu Gln Thr Thr 1890 1895 1900	5712
TTG TGC CTC CAC CAG CAT CAC ACT CAA CTT CCT TGT TRC AGA GCT TGG Leu Cys Leu His Gln His His Thr Gln Leu Pro Cys Xaa Arg Ala Trp 1905 1910 1915 1920	5760
AYG CTG CGT TCA CTT CAG CTT GGG ATA GCG TGT TCA CTC ACG GCC GTT Xaa Leu Arg Ser Leu Gln Leu Gly Ile Ala Cys Ser Leu Thr Ala Val 1925 1930 1935	5808
CCT TGC TTG TTG GGT TCA CAG CTG CTT ACG GCG CTC GGC GGA ACC CAC Pro Cys Leu Leu Gly Ser Gln Leu Leu Thr Ala Leu Gly Gly Thr His 1940 1945 1950	5856
CGC TGG GCG TCG GAG CCT CTT TCT TGC TGG GCA TGT CAT CGA GCC ACY Arg Trp Ala Ser Glu Pro Leu Ser Cys Trp Ala Cys His Arg Ala Xaa 1955 1960 1965	5904
TRA CTC ACG TCA GAC TTG CTG CTG CGT TGC TCC TCG GCG TCG GGG GTA Xaa Leu Thr Ser Asp Leu Leu Leu Arg Cys Ser Ser Ala Ser Gly Val 1970 1975 1980	5952
CCG TCC TAG GCA CGC CTG CTA CTG GGC TTG CTA TGG CGG GTG CCT ACT Pro Ser * Ala Arg Leu Leu Leu Gly Leu Leu Trp Arg Val Pro Thr 1985 1990 1995 2000	6000
TCG CKG GGG GCA GCG TTA CCG CTA ACT GGC TGA GTA TCA TTG TGG CTC Ser Xaa Gly Ala Ala Leu Pro Leu Thr Gly * Val Ser Leu Trp Leu 2005 2010 2015	6048
TAA TCG GAG GCT GGG AGG GGG CRG TKA ACG CAG CCT CAC TCA CCT TCG * Ser Glu Ala Gly Arg Gly Xaa Xaa Thr Gln Pro His Ser Pro Ser 2020 2025 2030	6096
AYC TCC TGG CKG GGA AGT TAC AAG CKA GYG AYG CTT GGT GCC TRG TCA Xaa Ser Trp Xaa Gly Ser Tyr Lys Xaa Xaa Xaa Leu Gly Ala Xaa Ser 2035 2040 2045	6144
GYT GCY TGG CCT CTC CGG GGG CTT CGG TGG CYG GTG TGG CDC TVG GYC Xaa Xaa Trp Pro Leu Arg Gly Leu Arg Trp Xaa Val Trp Xaa Xaa Xaa 2050 2055 2060	6192
TDY TGC TGT GGT CTG TCA ARA AGG GTG TGG GWC ARG AYT GGG TTA ACA Xaa Cys Xaa Gly Leu Ser Xaa Arg Val Trp Xaa Xaa Xaa Gly Leu Thr 2065 2070 2075 2080	6240
GAY TGT TGA CGA TGA TGC CAC GCA GTT CGG TGA TGC CTG ACG ATT TCT Xaa Cys * Arg * Cys His Ala Val Arg * Cys Leu Thr Ile Ser 2085 2090 2095	6288
TCC TCA AAG ATG AGT TCG TCA CCA AGG TGT CTA CTG TCC TGC GAA AGT	6336

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Ser Ser Lys Met Ser Ser Ser Pro Arg Cys Leu Leu Ser Cys Glu Ser	
2100 2105 2110	
TGT CAT TGT CAA GAT GGA TCA TGA CTC TTG TGG ACA AGC GGG AGA TGG	6384
Cys His Cys Gln Asp Gly Ser * Leu Leu Trp Thr Ser Gly Arg Trp	
2115 2120 2125	
AGA TGG AGA CMC CCG CTT CTC AGA TTG TTT GGG ACT TGC TTG ACT GGT	6432
Arg Trp Arg Xaa Pro Leu Leu Arg Leu Phe Gly Thr Cys Leu Thr Gly	
2130 2135 2140	
GCA TCC GGC TRG GTC GGT TCC TGT ACA ATA AAC TYA TGT TTG CTC TCC	6480
Ala Ser Gly Xaa Val Gly Ser Cys Thr Ile Asn Xaa Cys Leu Leu Ser	
2145 2150 2155 2160	
CTA GGT TGC GCC TGC CGC TTA TCG GTT GCA GTA CCG GTT GGG GTG GCC	6528
Leu Gly Cys Ala Cys Arg Leu Ser Val Ala Val Pro Val Gly Val Ala	
2165 2170 2175	
CGT GGG AGG GCA ATG GTC ATT TGG AAA CAA GGT GTA CTT GTG GCT GTG	6576
Arg Gly Arg Ala Met Val Ile Trp Lys Gln Gly Val Leu Val Ala Val	
2180 2185 2190	
TGA TTA CCG GTG ATA TTC ACG ATG GTA TAT TGC ACG ACC TAC ATT ATA	6624
* Leu Pro Val Ile Phe Thr Met Val Tyr Cys Thr Thr Tyr Ile Ile	
2195 2200 2205	
CCT CCC TAC TGT GCA GAC ATT ACT ACA AGA GGA CAG TGC CTG TTG GCG	6672
Pro Pro Tyr Cys Ala Asp Ile Thr Thr Arg Gly Gln Cys Leu Leu Ala	
2210 2215 2220	
TCA TGG GCA ATG CTG AGG GAG CAG TCC CCC TTG TGC CTA CTG GCG GTG	6720
Ser Trp Ala Met Leu Arg Glu Gln Ser Pro Leu Cys Leu Leu Ala Val	
2225 2230 2235 2240	
GAA TCA GGA CTT ACC AAA TTG GGA CTT CTG ACT GGT TTG AGG CTG TGG	6768
Glu Ser Gly Leu Thr Lys Leu Gly Leu Leu Thr Gly Leu Arg Leu Trp	
2245 2250 2255	
TCG TGC ATG GGA CAA TCA CGG TGC ACG CCA CCA GTT GCT ATG AGT TGA	6816
Ser Cys Met Gly Gln Ser Arg Cys Thr Pro Pro Val Ala Met Ser *	
2260 2265 2270	
AAG CTG CTG ACG TTC GGA GGG CGG TGC GAG CCG GCC CGA CTT ACG TTG	6864
Lys Leu Leu Thr Phe Gly Gly Arg Cys Glu Pro Ala Arg Leu Thr Leu	
2275 2280 2285	
GTG GCG TAC CTT GCA GCT GGA GCG CGC CGT GTA CTG CGC CTG CGC TCG	6912
Val Ala Tyr Leu Ala Ala Gly Ala Arg Arg Val Leu Arg Leu Arg Ser	
2290 2295 2300	
TTT ACA GGC TAG GCC AGG GCA TCA AAA TCG ATG GAG CGC GCC GAC TGT	6960
Phe Thr Gly * Ala Arg Ala Ser Lys Ser Met Glu Arg Ala Asp Cys	
2305 2310 2315 2320	
TGC CCT GTG ACT TAG CAC AGG GAG CGC GCC ACC CCC CGG TAT CTG GCA	7008
Cys Pro Val Thr * His Arg Glu Arg Ala Thr Pro Arg Tyr Leu Ala	

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2325	2330	2335	
GTG TTG CCG GTA GTG GTT GGA CAG ATG AGG ACG AGA GGG ACT TGG TGG Val Leu Pro Val Val Val Gly Gln Met Arg Thr Arg Gly Thr Trp Trp 2340 2345 2350			7056
AAA CCA AGG CTG CCG CCA TCG AGG CCA TTG GGG CGG CCT TGC ACC TCC Lys Pro Arg Leu Pro Pro Ser Arg Pro Leu Gly Arg Pro Cys Thr Ser 2355 2360 2365			7104
CTT CAC CGG AGG CTG CTC AGG CCG CTC TAG AGG CTT TGG AGG AGG CTG Leu His Arg Arg Leu Leu Arg Pro Leu * Arg Leu Trp Arg Arg Leu 2370 2375 2380			7152
CCG TGT CCC TGT TGC CCC ATG TGC CCG TCA TTA TGG GTG ATG ACT GTT Pro Cys Pro Cys Cys Pro Met Cys Pro Ser Leu Trp Val Met Thr Val 2385 2390 2395 2400			7200
CAT GCC GGG ATG AGG CGT TCC AAG GCC ACT TCA TCC CAG AAC CCA ATG His Ala Gly Met Arg Arg Ser Lys Ala Thr Ser Ser Gln Asn Pro Met 2405 2410 2415			7248
TGA CAG AGG TAC CCA TTG AGC CCA CGG TCG GAG ACG TGG AGG CAC TCA * Gln Arg Tyr Pro Leu Ser Pro Arg Ser Glu Thr Trp Arg His Ser 2420 2425 2430			7296
AGC TGC GGG CTG CAG ACC TGA CCG CCA GGT TGC AAG ACT TGG AGG CCA Ser Cys Gly Leu Gln Thr * Pro Pro Gly Cys Lys Thr Trp Arg Pro 2435 2440 2445			7344
TGG CTC TCG CCC GCG CTG AGT CAA TCG AGG ATG CTC GCG CAG CTT CGA Trp Leu Ser Pro Ala Leu Ser Gln Ser Arg Met Leu Ala Gln Leu Arg 2450 2455 2460			7392
TGC CTT CGC TCA CCG AGG TGG ACT CAA TGC CAT CAT TGG AGT CGA GCC Cys Leu Arg Ser Pro Arg Trp Thr Gln Cys His His Trp Ser Arg Ala 2465 2470 2475 2480			7440
CTT GCT CCT CCT TTG AAC AAA TCT CTT TAA CTG AAA GTG ACC CTG AGA Leu Ala Pro Pro Leu Asn Lys Ser Leu * Leu Lys Val Thr Leu Arg 2485 2490 2495			7488
CTG TCG TCG AGG CTG GCT TAC CCT TGG AGT TCG TGA ACT CCA ACA CCG Leu Ser Ser Arg Leu Ala Tyr Pro Trp Ser Ser * Thr Pro Thr Pro 2500 2505 2510			7536
GGC CGT CTC CGG CTC GGA GGA TTG TCA GAA TCC GAC AGG CTT GCT GTT Gly Arg Leu Arg Leu Gly Gly Leu Ser Glu Ser Asp Arg Leu Ala Val 2515 2520 2525			7584
GTG ACA GAT CCA CAA TGA AGG CCA TGC CGT TGT CGT TCA CTG TCG GGG Val Thr Asp Pro Gln * Arg Pro Cys Arg Cys Arg Ser Leu Ser Gly 2530 2535 2540			7632
AGT GCC TCT TCG TTA CTC GCT ATG ACC CGG ACG GTC ACC AAC TGT TTG Ser Ala Ser Ser Leu Leu Ala Met Thr Arg Thr Val Thr Asn Cys Leu 2545 2550 2555 2560			7680

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ACG AGC GAG GTC CGA TAG AGG TAT CTA CTC CTA TAT GTG AAG TGA TTG	7728
Thr Ser Glu Val Arg * Arg Tyr Leu Leu Leu Tyr Val Lys * Leu	
2565 2570 2575	
GGG ACA TCA GGC TTC AGT GTG ACC AAA TTG AGG AAA CTC CAA CAT CTT	7776
Gly Thr Ser Gly Phe Ser Val Thr Lys Leu Arg Lys Leu Gln His Leu	
2580 2585 2590	
ACT CTT ACA TCT GGT CAG GGG CGC CCT TGG GTA CTG GGA GAA GTG TCC	7824
Thr Leu Thr Ser Gly Gln Gly Arg Pro Trp Val Leu Gly Glu Val Ser	
2595 2600 2605	
CCC AAC CCA TGA CGC GCC CTA TAG GGA CCC ATC TGA CTT GTG ACA CTA	7872
Pro Asn Pro * Arg Ala Leu * Gly Pro Ile * Leu Val Thr Leu	
2610 2615 2620	
CCA AAG TTT ATG TTA CTG ACC CTG ATC GGG CCG CTG AGC GGG CCG AGA	7920
Pro Lys Phe Met Leu Leu Thr Leu Ile Gly Pro Leu Ser Gly Pro Arg	
2625 2630 2635 2640	
AGG TTA CAA TCT GGA GGG GTG ATA GGA AGT ATG ACA AGC ATT ATG AGG	7968
Arg Leu Gln Ser Gly Gly Val Ile Gly Ser Met Thr Ser Ile Met Arg	
2645 2650 2655	
CTG TCG TTG AGG CTG TCC TGA AAA AGG CAG CCG CGA CGA AGT CTC ATG	8016
Leu Ser Leu Arg Leu Ser * Lys Arg Gln Pro Arg Arg Ser Leu Met	
2660 2665 2670	
GCT GGA CCT ATT CCC AGG CTA TAG CTA AAG TTA GGC GCC GAG CAG CCG	8064
Ala Gly Pro Ile Pro Arg Leu * Leu Lys Leu Gly Ala Glu Gln Pro	
2675 2680 2685	
CTG GAT ACG GCA GCA AGG TGA CCG CCT CCA CAT TGG CCA CTG GTT GGC	8112
Leu Asp Thr Ala Ala Arg * Pro Pro Pro His Trp Pro Leu Val Gly	
2690 2695 2700	
CTC ACG TGG AGG AGA TGC TGG ACA AAA TAG CCA GGG GAC AGG AAG TTC	8160
Leu Thr Trp Arg Arg Cys Trp Thr Lys * Pro Gly Asp Arg Lys Phe	
2705 2710 2715 2720	
CTT TCA CTT TTG TGA CCA AGC GAG AGG TTT TCT TCT CCA AAA CTA CCC	8208
Leu Ser Leu Leu * Pro Ser Glu Arg Phe Ser Ser Pro Lys Leu Pro	
2725 2730 2735	
GTA AGC CCC CAA GAT TCA TAG TTT TCC CAC CTT TGG ACT TCA GGA TAG	8256
Val Ser Pro Gln Asp Ser * Phe Ser His Leu Trp Thr Ser Gly *	
2740 2745 2750	
CTG AAA AGA TGA TTC TGG GTG ACC CCG GCA TCG TTG CAA AGT CAA TTC	8304
Leu Lys Arg * Phe Trp Val Thr Pro Ala Ser Leu Gln Ser Gln Phe	
2755 2760 2765	
TGG GTG ACG CTT ATC TGT TCC AGT ACA CGC CCA ATC AGA GGG TCA AAG	8352
Trp Val Thr Leu Ile Cys Ser Ser Thr Arg Pro Ile Arg Gly Ser Lys	
2770 2775 2780	
CTC TGG TTA AGG CGT GGG AGG GGA AGT TGC ATC CCG CTG CGA TCA CTG	8400
Leu Trp Leu Arg Arg Gly Arg Gly Ser Cys Ile Pro Leu Arg Ser Leu	

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2785	2790	2795	2800	
TGG ACG CCA CTT GTT TCG ACT CAT CGA TTG ATG AGC ACG ACA TGC AGG				8448
Trp Thr Pro Leu Val Ser Thr His Arg Leu Met Ser Thr Thr Cys Arg				
2805		2810	2815	
TGG AGG CTT CGG TGT TTG CGG CGG CTA GTG ACA ACC CCT CAA TGG TAC				8496
Trp Arg Leu Arg Cys Leu Arg Arg Leu Val Thr Thr Pro Gln Trp Tyr				
2820	2825		2830	
ATG CTT TGT GCA AGT ACT ACT CTG GTG GCC CTA TGG TTT CCC CAG ATG				8544
Met Leu Cys Ala Ser Thr Thr Leu Val Ala Leu Trp Phe Pro Gln Met				
2835	2840		2845	
GGG TTC CCT TGG GGT ACC GCC AGT GTA GGT CGT CGG GCG TGT TAA CAA				8592
Gly Phe Pro Trp Gly Thr Ala Ser Val Gly Arg Arg Ala Cys * Gln				
2850	2855		2860	
CTA GCT CGG CGA ACA GCA TCA CTT GTT ACA TTA AGG TCA GCG CGG CCT				8640
Leu Ala Arg Arg Thr Ala Ser Leu Val Thr Leu Arg Ser Ala Arg Pro				
2865	2870	2875	2880	
GCA GGC GGG TGG GGA TTA AGG CAC CAT CAT TCT TTA TAG CTG GAG ATG				8688
Ala Gly Gly Trp Gly Leu Arg His His His Ser Leu * Leu Glu Met				
2885	2890		2895	
ATT GCT TGA TCA TCT ATG AAA ATG ATG GAA CTG ATC CCT GCC CTG CTC				8736
Ile Ala * Ser Ser Met Lys Met Met Glu Leu Ile Pro Ala Leu Leu				
2900	2905		2910	
TTA AGG CTG CCC TGG CCA ACT ATG GAT ACA GGT GTG AAC CAA CAA AGC				8784
Leu Arg Leu Pro Trp Pro Thr Met Asp Thr Gly Val Asn Gln Gln Ser				
2915	2920		2925	
ATG CTT CAC TGG ACA CAG CTG AGT GTT GCT CGG CCT ACT TGG CTG AGT				8832
Met Leu His Trp Thr Gln Leu Ser Val Ala Arg Pro Thr Trp Leu Ser				
2930	2935		2940	
GCG TAG CTG GGG GTG CCA AGC GCT GGT GGT TGA GCA CGG ACA TGA GGA				8880
Ala * Leu Gly Val Pro Ser Ala Gly Gly * Ala Arg Thr * Gly				
2945	2950	2955	2960	
AGC CGC TCG CAA GGG CGT CTT CCG AAT ATT CGG ACC CAA TCG GCA GTG				8928
Ser Arg Ser Gln Gly Arg Leu Pro Asn Ile Arg Thr Gln Ser Ala Val				
2965	2970		2975	
CTT TAG GGA CCA TCT TGA TGT ATC CCC GGC ATC CAA TCG TGC GGT ATG				8976
Leu * Gly Pro Ser * Cys Ile Pro Gly Ile Gln Ser Cys Gly Met				
2980	2985		2990	
TTC TAA TAC CAC ACG TAC TAA TAA TGG CTT ACA GGA GTG GCA GCA CAC				9024
Phe * Tyr His Thr Tyr * * Trp Leu Thr Gly Val Ala Ala His				
2995	3000		3005	
CGG ATG AGT TGG TTA TGT GTC AGG TTC AGG GAA ATC ATT ACT CTT TCC				9072
Arg Met Ser Trp Leu Cys Val Arg Phe Arg Glu Ile Ile Thr Leu Ser				
3010	3015		3020	

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

BNSDOCID: <WO__9521922A2_I_>

308

50

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Val Val Asn Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Lys Arg Tyr Arg Ile Gly Leu Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Leu Pro Arg Asn Gln Pro Arg Xaa Ser Leu Asp Thr Val His Arg
1 5 10 15

Leu Gly Val Pro Val
20

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

309

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Ile Thr Pro Arg Leu Lys Arg Gln Ser Leu Asn Gly Asp Gly Leu Leu
 1 5 10 15

Arg Ser Gln Arg Arg Pro Thr Tyr Gly Asn Ala Ala Lys Thr Phe Gly
 20 25 30

Thr Ala Met Arg Val Asp Asn Pro Ser Gly Gly Pro Gly Thr Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Leu Leu Val Leu Arg Val Pro Leu Glu Thr Gly Arg Lys Ala Ala Thr
 1 5 10 15

Gly Pro Pro Arg Arg Arg Ser Ala Ala Cys Gly Lys Gly Lys Asn Pro
 20 25 25

Ser Gly Asp Pro Trp Trp Gln Ser Leu Pro Leu Gly Ala
 30 35 40

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Val Trp Ser Thr His Ser Pro Trp Leu Gly Cys Gly Cys Trp Phe Ala
 1 5 10 15

Ser Pro Ser Arg Gly Gly Cys Ser Ser Thr Arg Gly Thr Ser Ala Ser
 20 25 30

310

Met Gly Thr Ile Met Cys Phe Pro Ile Val Val Pro Glu Thr Arg Phe
 35 40 45

Thr Ser Val Ser Gly Thr Asp Val Trp Trp Leu Met Ala Val Leu Phe
 50 55 60

Ala His Ser Leu Ala Gly Ser Ser Thr Gly Leu Gly Trp Leu Leu Gly
 65 70 75 80

Pro Gly Pro Asn Gln Val Ser Cys Trp Gly Asp Leu Gly Val
 85 90

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Leu Val Arg Cys Arg Leu Arg Leu Thr Pro Leu Glu Ser Ser Gly Trp
 1 5 10 15

Val Asn Leu Thr Val Trp Pro Ser Trp Gly Arg Ser Ser Pro Val Ala
 20 25 30

Ser His Gly Phe Pro Thr Ser Pro Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Arg Leu Val Thr Leu Ser Leu Pro Thr Gln Ala Cys Pro Ser Ile Leu
 1 5 10 15

Thr Gly Arg Leu Pro Arg Ser Cys Ser Cys Arg Pro Ser Cys Gly Glu
 20 25 30

Ala

311

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Arg Xaa Xaa Arg Ser
1 5

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Ser Ser Cys Trp Ser Ser Ser Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Ser Tyr Cys Phe Trp
1 5

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

312

Trp Ala Arg Leu Arg Gly Gly Cys Ser Thr Thr Ala Cys Val Val Thr
 1 5 10 15

Gly Gly Ala Arg Gly Pro Arg Arg
 20

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Pro Arg Cys Thr Val Ala Thr Val Leu Trp Cys Val Thr Val Ile Leu
 1 5 10 15

Glu Lys Cys Ile Gly Pro Pro Pro Cys Val Pro Xaa Trp Cys Gly Gly
 20 25 30

Thr Val Ile Gly Gly Ala Pro Cys Ala Thr Ser Pro Arg Phe Ala Pro
 35 40 45

Gly Arg Phe Ser Ala Arg
 50

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Gln Ser Cys Val Ser Gly Val Leu Pro Thr Gly Phe Gly Asp Leu Gly
 1 5 10 15

Thr Gly Leu His Cys Thr Thr Ser Tyr His Asp Gln Leu Ser Val Leu
 20 25 30

Ser Ser Gln Val Met Val His Asn Leu Lys Ile Ser Gln Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

313

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Ile His Pro Gly His Leu Val Leu Leu Ala Ser Leu Thr Arg Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Asn Val Val Pro Ala Ser Ala Thr Ala Gly Arg Arg Gly Val Leu Gly
1 5 10 15

Ser Met Ser Ala Val Ser Val Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Arg Ser Thr Ser Arg Pro Ser Trp Leu Met Glu Val Trp Ser Pro Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

314

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Gln Arg Pro Arg Val Ser Ala Pro Asn Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Val Ser Thr Val Trp Glu Pro Thr Thr Ala Leu Ser Val Ala Ser Thr
1 5 10 15

Ser Val Thr

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Leu Arg Trp Gly Ala Ile Gly Met Arg
1 5

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Ser Ala Arg Ala Thr Leu Cys Pro Glu Cys Ser Gln Lys Glu Phe Gln
1 5 10 15

315

Val Gly Leu

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met His Val

1

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Leu Gly Ser Leu Arg Thr Arg Ser Gln Val Gly Leu Pro Val Gly Phe
 1 5 10 15

Thr Pro Pro Cys Ser Pro Ser Ala Thr Gly Arg Arg Pro Pro Glu Trp
 20 25 30

Met Cys Val Leu Gly Leu Leu Ser Ile Ser Leu Val Ile Thr Thr Ala
 35 40 45

Ser Ser Met Leu Lys Ala Thr Asp Ser Arg Phe Thr Val Val Ser Glu
 50 55 60

Gly Leu Arg Arg Leu Gly Cys Leu Leu Thr Trp Ser Trp Pro Cys Trp
 65 70 75 80

Trp

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Ser Trp Leu Arg Leu Glu Leu Ser Pro Cys Leu Cys Trp Gln Cys Gly
 1 5 10 15

Gly Gly

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Glu His Leu Leu Pro Leu Leu Ser Ser Tyr Thr Leu Leu Ser Arg
 1 5 10 15

Ser Pro Leu Lys Val Phe His Cys Gly Leu Arg Pro Leu Phe Gln Leu
 20 25 30

His Leu Ala Arg Ile Leu Pro Pro Glu Ser Arg Thr Leu Pro Thr Met
 35 40 45

Leu Val Ala Thr Trp Trp Gln Ala Trp Arg Pro Gly Leu Arg Arg Ser
 50 55 60

Gly Val Leu Pro Met Met Val Leu Arg Pro Ser Leu Val Ala Ser Gly
 65 70 75 80

Pro Arg Gly Ser Ser Cys Glu Ala Ser Leu Pro Val Trp Pro Gly Cys
 85 90 95

Gln Met Leu Gly Leu Thr Cys Arg Ser Ser Arg Pro Xaa Trp Leu Pro
 100 105 110

Ser Trp Cys Ala Pro Arg Trp Ser Ala Gly Gln Pro Arg Ser Gly Gly
 115 120 125

Ser Leu Val Val Trp Val
 130

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Cys Val Ser Trp Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met Ser Trp Ala Leu Xaa Gly Leu Pro Cys Leu Trp Arg Cys Thr Ser
1 5 10 15
Gln Gly Val Leu Cys Arg Trp Tyr Trp Trp
20 25

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu Pro Gly Xaa Pro Gly Ser Gly Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Gly Leu Arg Cys Ala Ser Ile Trp Met Val Glu Thr Gly Xaa Thr Pro
1 5 10 15
Val Gly Leu Gly Val
20

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Ala Gly Pro Ser Trp Trp Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Pro Thr Val Ala Asp Gln Pro Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Leu Gly Xaa Pro Gly Gly Pro Ser Ile Xaa Arg Gly Phe Xaa Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

319

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Thr Thr His Arg Leu Glu Xaa Leu Xaa Val Xaa Gly Xaa Pro Gly Lys
 1 5 10 15
 Xaa Gly Xaa Xaa Trp Leu Gly Ser Ser Pro Arg Gln Leu Pro Gln Xaa
 20 25 30
 Pro Ser Ser Ser Tyr Ser Val
 35

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Ser Leu Ile Ser Ser Trp Xaa Tyr Ser Trp Leu Thr His Gln Ile
 1 5 10 15
 Ser Arg Ala Trp Arg Xaa Cys Trp Thr Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Leu Xaa Leu Arg Ser Gly Trp Pro Ala Leu Gly Trp Trp Ala Ser Cys
 1 5 10 15
 Ala Ser Gly Ala Ser Ser Ser Thr Ser Thr Xaa Val Thr Leu Ala Gly
 20 25 30
 Ala Val Leu Pro Ala Cys Glu Ser Gly Xaa Leu Arg Xaa
 35 40 45

(2) INFORMATION FOR SEQ ID NO:201:

320

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ser Xaa Leu Xaa
1

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Pro Arg Lys Ile Xaa Xaa Leu Phe Gly Thr Leu Leu Val Cys Trp Ala
1 5 10 15
Val Asp Asn Trp Ser Met Gly Asn Gln Trp Ser Arg Gly Glu Ala Thr
 20 25 30
Arg Cys

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Thr Val Gly Ser Thr Phe Arg Leu Ala Leu Phe Pro Leu Leu Pro Trp
1 5 10 15
Xaa Phe Ile Xaa Xaa Ala Xaa Xaa Xaa Xaa Gly Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:

321

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gln Ala Arg Thr Arg Pro Asn Thr Thr Xaa Thr Trp Trp Ser Xaa Gly
1 5 10 15

Leu Gln Gln Xaa Val Pro Trp Ala Ala Ala
20 25

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Cys Thr Xaa His Thr Met Xaa Pro Thr Pro Xaa,Xaa Trp Arg Gly Xaa
1 5 10 15
Leu Xaa Xaa Ser Xaa Leu Gly Gly Gly Xaa Arg Xaa Thr Thr Ser Arg
20 25 30
Xaa Thr Arg Ser Xaa Met Xaa Leu Leu Ala Xaa Xaa Xaa Xaa Ser Ala
35 40 45
Asn Gln Leu Gly Cys Gly
50

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ser Gly Met Thr Glu Leu Phe Ala Met Glu Leu Ser Ala Arg Trp Trp
1 5 10 15
Ile

322

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```

Ile Cys Pro Leu Ser Cys Gln Thr Phe Ala Gly Leu Leu Asp His Gln
 1             5             10             15
Ser Cys Ala Met Arg Val Met Leu Leu Ala Cys
          20             25

```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Phe Arg Cys Phe Ile Gly Gly Val Gly Phe Pro Arg Cys Gly Ile Pro
 1             5             10             15
Asn Leu Gly Lys Leu Ser Leu Gly Arg Leu Arg Leu Asp Arg Arg Pro
          20             25             30
Pro Leu Cys Gln Glu Pro Leu Asp Thr Gly Arg Arg His Cys Ser Cys
          35             40             45
Pro Pro Glu Leu Ala Ser Arg Arg Ala Cys Arg Met Ser Thr Ser Arg
          50             55             60
Leu Asp Thr Xaa Cys Leu Tyr
65             70

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

Thr His Pro Leu Pro Gln
 1             5

```


323

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Gly Pro Trp Ala Leu Thr Trp Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Pro Ala Asn Ile Arg Arg Cys Thr Val Ala Met Thr Leu Leu His Ile
1 5 10 15

Pro Gly Leu Leu Thr His Leu
20

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Pro Thr Val His Thr Ala Gly Leu Trp Pro Ile Pro Gly Asn Thr Cys
1 5 10 15

Gly Gly Thr Thr Ser
20

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

324

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Phe Ala Thr Ser Cys Thr Ser Pro Thr Arg Pro Gln Phe Trp Gly Trp
 1 5 10 15
 Val Gly Arg Gly Tyr Ser Leu Ala Ser Ala Ala Tyr Ala Ser Cys Phe
 20 25 30
 Ser Leu Arg Arg Pro His Arg Ser Leu Arg Trp Arg Ser Met Asn Leu
 35 40 45
 Phe Met Arg Arg Cys Trp Ala Val Arg Gly Arg Ser Pro Ser Ile Ala
 50 55 60
 Asn Ser Ser His
 65

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Val Gly Met Leu Leu Gly Asp Thr Cys Cys Phe Val Ile Pro Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Xaa Ala Leu Gly Tyr Pro Gln Leu Trp Pro Ala Leu Val Ser Thr Pro
 1 5 10 15
 Leu Cys Thr Ser Glu Ala Lys Lys Leu Thr Phe Gln Leu Val Thr Cys
 20 25 30
 Ala Phe Ala Pro Gln Thr His Phe Pro Leu Val Thr Leu Ala Ile Leu
 35 40 45

325

Thr Pro
50

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Gln Thr Val Val
1

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Trp Leu Arg Arg
1

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Pro Trp Thr Arg Pro Ser Leu Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Arg Pro Ser Arg Pro Leu Pro Asn
1 5

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Gly Leu Arg Gly Val Val Gly Val Ala Val Gly Lys Arg Ala Leu Thr
1 5 10 15

Ile Arg His

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Cys Leu Arg Arg Arg Arg Glu Xaa Phe Gly Leu Gly Leu Ser Gly Gln
1 5 10 15

Leu Leu Arg Leu Xaa Ser Arg Gly Met Ala
20 25

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

327

Ser Pro Met Leu Leu Glu Thr Cys Leu Gly Pro Thr Thr Arg Val Leu
 1 5 10 15
 Ile Leu Leu Pro Ser Val Arg Pro Ser Glu Arg Pro Leu Pro Phe Leu
 20 25 30
 Leu Xaa

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Gly Ile Ile Leu Arg Trp Phe Gly Pro Ser Arg Arg Xaa Thr Thr Gly
 1 5 10 15
 His Ser Trp Trp Val Cys Arg Gly Thr Cys Val Arg Thr Arg Ala Val
 20 25 30
 Val Xaa Pro Leu Met Val Pro Asn Gly Ala Ala Ser Gly Glu Lys Gly
 35 40 45
 Leu Phe Pro Cys Cys Ala Asp Gly Val Val Thr Cys Leu Ser Arg Trp
 50 55 60
 Leu Arg Ile Thr Gly Leu Met Thr Tyr Arg Pro Gly Ser Val Trp Pro
 65 70 75 80
 Arg Val Thr Leu Pro Ala Leu Leu Asp Arg Cys Phe Trp Ser Val Trp
 85 90 95
 Arg Trp Arg Gly Gly Leu Ser Trp His Thr Gly Arg Gly Leu Trp Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Pro Val Gly Leu Ser Met Gly Thr Val Thr Arg

328

1 5 10

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Tyr Lys Ala Pro Leu Gly Ala Trp Xaa Xaa Ala Val His Thr Gln Tyr
1 5 10 15
Pro Gln Met Val Val Asn Gly Thr His Gln Thr Ser Ser Gln Xaa Leu
20 25 30
Arg Leu

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Pro Pro Leu Arg Leu Arg Ala Xaa Gly Ala Gln Pro Arg Xaa Val Trp
1 5 10 15
Leu Met

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Arg Pro Val Lys Leu Glu Pro Cys Trp Leu Thr Xaa Arg Val L u Arg

329

1	5	10	15
Gly Arg Leu Gly Leu Gln Thr Thr Leu Cys Leu His Gln His His Thr	20	25	30
Gln Leu Pro Cys Xaa Arg Ala Trp Xaa Leu Arg Ser Leu Gln Leu Gly	35	40	45
Ile Ala Cys Ser Leu Thr Ala Val Pro Cys Leu Leu Gly Ser Gln Leu	50	55	60
Leu Thr Ala Leu Gly Gly Thr His Arg Trp Ala Ser Glu Pro Leu Ser	65	70	75
Cys Trp Ala Cys His Arg Ala Xaa Xaa Leu Thr Ser Asp Leu Leu Leu	85	90	95
Arg Cys Ser Ser Ala Ser Gly Val Pro Ser	100	105	

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Ala Arg Leu Leu Leu Gly Leu Leu Trp Arg Val Pro Thr Ser Xaa Gly	1	5	10	15
Ala Ala Leu Pro Leu Thr Gly	20			

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Val Ser Leu Trp Leu	1	5
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(2) INFORMATION FOR SEQ ID NO:230:

330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ser Glu Ala Gly Arg Gly Xaa Xaa Thr Gln Pro His Ser Pro Ser Xaa
1 5 10 15
Ser Trp Xaa Gly Ser Tyr Lys Xaa Xaa Xaa Leu Gly Ala Xaa Ser Xaa
20 25 30
Xaa Trp Pro Leu Arg Gly Leu Arg Trp Xaa Val Trp Xaa Xaa Xaa Xaa
35 40 45
Cys Xaa Gly Leu Ser Xaa Arg Val Trp Xaa Xaa Xaa Gly Leu Thr Xaa
50 55 60
Cys
65

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Cys His Ala Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Cys Leu Thr Ile Ser Ser Ser Lys Met Ser Ser Ser Pro Arg Cys Leu
1 5 10 15
Leu Ser Cys Glu Ser
20

331

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Cys His Cys Gln Asp Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Leu Leu Trp Thr Ser Gly Arg Trp Arg Trp Arg Xaa Pro Leu Leu Arg
1 5 10 15
Leu Phe Gly Thr Cys Leu Thr Gly Ala Ser Gly Xaa Val Gly Ser Cys
20 25 30
Thr Ile Asn Xaa Cys Leu Leu Ser Leu Gly Cys Ala Cys Arg Leu Ser
35 40 45
Val Ala Val Pro Val Gly Val Ala Arg Gly Arg Ala Met Val Ile Trp
50 55 60
Lys Gln Gly Val Leu Val Ala Val
65 70

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Leu Pro Val Ile Phe Thr Met Val Tyr Cys Thr Thr Tyr Ile Ile Pro

332

1	5	10	15
Pro Tyr Cys Ala Asp Ile Thr Thr Arg Gly Gln Cys Leu Leu Ala Ser	20	25	30
Trp Ala Met Leu Arg Glu Gln Ser Pro Leu Cys Leu Leu Ala Val Glu	35	40	45
Ser Gly Leu Thr Lys Leu Gly Leu Leu Thr Gly Leu Arg Leu Trp Ser	50	55	60
Cys Met Gly Gln Ser Arg Cys Thr Pro Pro Val Ala Met Ser	65	70	75

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Lys Leu Leu Thr Phe Gly Gly Arg Cys Glu Pro Ala Arg Leu Thr Leu	1	5	10	15
Val Ala Tyr Leu Ala Ala Gly Ala Arg Arg Val Leu Arg Leu Arg Ser	20	25	30	
Phe Thr Gly	35			

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Ala Arg Ala Ser Lys Ser Met Glu Arg Ala Asp Cys Cys Pro Val Thr	1	5	10	15
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(2) INFORMATION FOR SEQ ID NO:238:

333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

His Arg Glu Arg Ala Thr Pro Arg Tyr Leu Ala Val Leu Pro Val Val
1 5 10 15
Val Gly Gln Met Arg Thr Arg Gly Thr Trp Trp Lys Pro Arg Leu Pro
20 25 30
Pro Ser Arg Pro Leu Gly Arg Pro Cys Thr Ser Leu His Arg Arg Leu
35 40 45
Leu Arg Pro Leu
50

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Arg Leu Trp Arg Arg Leu Pro Cys Pro Cys Cys Pro Met Cys Pro Ser
1 5 10 15
Leu Trp Val Met Thr Val His Ala Gly Met Arg Arg Ser Lys Ala Thr
20 25 30
Ser Ser Gln Asn Pro Met
35

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

334

Gln Arg Tyr Pro Leu Ser Pro Arg Ser Glu Thr Trp Arg His Ser Ser
1 5 10 15

Cys Gly Leu Gln Thr
20

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Pro Pro Gly Cys Lys Thr Trp Arg Pro Trp Leu Ser Pro Ala Leu Ser
1 5 10 15

Gln Ser Arg Met Leu Ala Gln Leu Arg Cys Leu Arg Ser Pro Arg Trp
20 25 30

Thr Gln Cys His His Trp Ser Arg Ala Leu Ala Pro Pro Leu Asn Lys
35 40 45

Ser Leu
50

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Leu Lys Val Thr Leu Arg Leu Ser Ser Arg Leu Ala Tyr Pro Trp Ser
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

335

Thr Pro Thr Pro Gly Arg Leu Arg Leu Gly Gly Leu Ser Glu Ser Asp
1 5 10 15
Arg Leu Ala Val Val Thr Asp Pro Gln
20 25

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Arg Pro Cys Arg Cys Arg Ser Leu Ser Gly Ser Ala Ser Ser Leu Leu
1 5 10 15
Ala Met Thr Arg Thr Val Thr Asn Cys Leu Thr Ser Glu Val Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Arg Tyr Leu Leu Leu Tyr Val Lys
1 5

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

336

Leu Gly Thr Ser Gly Phe Ser Val Thr Lys Leu Arg Lys Leu Gln His
1 5 10 15
Leu Thr Leu Thr Ser Gly Gln Gly Arg Pro Trp Val Leu Gly Glu Val
20 25 30
Ser Pro Asn Pro
35

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Leu Val Thr Leu Pro Lys Phe Met Leu Leu Thr Leu Ile Gly Pro Leu
1 5 10 15
Ser Gly Pro Arg Arg Leu Gln Ser Gly Gly Val Ile Gly Ser Met Thr
20 25 30
Ser Ile Met Arg Leu Ser Leu Arg Leu Ser
35 40

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Lys Arg Gln Pro Arg Arg Ser Leu Met Ala Gly Pro Ile Pro Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

337

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Leu Lys Leu Gly Ala Glu Gln Pro Leu Asp Thr Ala Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Pro Pro Pro His Trp Pro Leu Val Gly Leu Thr Trp Arg Arg Cys Trp
1 5 10 15
Thr Lys

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Pro Gly Asp Arg Lys Phe Leu Ser Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Pro Ser Glu Arg Phe Ser Ser Pro Lys Leu Pro Val Ser Pro Gln Asp
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Phe Ser His Leu Trp Thr Ser Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Phe Trp Val Thr Pro Ala Ser Leu Gln Ser Gln Phe Trp Val Thr Leu
 1 5 10 15

Ile Cys Ser Ser Thr Arg Pro Ile Arg Gly Ser Lys Leu Trp Leu Arg
 20 25 30

Arg Gly Arg Gly Ser Cys Ile Pro Leu Arg Ser Leu Trp Thr Pro Leu
 35 40 45

Val Ser Thr His Arg Leu Met Ser Thr Thr Cys Arg Trp Arg Leu Arg
 50 55 60

Cys Leu Arg Arg Leu Val Thr Thr Pro Gln Trp Tyr Met Leu Cys Ala
 65 70 75 80

Ser Thr Thr Leu Val Ala Leu Trp Phe Pro Gln Met Gly Phe Pro Trp
 85 90 95

Gly Thr Ala Ser Val Gly Arg Arg Ala Cys
 100 110

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids

339

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Gln Leu Ala Arg Arg Thr Ala Ser Leu Val Thr Leu Arg Ser Ala Arg
1 5 10 15
Pro Ala Gly Gly Trp Gly Leu Arg His His His Ser Leu
20 25

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Leu Glu Met Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Ser Ser Met Lys Met Met Glu Leu Ile Pro Ala Leu Leu Leu Arg Leu
1 5 10 15
Pro Trp Pro Thr Met Asp Thr Gly Val Asn Gln Gln Ser Met Leu His
20 25 30
Trp Thr Gln Leu Ser Val Ala Arg Pro Thr Trp Leu Ser Ala
35 40 45

340

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Leu Gly Val Pro Ser Ala Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Gly Ser Arg Ser Gln Gly Arg Leu Pro Asn Ile Arg Thr Gln Ser Ala
1 5 10 15

Val Leu

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Cys Ile Pro Gly Ile Gln Ser Cys Gly Met Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

341

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Tyr His Thr Tyr
1

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Trp Leu Thr Gly Val Ala Ala His Arg Met Ser Trp Leu Cys Val Arg
1 5 10 15
Phe Arg Glu Ile Ile Thr Leu Ser Arg Cys Gly Cys Cys Leu Ala Ser
20 25 30
Trp Ser Leu Tyr Met Val Arg Gly Ala Tyr Lys Ser Pro Arg Thr Val
35 40 45
Arg Arg Leu Gly Trp Arg Gln Ala Gln Xaa Cys Gly Ile
50 55 60

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Pro Gly Thr Ala Asp Val Pro Glu Met Cys Ala Leu Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

342

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Gly	Glu	Ala	Arg	Ser	Gly	Gly	Thr	Trp	Pro	Glu	Pro	Ser	Ser	Gly	Xaa
1				5					10					15	

Gln Xaa

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Arg	Ser	Xaa	Pro	Xaa	Pro
1			5		

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Ile	His	Phe	Gln	Val	Phe	Ser	Trp	Arg	Arg	Leu	Thr	Asn	Thr	Met	Lys
1				5					10					15	

Arg Ser

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Ser Arg Ser Arg Val Asp His Leu Gly

343

1

5

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Gly	Gly	Phe	Leu	Val	Leu	Val	Ser	Arg	Cys	Trp	Pro	Pro	Cys	Cys	Glu
1				5					10					15	
Phe	Ala	Pro	Gly	Ser	Arg	Thr	Phe	Gly	Ser	Gly					
			20						25						

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..9493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

C GTG GGA GTC CGG GGC CCC GGA CCT CCC ACC GAG GTG GGG GGA AAG	46
Val Gly Val Arg Gly Pro Gly Pro Pro Thr Glu Val Gly Gly Lys	
1 5 10 15	
GGG CCC TGG ACC GGC CGG GTG GAA GGC CCG GAA CCG GTC CAT CTT CCT	94
Gly Pro Trp Thr Gly Arg Val Glu Gly Pro Glu Pro Val His Leu Pro	
20 25 30	
CAA GGT TGA GGA AGG GGT ACG TCT ATC GGT CCG GTC GGT CCG AAA GGC	142
Gln Gly * Gly Arg Gly Thr Ser Ile Gly Pro Val Gly Pro Lys Gly	
35 40 45	
GTC TGG ATG CCT AGT GTT AGG GTT CGT AGG TGG TAA ATC CCA GCT AGG	190
Val Trp Met Pro Ser Val Arg Val Arg Arg Trp * Ile Pro Ala Arg	
50 55 60	
CGT GAA AGC GCT ATA GGA TAG GCT TAT CCC GGT GAC CGC TGC CCC GGA	238
Arg Glu Ser Ala Il Gly * Ala Tyr Pro Gly Asp Arg Cys Pro Gly	

344

65	70	75	
ACC AGC CCC GCG GKT CTT TGG ACA CGG TCC ACA GGT TGG GGG TAC CGG			286
Thr Ser Pro Ala Xaa Leu Trp Thr Arg Ser Thr Gly Trp Gly Tyr Arg			
80	85	90	95
TGT GAA TAA CCC CCC GAC TGA AGC GTC AGT CGT TAA ACG GAG ACG GTC			334
Cys Glu * Pro Pro Asp * Ser Val Ser Arg * Thr Glu Thr Val			
	100	105	110
TCC TGA GAT CGC AAC GAC GCC CCA CGT ACG GGA ACG CCG CCA AAA CCT			382
Ser * Asp Arg Asn Asp Ala Pro Arg Thr Gly Thr Pro Pro Lys Pro			
	115	120	125
TCG GGA CAG CTA TGC GGG TTG ACA ATC CCA GTG GGG GGC CGG GGA CCA			430
Ser Gly Gln Leu Cys Gly Leu Thr Ile Pro Val Gly Gly Arg Gly Pro			
	130	135	140
GCT GAT TAC TTG TCC TGC GAG TTC CTC TTG AGA CTG GCC GAA AGG CAG			478
Ala Asp Tyr Leu Ser Cys Glu Phe Leu Leu Arg Leu Ala Glu Arg Gln			
	145	150	155
CCA CGG GGC CAC CAA GGC GGC GCA GCG CTG CAT GCG GCA AGG GGA AAA			526
Pro Arg Gly His Gln Gly Gly Ala Ala Leu His Ala Ala Arg Gly Lys			
160	165	170	175
ATC CTT CGG GTG ACC CCT GGT GGC AAT CCC TTC CCT TAG GAG CAT GAG			574
Ile Leu Arg Val Thr Pro Gly Gly Asn Pro Phe Pro * Glu His Glu			
	180	185	190
TGT GGT CGA CAC ATT CAC CAT GGC TTG GCT GTG GTT GCT GGT TTG CTT			622
Cys Gly Arg His Ile His His Gly Leu Ala Val Val Ala Gly Leu Leu			
	195	200	205
CCC CCT CGC GGG GGG GGT GCT CTT CAA CTC GCG GCA CCA GTG CTT CAA			670
Pro Pro Arg Gly Gly Gly Ala Leu Gln Leu Ala Ala Pro Val Leu Gln			
	210	215	220
TGG GGA CCA TTA TGT GCT TTC CAA TTG TTG TTC CCG AGA CGA GGT TTA			718
Trp Gly Pro Leu Cys Ala Phe Gln Leu Leu Phe Pro Arg Arg Gly Leu			
	225	230	235
CTT CTG TTT CGG GGA CGG ATG TCT GGT GGC TTA TGG CTG TAC TGT TTG			766
Leu Leu Phe Arg Gly Arg Met Ser Gly Gly Leu Trp Leu Tyr Cys Leu			
	240	245	255
CAC ACA GTC TTG CTG GAA GCT CTA CCG GCC TGG GGT GGC TAC TCG GCC			814
His Thr Val Leu Leu Glu Ala Leu Pro Ala Trp Gly Gly Tyr Ser Ala			
	260	265	270
CGG GTC CGA ACC AGG TGA GCT GCT GGG GAG ATT TGG GAG TGT AAT TGG			862
Arg Val Arg Thr Arg * Ala Ala Gly Glu Ile Trp Glu Cys Asn Trp			
	275	280	285
TCC GGT GTC GGC TTC GGC TTA CAC CGC TGG AGT CCT CGG GTT GGG TGA			910
Ser Gly Val Gly Phe Gly Leu His Arg Trp Ser Pro Arg Val Gly *			
	290	295	300

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ACC TTA CAG TTT GGC CTT CTT GGG GAC GTT CCT CAC CAG TCG CCT CTC Thr Leu Gln Phe Gly Leu Leu Gly Asp Val Pro His Gln Ser Pro Leu 305 310 315	958
ACG GAT TCC CAA CGT CAC CTG CGT GAA GGC TTG TGA CCT TGA GTT TAC Thr Asp Ser Gln Arg His Leu Arg Glu Gly Leu * Pro * Val Tyr 320 325 330 335	1006
CTA CCC AGG CTT GTC CAT CGA TTT TGA CTG GGC GTT TAC CAA GAT CTT Leu Pro Arg Leu Val His Arg Phe * Leu Gly Val Tyr Gln Asp Leu 340 345 350	1054
GCA GTT GCC GGC CAA GCT GTG GCG AGG CCT AAC GGC RGC WCC GGT CTT Ala Val Ala Gly Gln Ala Val Ala Arg Pro Asn Gly Xaa Xaa Gly Leu 355 360 365	1102
GAG CCT CCT CGT GAT CCT CAT GCT GGT CCT CGA GCA GCG CCT CCT GAT Glu Pro Pro Arg Asp Pro His Ala Gly Pro Arg Ala Ala Pro Pro Asp 370 375 380	1150
AGC CTT CCT ACT GCT TTT GGT AGT GGG CGA GGC TCA GAG GGG GAT GTT Ser Leu Pro Thr Ala Phe Gly Ser Gly Arg Gly Ser Glu Gly Asp Val 385 390 395	1198
CGA CAA CTG CGT GTG TGG TTA CTG GGG GGG CAA GAG GCC CCC GTC GGT Arg Gln Leu Arg Val Trp Leu Leu Gly Gly Gln Glu Ala Pro Val Gly 400 405 410 415	1246
GAC CCC GCT GTA CCG TGG CAA CGG TAC TGT GGT GTG TGA CTG TGA TTT Asp Pro Ala Val Pro Trp Gln Arg Tyr Cys Gly Val * Leu * Phe 420 425 430	1294
TGG AAA AAT GCA TTG GGC CCC CCC CTT GTG TTC CGG YCT GGT GTG GCG Trp Lys Asn Ala Leu Gly Pro Pro Leu Val Phe Arg Xaa Gly Val Ala 435 440 445	1342
GGA CGG TCA TAG GAG GGG CAC CGT GCG CGA CCT CCC CCC GGT TTG CCC Gly Arg Ser * Glu Gly His Arg Ala Arg Pro Pro Pro Gly Leu Pro 450 455 460	1390
CCG GGA GGT TCT CGG CAC GGT GAC AGT CAT GTG TCA GTG GGG TTC TGC Pro Gly Gly Ser Arg His Gly Asp Ser His Val Ser Val Gly Phe Cys 465 470 475	1438
CTA CTG GAT TTG GAG ATT TGG GGA CTG GGT TGC ATT GTA CGA CGA GCT Leu Leu Asp Leu Glu Ile Trp Gly Leu Gly Cys Ile Val Arg Arg Ala 480 485 490 495	1486
ACC ACG ATC AGC TCT CTG TAC TTT CTT CTC AGG TCA TGG TCC ACA ACC Thr Thr Ile Ser Ser Leu Tyr Phe Leu Leu Arg Ser Trp Ser Thr Thr 500 505 510	1534
TAA AGA TCT CTC AGT CTT GAA TCC ATC CGG GGC ACC TTG TGC TTC TTG * Arg Ser Leu Ser Leu Glu Ser Ile Arg Gly Thr Leu Cys Phe Leu 515 520 525	1582
CGT CGT TGA CCA GAG GCC GCT GAA ATG TGG TTC CTG CGT CCG CGA CTG	1630

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Arg Arg * Pro Glu Ala Ala Glu Met Trp Phe Leu Arg Pro Arg Leu	1678
530 535 540	
CTG GGA GAC GGG GGG TCC TGG GTT CGA TGA GTG CGG TGT CGG TAC TCG	
Leu Gly Asp Gly Gly Ser Trp Val Arg * Val Arg Cys Arg Tyr Ser	
545 550 555	
GAT GAC GAA GCA CCT CGA GGC CGT CCT GGT TGA TGG AGG TGT GGA GTC	1726
Asp Asp Glu Ala Pro Arg Gly Arg Pro Gly * Trp Arg Cys Gly Val	
560 565 570 575	
CAA GGT GAC AAC GCC CAA GGG TGA GCG CCC CAA ATA CAT AGG TCA GCA	1774
Gln Gly Asp Asn Ala Gln Gly * Ala Pro Gln Ile His Arg Ser Ala	
580 585 590	
CGG TGT GGG AAC CTA CTA CGG CGC TGT CCG TAG CCT CAA CAT CAG TTA	1822
Arg Cys Gly Asn Leu Leu Arg Arg Cys Pro * Pro Gln His Gln Leu	
595 600 605	
CCT AGT GAC TGA GGT GGG GGG CTA TTG GCA TGC GCT GAA GTG CCC GTG	1870
Pro Ser Asp * Gly Gly Gly Leu Leu Ala Cys Ala Glu Val Pro Val	
610 615 620	
CGA CTT TGT GCC CCG AGT GCT CCC AGA AAG AAT TCC AGG TAG GCC TGT	1918
Arg Leu Cys Ala Pro Ser Ala Pro Arg Lys Asn Ser Arg * Ala Cys	
625 630 635	
GAA TGC ATG TCT AGC TGG GAA GTC TCC GCA CCC GTT CGC AAG TTG GGC	1966
Glu Cys Met Ser Ser Trp Glu Val Ser Ala Pro Val Arg Lys Leu Gly	
640 645 650 655	
TCC CGG TGG GTT TTA CGC CCC CGT GTT CAC CAA GTG CAA CTG GCC GAA	2014
Ser Arg Trp Val Leu Arg Pro Arg Val His Gln Val Gln Leu Ala Glu	
660 665 670	
GAC CTC CGG AGT GGA TGT GTG TCC TGG GTT TGC TTT CGA TTT CCC TGG	2062
Asp Leu Arg Ser Gly Cys Val Ser Trp Val Cys Phe Arg Phe Pro Trp	
675 680 685	
TGA TCA CAA CGG CTT CAT CCA TGT TAA AGG CAA CAG ACA GCA GGT TTA	2110
* Ser Gln Arg Leu His Pro Cys * Arg Gln Gln Thr Ala Gly Leu	
690 695 700	
CAG TGG TCA GCG AAG GTC TTC GCC GGC TTG GTT GCT TAC TGA CAT GGT	2158
Gln Trp Ser Ala Lys Val Phe Ala Gly Leu Val Ala Tyr * His Gly	
705 710 715	
CCT GGC CCT GTT GGT GGT GAT GAA GTT GGC TGA GGC TAG AGT TGT CCC	2206
Pro Gly Pro Val Gly Gly Asp Glu Val Gly * Gly * Ser Cys Pro	
720 725 730 735	
CCT GTT TAT GCT GGC AAT GTG GTG GTG GTT GAA TGG AGC ATC TGC TGC	2254
Pro Val Tyr Ala Gly Asn Val Val Val Val Glu Trp Ser Ile Cys Cys	
740 745 750	
CAC TAT TGT CAT CAT ACA CCC TAC TGT CAC GAA GTC CAC TGA AAG TGT	2302
His Tyr Cys His His Thr Pro Tyr Cys His Glu Val His * Lys Cys	
755 760 765	

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TCC	ATT	GTG	GAC	TCC	GCC	CAC	TGT	TCC	AAC	TCC	ATC	TTG	CCC	GAA	TTC	2350
Ser	Ile	Val	Asp	Ser	Ala	His	Cys	Ser	Asn	Ser	Ile	Leu	Pro	Glu	Phe	
		770					775					780				
TAC	CAC	CGG	AGT	CGC	GGA	CTC	TAC	CTA	CAA	TGC	TGG	TTG	CTA	CAT	GGT	2398
Tyr	His	Arg	Ser	Arg	Gly	Leu	Tyr	Leu	Gln	Cys	Trp	Leu	Leu	His	Gly	
		785				790					795					
GGC	AGG	CCT	GGC	GGC	CGG	GGC	TCA	GGC	GGT	CTG	GGG	TGC	TGC	CAA	TGA	2446
Gly	Arg	Pro	Gly	Gly	Arg	Gly	Ser	Gly	Gly	Leu	Gly	Cys	Cys	Gln	*	
800					805					810					815	
TGG	TGC	TCA	GGC	CGT	CGT	TGG	TGG	CAT	CTG	GCC	CGC	GTG	GCT	CAA	GCT	2494
Trp	Cys	Ser	Gly	Arg	Arg	Trp	Trp	His	Leu	Ala	Arg	Val	Ala	Gln	Ala	
				820					825					830		
GCG	AAG	CTT	CGC	TGC	CGG	TCT	GGC	CTG	GTT	GTC	AAA	TGT	TGG	GGC	TTA	2542
Ala	Lys	Leu	Arg	Cys	Arg	Ser	Gly	Leu	Val	Val	Lys	Cys	Trp	Gly	Leu	
			835					840					845			
CTT	GCC	GGT	CGT	CGA	GGC	CGC	VCT	GGC	TCC	CGA	GCT	GGT	GTG	CAC	CCC	2590
Leu	Ala	Gly	Arg	Arg	Gly	Arg	Xaa	Gly	Ser	Arg	Ala	Gly	Val	His	Pro	
		850					855					860				
GGT	GGT	CGG	CTG	GGC	AGC	CCA	GGA	GTG	GTG	GTT	CAC	TGG	TTG	TCT	GGG	2638
Gly	Gly	Arg	Leu	Gly	Ser	Pro	Gly	Val	Val	Val	His	Trp	Leu	Ser	Gly	
		865				870					875					
TGT	GAT	GTG	TGT	CGT	GGC	GTA	CCT	GAA	TGT	CCT	GGG	CTC	TGT	RAG	GGC	2686
Cys	Asp	Val	Cys	Arg	Gly	Val	Pro	Glu	Cys	Pro	Gly	Leu	Cys	Xaa	Gly	
880					885					890					895	
TGC	CGT	GCT	TGT	GGC	GAT	GCA	CTT	CGC	AAG	GGG	TGC	TCT	GCC	GCT	GGT	2734
Cys	Arg	Ala	Cys	Gly	Asp	Ala	Leu	Arg	Lys	Gly	Cys	Ser	Ala	Ala	Gly	
				900					905					910		
ATT	GGT	GGT	AGC	TGC	CGG	GGT	RAC	CCG	GGA	GCG	GCA	CAG	CGT	CTT	AGG	2782
Ile	Gly	Gly	Ser	Cys	Arg	Gly	Xaa	Pro	Gly	Ala	Ala	Gln	Arg	Leu	Arg	
			915					920					925			
GCT	TGA	GGT	GTG	CTT	CGA	TCT	GGA	TGG	TGG	AGA	CTG	GCC	RGA	CGC	CAG	2830
Ala	*	Gly	Val	Leu	Arg	Ser	Gly	Trp	Trp	Arg	Leu	Ala	Xaa	Arg	Gln	
		930					935					940				
TTG	GTC	TTG	GGG	TTT	AGC	AGG	CGT	GGT	GAG	CTG	GGC	CCT	CCT	GGT	GGG	2878
Leu	Val	Leu	Gly	Phe	Ser	Arg	Arg	Gly	Glu	Leu	Gly	Pro	Pro	Gly	Gly	
		945				950					955					
GGG	TCT	GAT	GAC	CCA	CGG	TGG	CCG	ATC	AGC	CAG	AYT	GAC	TTG	GTA	YGC	2926
Gly	Ser	Asp	Asp	Pro	Arg	Trp	Pro	Ile	Ser	Gln	Xaa	Asp	Leu	Val	Xaa	
960					965					970					975	
CAG	GTG	GGC	CGT	CAA	TTA	YCA	GAG	GGT	TCG	YCG	GTG	GGT	GAA	CAA	CTC	2974
Gln	Val	Gly	Arg	Gln	Leu	Xaa	Glu	Gly	Ser	Xaa	Val	Gly	Glu	Gln	L u	
				980				985						990		
ACC	GGT	TGG	AGC	YTT	TGG	YCG	TTG	GMG	GCG	YGC	CTG	GAA	AGC	YTG	GTT	3022
Thr	Gly	Trp	Ser	Xaa	Trp	Xaa	Leu	Xaa	Ala	Xaa	Leu	Glu	Ser	Xaa	Val	

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995	1000	1005	
RGT KGT GGC TTG GTT CTT CCC CCA GAC AGT TGC CAC AGT YTC CGT CAT Xaa Xaa Gly Leu Val Leu Pro Pro Asp Ser Cys His Ser Xaa Arg His 1010	1015	1020	3070
CTT CAT ACT CTG TTT GAG CAG TTT AGA TGT CAT TGA TTT CAT CTT GGA Leu His Thr Leu Phe Glu Gln Phe Arg Cys His * Phe His Leu Gly 1025	1030	1035	3118
RGT ACT CTT GGT TAA CTC ACC AAA TCT CGC GCG CTT GGC GCG RGT GCT Xaa Thr Leu Gly * Leu Thr Lys Ser Arg Ala Leu Gly Ala Xaa Ala 1040	1045	1050	3166
GGA CTC CTT AGC TCT HGC TGA GGA GCG GCT GGC CTG CTC TTG GCT GGT Gly Leu Leu Ser Ser Xaa * Gly Ala Ala Gly Leu Leu Leu Ala Gly 1060	1065	1070	3214
GGG CGT CCT GCG CAA GCG GGG CGT CCT CCT CTA CGA GCA CGC YGG TCA Gly Arg Pro Ala Gln Ala Gly Arg Pro Pro Leu Arg Ala Arg Xaa Ser 1075	1080	1085	3262
CAC TAG CAG GCG CGG TGC TGC CCG CTT GCG AGA GTG GGG YTT TGC GCT His * Gln Ala Arg Cys Cys Pro Leu Ala Arg Val Gly Xaa Cys Ala 1090	1095	1100	3310
YGA GCC KGT TAG YAT AAC CAA GGA AGA TTG YGC YAT TGT TCG GGA CTC Xaa Ala Xaa * Xaa Asn Gln Gly Arg Leu Xaa Xaa Cys Ser Gly Leu 1105	1110	1115	3358
TGC TCG TGT GTT GGG CTG TGG ACA ATT GGT CCA TGG GAA ACC AGT GGT Cys Ser Cys Val Gly Leu Trp Thr Ile Gly Pro Trp Glu Thr Ser Gly 1120	1125	1130	3406
CGC GAG GCG AGG CGA CGA GGT GTT GAT CGG CTG TGT GAA CAG TCG GTT Arg Glu Ala Arg Arg Arg Gly Val Asp Arg Leu Cys Glu Gln Ser Val 1140	1145	1150	3454
CGA CCT TCC GCC TGG CTT TGT TCC CAC TGC TCC CGT GGT SCT TCA TCA Arg Pro Ser Ala Trp Leu Cys Ser His Cys Ser Arg Gly Xaa Ser Ser 1155	1160	1165	3502
RGC WGG CAA RGG RTT YTT YGG GGT TGT GAA GAC MTC CAT GAC AGG CAA Xaa Xaa Gln Xaa Xaa Xaa Xaa Gly Cys Glu Asp Xaa His Asp Arg Gln 1170	1175	1180	3550
GGA CCC GTC CGA ACA CCA CGG RAA CGT GGT GGT CCT WGG GAC TTC AAC Gly Pro Val Arg Thr Pro Arg Xaa Arg Gly Gly Pro Xaa Asp Phe Asn 1185	1190	1195	3598
AAC KCG TTC CAT GGG CTG CTG CGT GAA CGG AGT AGT GTA CAC RAC ATA Asn Xaa Phe His Gly Leu Leu Arg Glu Arg Ser Ser Val His Xaa Ile 1200	1205	1210	3646
CCA TGG YAC CAA CGC CCG RCC KAT GGC GGG GCC KTT TGG KCC YGT CAA Pro Trp Xaa Gln Arg Pro Xaa Xaa Gly Gly Ala Xaa Trp Xaa Xaa Gln 1220	1225	1230	3694

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YGC TCG GTG GTG GTC WGC GAG YGA CGA CGT CAC GGT YTA CCC GCT CCC Xaa Ser Val Val Val Xaa Glu Xaa Arg Arg His Gly Xaa Pro Ala Pro 1235 1240 1245	3742
WAA TGG YGC TTC TTG CCT YCA RGC WTC YAA GTG CCA ACC AAC TGG GGT Xaa Trp Xaa Phe Leu Pro Xaa Xaa Xaa Xaa Val Pro Thr Asn Trp Gly 1250 1255 1260	3790
GTG GGT GAT CCG GAA TGA CGG AGC TCT TTG CCA TGG AAC TCT CGG CAA Val Gly Asp Pro Glu * Arg Ser Ser Leu Pro Trp Asn Ser Arg Gln 1265 1270 1275	3838
GGT GGT GGA TTT AGA TAT GCC CGC TGA GTT GTC AGA CTT TCG CGG GTC Gly Gly Gly Phe Arg Tyr Ala Arg * Val Val Arg Leu Ser Arg Val 1280 1285 1290 1295	3886
TTC TGG ATC ACC AAT CTT GTG CGA TGA GGG TCA TGC TGT TGG CAT GCT Phe Trp Ile Thr Asn Leu Val Arg * Gly Ser Cys Cys Trp His Ala 1300 1305 1310	3934
GAT TTC GGT GCT TCA TAG GGG GAG TAG GGT TTC CTC GGT GCG GTA TAC Asp Phe Gly Ala Ser * Gly Glu * Gly Phe Leu Gly Ala Val Tyr 1315 1320 1325	3982
CAA ACC TTG GGA AAC TCT CCC TCG GGA GAT TGA GGC TCG ATC GGA GGC Gln Thr Leu Gly Asn Ser Pro Ser Gly Asp * Gly Ser Ile Gly Gly 1330 1335 1340	4030
CCC CCC TGT GCC AGG AAC CAC TGG ATA CAG GGA GGC GCC ACT GTT CCT Pro Pro Cys Ala Arg Asn His Trp Ile Gln Gly Gly Ala Thr Val Pro 1345 1350 1355	4078
GCC CAC CGG AGC TGG CAA GTC GAC GCG CGT GCC GAA TGA GTA CGT CAA Ala His Arg Ser Trp Gln Val Asp Ala Arg Ala Glu * Val Arg Gln 1360 1365 1370 1375	4126
GGC TGG ACA CAA RGT GCT TGT ACT AAA CCC ATC CAT TGC CAC AGT GAG Gly Trp Thr Gln Xaa Ala Cys Thr Lys Pro Ile His Cys His Ser Glu 1380 1385 1390	4174
GGC CAT GGG CCC TTA CAT GGA AAA GTT AAC CGG CAA ACA TCC GTC GGT Gly His Gly Pro Leu His Gly Lys Val Asn Arg Gln Thr Ser Val Gly 1395 1400 1405	4222
GTA CTG TGG CCA TGA CAC TAC TGC ATA TTC CAG GAC TAC TGA CTC ATC Val Leu Trp Pro * His Tyr Cys Ile Phe Gln Asp Tyr * Leu Ile 1410 1415 1420	4270
TTT GAC CTA CTG TAC ATA CGG CAG GTT TAT GGC CAA TCC CAG GAA ATA Phe Asp Leu Leu Tyr Ile Arg Gln Val Tyr Gly Gln Ser Gln Glu Ile 1425 1430 1435	4318
CTT GCG GGG GAA CGA CGT CGT AAT TTG CGA CGA GTT GCA CGT CAC CGA Leu Ala Gly Glu Arg Arg Arg Asn Leu Arg Val Ala Arg His Arg 1440 1445 1450 1455	4366
CCC GAC CTC AAT TTT GGG GAT GGG TCG GGC GAG GTT ACT CGC TCG CGA Pro Asp Leu Asn Phe Gly Asp Gly Ser Gly Glu Val Thr Arg Ser Arg	4414

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1460										1465					1470					
GTG	CGG	CGT	ACG	CCT	CCT	GCT	TTT	CGC	TAC	GGC	GAC	CCC	ACC	GGT	CTC	4462				
Val	Arg	Arg	Thr	Pro	Pro	Ala	Phe	Arg	Tyr	Gly	Asp	Pro	Thr	Gly	Leu					
1475					1480					1485										
TCC	GAT	GGC	GAA	GCA	TGA	ATC	TAT	TCA	TGA	GGA	GAT	GTT	GGG	CAG	TGA	4510				
Ser	Asp	Gly	Glu	Ala	*	Ile	Tyr	Ser	*	Gly	Asp	Val	Gly	Gln	*					
1490					1495					1500										
GGG	GGA	GGT	CCC	CTT	CTA	TTG	CCA	ATT	CCT	CCC	ACT	GAG	TAG	GTA	TGC	4558				
Gly	Gly	Gly	Pro	Leu	Leu	Leu	Pro	Ile	Pro	Pro	Thr	Glu	*	Val	Cys					
1505					1510					1515										
TAC	TGG	GAG	ACA	CCT	GCT	GTT	TTG	TCA	TTC	CAA	GGT	AGA	RTG	CAC	TAG	4606				
Tyr	Trp	Glu	Thr	Pro	Ala	Val	Leu	Ser	Phe	Gln	Gly	Arg	Xaa	His	*					
1520					1525					1530					1535					
GTT	ATC	CTC	AGC	TTT	GGC	CAG	CTT	TGG	TGT	CAA	CAC	CGT	TGT	GTA	CTT	4654				
Val	Ile	Leu	Ser	Phe	Gly	Gln	Leu	Trp	Cys	Gln	His	Arg	Cys	Val	Leu					
1540					1545					1550										
CAG	AGG	CAA	AGA	AAC	TGA	CAT	TCC	AAC	TGG	TGA	CGT	GTG	CGT	TTG	CGC	4702				
Gln	Arg	Gln	Arg	Asn	*	His	Ser	Asn	Trp	*	Arg	Val	Arg	Leu	Arg					
1555					1560					1565										
CAC	AGA	CGC	ACT	TTC	CAC	TGG	TTA	CAC	TGG	CAA	TTT	TGA	CAC	CGT	AAC	4750				
His	Arg	Arg	Thr	Phe	His	Trp	Leu	His	Trp	Gln	Phe	*	His	Arg	Asn					
1570					1575					1580										
AGA	CTG	TGG	TTT	AAT	GGT	TGA	GGA	GGT	AGT	GGA	AGT	GAC	CCT	GGA	CCC	4798				
Arg	Leu	Trp	Phe	Asn	Gly	*	Gly	Gly	Ser	Gly	Ser	Asp	Pro	Gly	Pro					
1585					1590					1595										
GAC	CAT	CAC	TAT	CGG	TGT	GAA	GAC	CGT	CCC	GGC	CCC	TGC	CGA	ACT	GAG	4846				
Asp	His	His	Tyr	Arg	Cys	Glu	Asp	Arg	Pro	Gly	Pro	Cys	Arg	Thr	Glu					
1600					1605					1610					1615					
GGC	TCA	GAG	GCG	TGG	TAG	GTG	TGG	CCG	TGG	GAA	AGC	GGG	CAC	TTA	CTA	4894				
Gly	Ser	Glu	Ala	Trp	*	Val	Trp	Pro	Trp	Glu	Ser	Gly	His	Leu	Leu					
1620					1625					1630										
TCA	GGC	ATT	GAT	GTC	TTC	GGC	GCC	GGC	GGG	AAC	SGT	TCG	GTC	TGG	GGC	4942				
Ser	Gly	Ile	Asp	Val	Phe	Gly	Ala	Gly	Gly	Asn	Xaa	Ser	Val	Trp	Gly					
1635					1640					1645										
TCT	CTG	GGC	AGC	TGT	TGA	GGC	TGG	HGT	CTC	GTG	GTA	TGG	CCT	AGA	GCC	4990				
Ser	Leu	Gly	Ser	Cys	*	Gly	Trp	Xaa	Leu	Val	Val	Trp	Pro	Arg	Ala					
1650					1655					1660										
CGA	TGC	TAT	TGG	AGA	CCT	GCT	TAG	GGC	CTA	CGA	CTC	GTG	TCC	TTA	TAC	5038				
Arg	Cys	Tyr	Trp	Arg	Pro	Ala	*	Gly	Leu	Arg	Leu	Val	Ser	Leu	Tyr					
1665					1670					1675										
TGC	TGC	CAT	CAG	TGC	GTC	CAT	CGG	AGA	GGC	CAT	TGC	CTT	TTT	TAC	TGG	5086				
Cys	Cys	His	Gln	Cys	Val	His	Arg	Arg	Gly	His	Cys	Leu	Phe	Tyr	Trp					
1680					1685					1690					1695					

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YCT AGT GCC AAT GAG GAA TTA TCC TCA GGT GGT TTG GGC CAA GCA GAA Xaa Ser Ala Asn Glu Glu Leu Ser Ser Gly Gly Leu Gly Gln Ala Glu 1700 1705 1710	5134
GGG RCA CAA CTG GCC ACT CTT GGT GGG TGT GCA GAG GCA CAT GTG TGA Gly Xaa Gln Leu Ala Thr Leu Gly Gly Cys Ala Glu Ala His Val * 1715 1720 1725	5182
GGA CGC GGG CTG TGG TCC KCC CGC TAA TGG TCC CGA ATG GAG CGG CAT Gly Arg Gly Leu Trp Ser Xaa Arg * Trp Ser Arg Met Glu Arg His 1730 1735 1740	5230
CAG GGG AAA AGG GCC TGT TCC CCT GTT GTG CCG ATG GGG TGG TGA CTT Gln Gly Lys Arg Ala Cys Ser Pro Val Val Pro Met Gly Trp * Leu 1745 1750 1755	5278
GCC TGA GTC GGT GGC TCC GCA TCA CTG GGT TGA TGA CCT ACA GGC CCG Ala * Val Gly Gly Ser Ala Ser Leu Gly * * Pro Thr Gly Pro 1760 1765 1770 1775	5326
GCT CGG TGT GGC CGA GGG TTA CAC TCC CTG CAT TGC TGG ACC GGT GCT Ala Arg Cys Gly Arg Gly Leu His Ser Leu His Cys Trp Thr Gly Ala 1780 1785 1790	5374
TTT GGT CGG TTT GGC GAT GGC GGG GGG GGC TAT CCT GGC ACA CTG GAC Phe Gly Arg Phe Gly Asp Gly Gly Gly Gly Tyr Pro Gly Thr Leu Asp 1795 1800 1805	5422
GGG GTC TCT GGT TGT AGT GAC CAG TTG GGT TGT CAA TGG GAA CGG TAA Gly Val Ser Gly Cys Ser Asp Gln Leu Gly Cys Gln Trp Glu Arg * 1810 1815 1820	5470
CCC GCT GAT ACA AAG CGC CTC TAG GGG CGT GGC KAC YAG CGG TCC ATA Pro Ala Asp Thr Lys Arg Leu * Gly Arg Gly Xaa Xaa Arg Ser Ile 1825 1830 1835	5518
CCC AGT ACC CCC AGA TGG TGG TGA ACG GTA CCC ATC AGA CAT CAA GCC Pro Ser Thr Pro Arg Trp Trp * Thr Val Pro Ile Arg His Gln Ala 1840 1845 1850 1855	5566
AAT YAC TGA GGC TGT GAC CAC CCT TGA GAC TGC GTG CGG YTG GGG CCC Asn Xaa * Gly Cys Asp His Pro * Asp Cys Val Arg Xaa Gly Pro 1860 1865 1870	5614
AGC CGC GGC BAG TCT GGC TTA TGT GAA GGC CTG TGA AAC TGG AAC CAT Ser Arg Gly Xaa Ser Gly Leu Cys Glu Gly Leu * Asn Trp Asn His 1875 1880 1885	5662
GTT GGC TGA CAA RGC GAG TGC TGC GTG GCA GGC TTG GGC TGC AAA CAA Val Gly * Gln Xaa Glu Cys Cys Val Ala Gly Leu Gly Cys Lys Gln 1890 1895 1900	5710
CTT TGT GCC TCC ACC AGC ATC ACA CTC AAC TTC CTT GTT RCA GAG CTT Leu Cys Ala Ser Thr Ser Ile Thr Leu Asn Phe Leu Val Xaa Glu Leu 1905 1910 1915	5758
GGA YGC TGC GTT CAC TTC AGC TTG GGA TAG CGT GTT CAC TCA CGG CCG Gly Xaa Cys Val His Phe Ser Leu Gly * Arg Val His Ser Arg Pro	5806

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1920	1925	1930	1935	
TTC CTT GCT TGT TGG GTT CAC AGC TGC TTA CGG CGC TCG GCG GAA CCC				5854
Phe Leu Ala Cys Trp Val His Ser Cys Leu Arg Arg Ser Ala Glu Pro				
1940		1945	1950	
ACC GCT GGG CGT CGG AGC CTC TTT CTT GCT GGG CAT GTC ATC GAG CCA				5902
Thr Ala Gly Arg Arg Ser Leu Phe Leu Ala Gly His Val Ile Glu Pro				
1955		1960	1965	
CYT RAC TCA CGT CAG ACT TGC TGC TGC GTT GCT CCT CGG CGT CGG GGG				5950
Xaa Xaa Ser Arg Gln Thr Cys Cys Cys Val Ala Pro Arg Arg Arg Gly				
1970		1975	1980	
TAC CGT CCT AGG CAC GCC TGC TAC TGG GCT TGC TAT GGC GGG TGC CTA				5998
Tyr Arg Pro Arg His Ala Cys Tyr Trp Ala Cys Tyr Gly Gly Cys Leu				
1985		1990	1995	
CTT CGC KGG GGG CAG CGT TAC CGC TAA CTG GCT GAG TAT CAT TGT GGC				6046
Leu Arg Xaa Gly Gln Arg Tyr Arg * Leu Ala Glu Tyr His Cys Gly				
2000		2005	2010	2015
TCT AAT CGG AGG CTG GGA GGG GGC RGT KAA CGC AGC CTC ACT CAC CTT				6094
Ser Asn Arg Arg Leu Gly Gly Gly Xaa Xaa Arg Ser Leu Thr His Leu				
2020		2025	2030	
CGA YCT CCT GGC KGG GAA GTT ACA AGC KAG YGA YGC TTG GTG CCT RGT				6142
Arg Xaa Pro Gly Xaa Glu Val Thr Ser Xaa Xaa Xaa Leu Val Pro Xaa				
2035		2040	2045	
CAG YTG CYT GGC CTC TCC GGG GGC TTC GGT GGC YGG TGT GGC DCT VGG				6190
Gln Xaa Xaa Gly Leu Ser Gly Gly Phe Gly Gly Xaa Cys Gly Xaa Xaa				
2050		2055	2060	
YCT DYT GCT VTG GTC TGT CAA RAA GGG TGT GGG WCA RGA YTG GGT TAA				6238
Xaa Xaa Ala Xaa Val Cys Gln Xaa Gly Cys Gly Xaa Xaa Xaa Gly *				
2065		2070	2075	
CAG AYT GTT GAC GAT GAT GCC ACG CAG TTC GGT GAT GCC TGA CGA TTT				6286
Gln Xaa Val Asp Asp Asp Ala Thr Gln Phe Gly Asp Ala * Arg Phe				
2080		2085	2090	2095
CTT CCT CAA AGA TGA GTT CGT CAC CAA GGT GTC TAC TGT CCT GCG AAA				6334
Leu Pro Gln Arg * Val Arg His Gln Gly Val Tyr Cys Pro Ala Lys				
2100		2105	2110	
GTT GTC ATT GTC AAG ATG GAT CAT GAC TCT TGT GGA CAA GCG GGA GAT				6382
Val Val Ile Val Lys Met Asp His Asp Ser Cys Gly Gln Ala Gly Asp				
2115		2120	2125	
GGA GAT GGA GAC MCC CGC TTC TCA GAT TGT TTG GGA CTT GCT TGA CTG				6430
Gly Asp Gly Asp Xaa Arg Phe Ser Asp Cys Leu Gly Leu Ala * Leu				
2130		2135	2140	
GTG CAT CCG GCT RGG TCG GTT CCT GTA CAA TAA ACT YAT GTT TGC TCT				6478
Val His Pro Ala Xaa Ser Val Pro Val Gln * Thr Xaa Val Cys Ser				
2145		2150	2155	

353

CCC TAG GTT GCG CCT GCC GCT TAT CGG TTG CAG TAC CGG TTG GGG TGG	6526
Pro * Val Ala Pro Ala Ala Tyr Arg Leu Gln Tyr Arg Leu Gly Trp	
2160 2165 2170 2175	
CCC GTG GGA GGG CAA TGG TCA TTT GGA AAC AAG GTG TAC TTG TGG CTG	6574
Pro Val Gly Gly Gln Trp Ser Phe Gly Asn Lys Val Tyr Leu Trp Leu	
2180 2185 2190	
TGT GAT TAC CGG TGA TAT TCA CGA TGG TAT ATT GCA CGA CCT ACA TTA	6622
Cys Asp Tyr Arg * Tyr Ser Arg Trp Tyr Ile Ala Arg Pro Thr Leu	
2195 2200 2205	
TAC CTC CCT ACT GTG CAG ACA TTA CTA CAA GAG GAC AGT GCC TGT TGG	6670
Tyr Leu Pro Thr Val Gln Thr Leu Leu Gln Glu Asp Ser Ala Cys Trp	
2210 2215 2220	
CGT CAT GGG CAA TGC TGA GGG AGC AGT CCC CCT TGT GCC TAC TGG CGG	6718
Arg His Gly Gln Cys * Gly Ser Ser Pro Pro Cys Ala Tyr Trp Arg	
2225 2230 2235	
TGG AAT CAG GAC TTA CCA AAT TGG GAC TTC TGA CTG GTT TGA GGC TGT	6766
Trp Asn Gln Asp Leu Pro Asn Trp Asp Phe * Leu Val * Gly Cys	
2240 2245 2250 2255	
GGT CGT GCA TGG GAC AAT CAC GGT GCA CGC CAC CAG TTG CTA TGA GTT	6814
Gly Arg Ala Trp Asp Asn His Gly Ala Arg His Gln Leu Leu * Val	
2260 2265 2270	
GAA AGC TGC TGA CGT TCG GAG GGC GGT GCG AGC CGG CCC GAC TTA CGT	6862
Glu Ser Cys * Arg Ser Glu Gly Gly Ala Ser Arg Pro Asp Leu Arg	
2275 2280 2285	
TGG TGG CGT ACC TTG CAG CTG GAG CGC GCC GTG TAC TGC GCC TGC GCT	6910
Trp Trp Arg Thr Leu Gln Leu Glu Arg Ala Val Tyr Cys Ala Cys Ala	
2290 2295 2300	
CGT TTA CAG GCT AGG CCA GGG CAT CAA AAT CGA TGG AGC GCG CCG ACT	6958
Arg Leu Gln Ala Arg Pro Gly His Gln Asn Arg Trp Ser Ala Pro Thr	
2305 2310 2315	
GTT GCC CTG TGA CTT AGC ACA GGG AGC GCG CCA CCC CCC GGT ATC TGG	7006
Val Ala Leu * Leu Ser Thr Gly Ser Ala Pro Pro Pro Gly Ile Trp	
2320 2325 2330 2335	
CAG TGT TGC CGG TAG TGG TTG GAC AGA TGA GGA CGA GAG GGA CTT GGT	7054
Gln Cys Cys Arg * Trp Leu Asp Arg * Gly Arg Glu Gly Leu Gly	
2340 2345 2350	
GGA AAC CAA GGC TGC CGC CAT CGA GGC CAT TGG GGC GGC CTT GCA CCT	7102
Gly Asn Gln Gly Cys Arg His Arg Gly His Trp Gly Gly Leu Ala Pro	
2355 2360 2365	
CCC TTC ACC GGA GGC TGC TCA GGC CGC TCT AGA GGC TTT GGA GGA GGC	7150
Pro Phe Thr Gly Gly Cys Ser Gly Arg Ser Arg Gly Phe Gly Gly Gly	
2370 2375 2380	
TGC CGT GTC CCT GTT GCC CCA TGT GCC CGT CAT TAT GGG TGA TGA CTG	7198
Cys Arg Val Pro Val Ala Pro Cys Ala Arg His Tyr Gly * * Leu	

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2385	2390	2395	
TTC ATG CCG GGA TGA GGC GTT CCA AGG CCA CTT CAT CCC AGA ACC CAA			7246
Phe Met Pro Gly * Gly Val Pro Arg Pro Leu His Pro Arg Thr Gln			
2400	2405	2410	2415
TGT GAC AGA GGT ACC CAT TGA GCC CAC GGT CGG AGA CGT GGA GGC ACT			7294
Cys Asp Arg Gly Thr His * Ala His Gly Arg Arg Arg Gly Gly Thr			
2420	2425	2430	
CAA GCT GCG GGC TGC AGA CCT GAC CGC CAG GTT GCA AGA CTT GGA GGC			7342
Gln Ala Ala Gly Cys Arg Pro Asp Arg Gln Val Ala Arg Leu Gly Gly			
2435	2440	2445	
CAT GGC TCT CGC CCG CGC TGA GTC AAT CGA GGA TGC TCG CGC AGC TTC			7390
His Gly Ser Arg Pro Arg * Val Asn Arg Gly Cys Ser Arg Ser Phe			
2450	2455	2460	
GAT GCC TTC GCT CAC CGA GGT GGA CTC AAT GCC ATC ATT GGA GTC GAG			7438
Asp Ala Phe Ala His Arg Gly Gly Leu Asn Ala Ile Ile Gly Val Glu			
2465	2470	2475	
CCC TTG CTC CTC CTT TGA ACA AAT CTC TTT AAC TGA AAG TGA CCC TGA			7486
Pro Leu Leu Leu Leu * Thr Asn Leu Phe Asn * Lys * Pro *			
2480	2485	2490	2495
GAC TGT CGT CGA GGC TGG CTT ACC CTT GGA GTT CGT GAA CTC CAA CAC			7534
Asp Cys Arg Arg Gly Trp Leu Thr Leu Gly Val Arg Glu Leu Gln His			
2500	2505	2510	
CGG GCC GTC TCC GGC TCG GAG GAT TGT CAG AAT CCG ACA GGC TTG CTG			7582
Arg Ala Val Ser Gly Ser Glu Asp Cys Gln Asn Pro Thr Gly Leu Leu			
2515	2520	2525	
TTG TGA CAG ATC CAC AAT GAA GGC CAT GCC GTT GTC GTT CAC TGT CGG			7630
Leu * Gln Ile His Asn Glu Gly His Ala Val Val Val His Cys Arg			
2530	2535	2540	
GGA GTG CCT CTT CGT TAC TCG CTA TGA CCC GGA CGG TCA CCA ACT GTT			7678
Gly Val Pro Leu Arg Tyr Ser Leu * Pro Gly Arg Ser Pro Thr Val			
2545	2550	2555	
TGA CGA GCG AGG TCC GAT AGA GGT ATC TAC TCC TAT ATG TGA AGT GAT			7726
* Arg Ala Arg Ser Asp Arg Gly Ile Tyr Ser Tyr Met * Ser Asp			
2560	2565	2570	2575
TGG GGA CAT CAG GCT TCA GTG TGA CCA AAT TGA GGA AAC TCC AAC ATC			7774
Trp Gly His Gln Ala Ser Val * Pro Asn * Gly Asn Ser Asn Ile			
2580	2585	2590	
TTA CTC TTA CAT CTG GTC AGG GGC GCC CTT GGG TAC TGG GAG AAG TGT			7822
Leu Leu Leu His Leu Val Arg Gly Ala Leu Gly Tyr Trp Glu Lys Cys			
2595	2600	2605	
CCC CCA ACC CAT GAC GCG CCC TAT AGG GAC CCA TCT GAC TTG TGA CAC			7870
Pro Pro Thr His Asp Ala Pro Tyr Arg Asp Pro Ser Asp Leu * His			
2610	2615	2620	

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GGG GCA CCT GGC CAG AGC CCT CCT CTG GCA YCC AGG KTT GAA GGA GCA 9310
 Gly Ala Pro Gly Gln Ser Pro Pro Leu Ala Xaa Arg Xaa Glu Gly Ala
 3090 3095 3100

YCC CCC RCC CAT AAA TTC ACT TCC AGG TTT TCA GCT GGC GAC GCC TTA 9358
 Xaa Pro Xaa His Lys Phe Thr Ser Arg Phe Ser Ala Gly Asp Ala Leu
 3105 3110 3115

CGA ACA CCA TGA AGA GGT CTT GAT CTC GAT CAA GAG TCG ACC ACC TTG 9406
 Arg Thr Pro * Arg Gly Leu Asp Leu Asp Gln Glu Ser Thr Thr Leu
 3120 3125 3130 3135

GAT AAG GTG GAT TCT TGG TGC TTG TCT CTC GTT GCT GGC CGC CTT GCT 9454
 Asp Lys Val Asp Ser Trp Cys Leu Ser Leu Val Ala Gly Arg Leu Ala
 3140 3145 3150

GTG AAT TCG CTC CAG GCA GTA GGA CCT TCG GGT CGG GGG 9493
 Val Asn Ser Leu Gln Ala Val Gly Pro Ser Gly Arg Gly
 3155 3160

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Val Gly Val Arg Gly Pro Gly Pro Pro Thr Glu Val Gly Gly Lys Gly
 1 5 10 15

Pro Trp Thr Gly Arg Val Glu Gly Pro Glu Pro Val His Leu Pro Gln
 20 25 30

Gly

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Gly Arg Gly Thr Ser Ile Gly Pro Val Gly Pro Lys Gly Val Trp Met
 1 5 10 15

Pro Ser Val Arg Val Arg Arg Trp
 20

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Ile Pro Ala Arg Arg Glu Ser Ala Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Ala Tyr Pro Gly Asp Arg Cys Pro Gly Thr Ser Pro Ala Xaa Leu Trp
1 5 10 15
Thr Arg Ser Thr Gly Trp Gly Tyr Arg Cys Glu
20 25

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Ser Val Ser Arg
1

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

359

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Thr Glu Thr Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Asp Arg Asn Asp Ala Pro Arg Thr Gly Thr Pro Pro Lys Pro Ser Gly
1 5 10 15

Gln Leu Cys Gly Leu Thr Ile Pro Val Gly Gly Arg Gly Pro Ala Asp
20 25 30

Tyr Leu Ser Cys Glu Phe Leu Leu Arg Leu Ala Glu Arg Gln Pro Arg
35 40 45

Gly His Gln Gly Gly Ala Ala Leu His Ala Ala Arg Gly Lys Ile Leu
50 55 60

Arg Val Thr Pro Gly Gly Asn Pro Phe Pro
65 70

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Glu His Glu Cys Gly Arg His Ile His His Gly Leu Ala Val Val Ala
1 5 10 15

Gly Leu Leu Pro Pro Arg Gly Gly Gly Ala Leu Gln Leu Ala Ala Pro
20 25 30

Val L u Gln Trp Gly Pro Leu Cys Ala Phe Gln Leu Leu Phe Pro Arg
35 40 45

Arg Gly Leu Leu Leu Phe Arg Gly Arg Met Ser Gly Gly Leu Trp Leu

50

55

60

Tyr Ser Ala Arg Val Arg Thr Arg
85

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Leu His Arg Trp Ser Pro Arg Val Gly
 20 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Thr Asp Ser Gln Arg His Leu Arg Glu Gly Leu
20 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

361

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Val Tyr Leu Pro Arg Leu Val His Arg Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Leu Gly Val Tyr Gln Asp Leu Ala Val Ala Gly Gln Ala Val Ala Arg
1 5 10 16
Pro Asn Gly Xaa Xaa Gly Leu Glu Pro Pro Arg Asp Pro His Ala Gly
20 25 30
Pro Arg Ala Ala Pro Pro Asp Ser Leu Pro Thr Ala Phe Gly Ser Gly
35 40 45
Arg Gly Ser Glu Gly Asp Val Arg Gln Leu Arg Val Trp Leu Leu Gly
50 55 60
Gly Gln Glu Ala Pro Val Gly Asp Pro Ala Val Pro Trp Gln Arg Tyr
65 70 75 80
Cys Gly Val

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Phe Trp Lys Asn Ala Leu Gly Pro Pro Leu Val Phe Arg Xaa Gly Val
1 5 10 15

362

Ala Gly Arg Ser
20

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Glu Gly His Arg Ala Arg Pro Pro Pro Gly Leu Pro Pro Gly Gly Ser
1 5 10 15
Arg His Gly Asp Ser His Val Ser Val Gly Phe Cys Leu Leu Asp Leu
20 25 30
Glu Ile Trp Gly Leu Gly Cys Ile Val Arg Arg Ala Thr Thr Ile Ser
35 40 45
Ser Leu Tyr Phe Leu Leu Arg Ser Trp Ser Thr Thr
50 60 65

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Arg Ser Leu Ser Leu Glu Ser Ile Arg Gly Thr Leu Cys Phe Leu Arg
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids

363

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Pro Glu Ala Ala Glu Met Trp Phe Leu Arg Pro Arg Leu Leu Gly Asp
1 5 10 15
Gly Gly Ser Trp Val Arg
20

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Val Arg Cys Arg Tyr Ser Asp Asp Glu Ala Pro Arg Gly Arg Pro Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Trp Arg Cys Gly Val Gln Gly Asp Asn Ala Gln Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

364

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Ala Pro Gln Ile His Arg Ser Ala Arg Cys Gly Asn Leu Leu Arg Arg
1 5 10 15

Cys Pro

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Pro Gln His Gln Leu Pro Ser Asp
1 5

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Gly Gly Gly Leu Leu Ala Cys Ala Glu Val Pro Val Arg Leu Cys Ala
1 5 10 15

Pro Ser Ala Pro Arg Lys Asn Ser Arg
20 25

365

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Ala Cys Glu Cys Met Ser Ser Trp Glu Val Ser Ala Pro Val Arg Lys
1 5 10 15
Leu Gly Ser Arg Trp Val Leu Arg Pro Arg Val His Gln Val Gln Leu
20 25 30
Ala Glu Asp Leu Arg Ser Gly Cys Val Ser Trp Val Cys Phe Arg Phe
35 40 45
Pro Trp
50

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Ser Gln Arg Leu His Pro Cys
1 5

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Arg Gln Gln Thr Ala Gly Leu Gln Trp Ser Ala Lys Val Phe Ala Gly
1 5 10 15
Leu Val Ala Tyr
20

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

His Gly Pro Gly Pro Val Gly Gly Asp Glu Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Ser Cys Pro Pro Val Tyr Ala Gly Asn Val Val Val Val Glu Trp Ser
1 5 10 15

Ile Cys Cys His Tyr Cys His His Thr Pro Tyr Cys His Glu Val His
20 25 30

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid

367

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Lys Cys Ser Ile Val Asp Ser Ala His Cys Ser Asn Ser Ile Leu Pro
 1 5 10 15
 Glu Phe Tyr His Arg Ser Arg Gly Leu Tyr Leu Gln Cys Trp Leu Leu
 20 25 30
 His Gly Gly Arg Pro Gly Gly Arg Gly Ser Gly Gly Leu Gly Cys Cys
 35 40 45
 Gln

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Trp Cys Ser Gly Arg Arg Trp Trp His Leu Ala Arg Val Ala Gln Ala
 1 5 10 15
 Ala Lys Leu Arg Cys Arg Ser Gly Leu Val Val Lys Cys Trp Gly Leu
 20 25 30
 Leu Ala Gly Arg Arg Gly Arg Xaa Gly Ser Arg Ala Gly Val His Pro
 35 40 45
 Gly Gly Arg Leu Gly Ser Pro Gly Val Val Val His Trp Leu Ser Gly
 50 55 60
 Cys Asp Val Cys Arg Gly Val Pro Glu Cys Pro Gly Leu Cys Xaa Gly
 65 70 75 80
 Cys Arg Ala Cys Gly Asp Ala Leu Arg Lys Gly Cys Ser Ala Ala Gly
 85 90 95
 Ile Gly Gly Ser Cys Arg Gly Xaa Pro Gly Ala Ala Gln Arg Leu Arg
 100 105 110
 Ala

368

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Gly Val Leu Arg Ser Gly Trp Trp Arg Leu Ala Xaa Arg Gln Leu Val
 1               5               10               15
Leu Gly Phe Ser Arg Arg Gly Glu Leu Gly Pro Pro Gly Gly Gly Ser
      20               25               30
Asp Asp Pro Arg Trp Pro Ile Ser Gln Xaa Asp Leu Val Xaa Gln Val
      35               40               45
Gly Arg Gln Leu Xaa Glu Gly Ser Xaa Val Gly Glu Gln Leu Thr Gly
      50               55               60
Trp Ser Xaa Trp Xaa Leu Xaa Ala Xaa Leu Glu Ser Xaa Val Xaa Xaa
      65               70               75               80
Gly Leu Val Leu Pro Pro Asp Ser Cys His Ser Xaa Arg His Leu His
      85               90               95
Thr Leu Phe Glu Gln Phe Arg Cys
      100               105

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe His Leu Gly Xaa Thr Leu Gly
 1               5

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

369

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Leu Thr Lys Ser Arg Ala Leu Gly Ala Xaa Ala Gly Leu Leu Ser Ser
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Gly Ala Ala Gly Leu Leu Leu Ala Gly Gly Arg Pro Ala Gln Ala Gly
1 5 10 15

Arg Pro Pro Leu Arg Ala Arg Xaa Ser His
20 25

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Gln Ala Arg Cys Cys Pro Leu Ala Arg Val Gly Xaa Cys Ala Xaa Ala
1 5 10 15

Xaa

370

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Xaa Asn Gln Gly Arg Leu Xaa Xaa Cys Ser Gly Leu Cys Ser Cys Val
 1 5 10 15
 Gly Leu Trp Thr Ile Gly Pro Trp Glu Thr Ser Gly Arg Glu Ala Arg
 20 25 30
 Arg Arg Gly Val Asp Arg Leu Cys Glu Gln Ser Val Arg Pro Ser Ala
 35 40 45
 Trp Leu Cys Ser His Cys Ser Arg Gly Xaa Ser Ser Xaa Xaa Gln Xaa
 50 55 60
 Xaa Xaa Xaa Gly Cys Glu Asp Xaa His Asp Arg Gln Gly Pro Val Arg
 65 70 75 80
 Thr Pro Arg Xaa Arg Gly Gly Pro Xaa Asp Phe Asn Asn Xaa Phe His
 85 90 95
 Gly Leu Leu Arg Glu Arg Ser Ser Val His Xaa Ile Pro Trp Xaa Gln
 100 105 110
 Arg Pro Xaa Xaa Gly Gly Ala Xaa Trp Xaa Xaa Gln Xaa Ser Val Val
 115 120 125
 Val Xaa Glu Xaa Arg Arg His Gly Xaa Pro Ala Pro Xaa Trp Xaa Phe
 130 135 140 145
 Leu Pro Xaa Xaa Xaa Xaa Val Pro Thr Asn Trp Gly Val Gly Asp Pro
 150 155 160
 Glu

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Arg Ser Ser Leu Pro Trp Asn Ser Arg Gln Gly Gly Gly Phe Arg Tyr
1 5 10 15
Ala Arg

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Val Val Arg Leu Ser Arg Val Phe Trp Ile Thr Asn Leu Val Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Gly Ser Cys Cys Trp His Ala Asp Phe Gly Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Gly Phe Leu Gly Ala Val Tyr Gln Thr Leu Gly Asn Ser Pro Ser Gly
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Gly Ser Ile Gly Gly Pro Pro Cys Ala Arg Asn His Trp Ile Gln Gly
1 5 10 15

Gly Ala Thr Val Pro Ala His Arg Ser Trp Gln Val Asp Ala Arg Ala
20 25 30

Glu

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Val Arg Gln Gly Trp Thr Gln Xaa Ala Cys Thr Lys Pro Ile His Cys
1 5 10 15

His Ser Glu Gly His Gly Pro Leu His Gly Lys Val Asn Arg Gln Thr
20 25 30

373

Ser Val Gly Val Leu Trp Pro
35

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

His Tyr Cys Ile Phe Gln Asp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Leu Ile Phe Asp Leu Leu Tyr Ile Arg Gln Val Tyr Gly Gln Ser Gln
1 5 10 15

Glu Ile Leu Ala Gly Glu Arg Arg Arg Asn Leu Arg Arg Val Ala Arg
20 25 30

His Arg Pro Asp Leu Asn Phe Gly Asp Gly Ser Gly Glu Val Thr Arg
35 40 45

Ser Arg Val Arg Arg Thr Pro Pro Ala Phe Arg Tyr Gly Asp Pro Thr
50 55 60

Gly Leu Ser Asp Gly Glu Ala
65 70

(2) INFORMATION FOR SEQ ID NO:312:

374

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Gly Asp Val Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Gly Gly Gly Pro Leu Leu Leu Pro Ile Pro Pro Thr Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Val Cys Tyr Trp Glu Thr Pro Ala Val Leu Ser Phe Gln Gly Arg Xaa
1 5 10 15

His

(2) INFORMATION FOR SEQ ID NO:315:

375

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Val Ile Leu Ser Phe Gly Gln Leu Trp Cys Gln His Arg Cys Val Leu
1 5 10 15

Gln Arg Gln Arg Asn
21

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

His Ser Asn Trp
1

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Arg Val Arg Leu Arg His Arg Arg Thr Phe His Trp Leu His Trp Gln Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:318:

376

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

His Arg Asn Arg Leu Trp Phe Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Gly Gly Ser Gly Ser Asp Pro Gly Pro Asp His His Tyr Arg Cys Glu
1 5 10 15
Asp Arg Pro Gly Pro Cys Arg Thr Glu Gly Ser Glu Ala Trp
20 25 30

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Val Trp Pro Trp Glu Ser Gly His Leu Leu Ser Gly Ile Asp Val Phe
1 5 10 15
Gly Ala Gly Gly Asn Xaa Ser Val Trp Gly Ser Leu Gly Ser Cys
20 25 30

377

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Gly Trp Xaa Leu Val Val Trp Pro Arg Ala Arg Cys Tyr Trp Arg Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Gly Leu Arg Leu Val Ser Leu Tyr Cys Cys His Gln Cys Val His Arg
1 5 10 15

Arg Gly His Cys Leu Phe Tyr Trp Xaa Ser Ala Asn Glu Glu Leu Ser
20 25 30

Ser Gly Gly Leu Gly Gln Ala Glu Gly Xaa Gln Leu Ala Thr Leu Gly
35 40 45

Gly Cys Ala Glu Ala His Val
50 55

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

378

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Gly Arg Gly Leu Trp Ser Xaa Arg
1 5

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Trp Ser Arg Met Glu Arg His Gln Gly Lys Arg Ala Cys Ser Pro Val
1 5 10 15

Val Pro Met Gly Trp
20

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Val Gly Gly Ser Ala Ser Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

379

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Pro Thr Gly Pro Ala Arg Cys Gly Arg Gly Leu His Ser Leu His Cys
1 5 10 15
Trp Thr Gly Ala Phe Gly Arg Phe Gly Asp Gly Gly Gly Tyr Pro
20 25 30
Gly Thr Leu Asp Gly Val Ser Gly Cys Ser Asp Gln Leu Gly Cys Gln
35 40 45
Trp Glu Arg
50

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Pro Ala Asp Thr Lys Arg Leu
1 5

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Gly Arg Gly Xaa Xaa Arg Ser Ile Pro Ser Thr Pro Arg Trp Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:329:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Thr Val Pro Ile Arg His Gln Ala Asn Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Gly Cys Asp His Pro
1 5

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Asp Cys Val Arg Xaa Gly Pro Ser Arg Gly Xaa Ser Gly Leu Cys Glu
1 5 10 15

Gly Leu

(2) INFORMATION FOR SEQ ID NO:332:

381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Asn Trp Asn His Val Gly
1 5

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Gln Xaa Glu Cys Cys Val Ala Gly Leu Gly Cys Lys Gln Leu Cys Ala
1 5 10 15
Ser Thr Ser Ile Thr Leu Asn Phe Leu Val Xaa Glu Leu Gly Xaa Cys
20 25 30
Val His Phe Ser Leu Gly
35

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Arg Val His Ser Arg Pro Phe Leu Ala Cys Trp Val His Ser Cys Leu
1 5 10 15

382

Arg Arg Ser Ala Glu Pro Thr Ala Gly Arg Arg Ser Leu Phe Leu Ala
 20 25 30

Gly His Val Ile Glu Pro Xaa Xaa Ser Arg Gln Thr Cys Cys Cys Val
 35 40 45

Ala Pro Arg Arg Arg Gly Tyr Arg Pro Arg His Ala Cys Tyr Trp Ala
 50 55 60

Cys Tyr Gly Gly Cys Leu LeuArg Xaa Gly Gln Arg Tyr Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Leu Ala Glu Tyr His Cys Gly Ser Asn Arg Arg Leu Gly Gly Gly Xaa
 1 5 10 15

Xaa Arg Ser Leu Thr His Leu Arg Xaa Pro Gly Xaa Glu Val Thr Ser
 20 25 30

Xaa Xaa Xaa Leu Val Pro Xaa Gln Xaa Xaa Gly Leu Ser Gly Gly Phe
 35 40 45

Gly Gly Xaa Cys Gly Xaa Xaa Xaa Xaa Ala Xaa Val Cys Gln Xaa Gly
 50 55 60

Cys Gly Xaa Xaa Xaa Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Gln Xaa Val Asp Asp Asp Ala Thr Gln Phe Gly Asp Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Arg Phe Leu Pro Gln Arg
1 5

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Val Arg His Gln Gly Val Tyr Cys Pro Ala Lys Val Val Ile Val Lys
1 5 10 15

Met Asp His Asp Ser Cys Gly Gln Ala Gly Asp Gly Asp Gly Asp Xaa
20 25 30

Arg Phe Ser Asp Cys Leu Gly Leu Ala
35 40

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

384

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Leu Val His Pro Ala Xaa Ser Val Pro Val Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Thr Xaa Val Cys Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Ala Pro Ala Ala Tyr Arg Leu Gln Tyr Arg Leu Gly Trp Pro Val
1 5 10 15

Gly Gly Gln Trp Ser Phe Gly Asn Lys Val Tyr Leu Trp Leu Cys Asp
20 25 30

Tyr Arg

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

385

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Tyr	Ser	Arg	Trp	Tyr	Ile	Ala	Arg	Pro	Thr	Leu	Tyr	Leu	Pro	Thr	Val
1				5					10					15	
Gln	Thr	Leu	Leu	Gln	Glu	Asp	Ser	Ala	Cys	Trp	Arg	His	Gly	Gln	Cys
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Gly	Ser	Ser	Pro	Pro	Cys	Ala	Tyr	Trp	Arg	Trp	Asn	Gln	Asp	Leu	Pro
1				5					10					15	
Asn	Trp	Asp	Phe												
			20												

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Gly	Cys	Gly	Arg	Ala	Trp	Asp	Asn	His	Gly	Ala	Arg	His	Gln	Leu	Leu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:345:

386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Val Glu Ser Cys

1

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Arg Ser Glu Gly Gly Ala Ser Arg Pro Asp Leu Arg Trp Trp Arg Thr
1 5 10 15

Leu Gln Leu Glu Arg Ala Val Tyr Cys Ala Cys Ala Arg Leu Gln Ala
20 25 30

Arg Pro Gly His Gln Asn Arg Trp Ser Ala Pro Thr Val Ala Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Leu Ser Thr Gly Ser Ala Pro Pro Pro Gly Ile Trp Gln Cys Cys Arg
1 5 10 15

387

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Trp Leu Asp Arg
1

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Gly Arg Glu Gly Leu Gly Gly Asn Gln Gly Cys Arg His Arg Gly His
1 5 10 15

Trp Gly Gly Leu Ala Pro Pro Phe Thr Gly Gly Cys Ser Gly Arg Ser
20 25 30

Arg Gly Phe Gly Gly Gly Cys Arg Val Pro Val Ala Pro Cys Ala Arg
35 40 45

His Tyr Gly
50

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

388

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Leu Phe Met Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Gly Val Pro Arg Pro Leu His Pro Arg Thr Gln Cys Asp Arg Gly Thr
1 5 10 15

His

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Ala His Gly Arg Arg Arg Gly Gly Thr GlnAla Ala Gly Cys Arg Pro Asp
1 5 10 15

Arg Gln Val Ala Arg Leu Gly Gly His Gly Ser Arg Pro Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:353:

389

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Val Asn Arg Gly Cys Ser Arg Ser Phe Asp Ala Phe Ala His Arg Gly
1 5 10 15

Gly Leu Asn Ala Ile Ile Gly Val Glu Pro Leu Leu Leu Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Thr Asn Leu Phe Asn
1 5

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Asp Cys Arg Arg Gly Trp Leu Thr Leu Gly Val Arg Glu Leu Gln His
1 5 10 15

Arg Ala Val Ser Gly Ser Glu Asp Cys Gln Asn Pro Thr Gly Leu Leu
20 25 30

390

Leu

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Gln Ile His Asn Glu Gly His Ala Val Val Val His Cys Arg Gly Val
1 5 10 15
Pro Leu Arg Tyr Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Pro Gly Arg Ser Pro Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

391

Arg Ala Arg Ser Asp Arg Gly Ile Tyr Ser Tyr Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Ser Asp Trp Gly His Gln Ala Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Gly Asn Ser Asn Ile Leu Leu Leu His Leu Val Arg Gly Ala Leu Gly
1 5 10 15

Tyr Trp Glu Lys Cys Pro Pro Thr His Asp Ala Pro Tyr Arg Asp Pro
20 25 30

Ser Asp Leu
35

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

His Tyr Gln Ser Leu Cys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Ala Gly Arg Glu Gly Tyr Asn Leu Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Gly Cys Pro Glu Lys Gly Ser Arg Asp Glu Val Ser Trp Leu Asp Leu
1 5 10 15

Phe Pro Gly Tyr Ser
20

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

393

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Ala Pro Ser Ser Arg Trp Ile Arg Gln Gln Gly Asp Arg Leu His Ile
1 5 10 15
Gly His Trp Leu Ala Ser Arg Gly Gly Asp Ala Gly Gln Asn Ser Gln
20 25 30
Gly Thr Gly Ser Ser Phe His Phe Cys Asp Gln Ala Arg Gly Phe Leu
35 40 45
Leu Gln Asn Tyr Pro
50

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Ala Pro Lys Ile His Ser Phe Pro Thr Phe Gly Leu Gln Asp Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

394

Lys Asp Asp Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Pro Arg His Arg Cys Lys Val Asn Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Arg Leu Ser Val Pro Val His Ala Gln Ser Glu Gly Gln Ser Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Gly Val Gly Gly Glu Val Ala Ser Arg Cys Asp His Cys Gly Arg His

395

1 5 10 15
Leu Phe Arg Leu Ile
 20

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Ala Arg His Ala Gly Gly Gly Phe Gly Val Cys Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Gln Pro Leu Asn Gly Thr Cys Phe Val Gln Val Leu Leu Trp Trp Pro
1 5 10 15
Tyr Gly Phe Pro Arg Trp Gly Ser Leu Gly Val Pro Pro Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

396

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Val Val Gly Arg Val Asn Asn
1 5

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Leu Gly Glu Gln His His Leu Leu His
1 5

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Gly Gln Arg Gly Leu Gln Ala Gly Gly Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

397

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Gly Thr Ile Ile Leu Tyr Ser Trp Arg
1 5

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Leu Leu Asp His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Ser Leu Pro Cys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

398

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Gly	Cys	Pro	Gly	Gln	Leu	Trp	Ile	Gln	Val
1				5					10

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Thr	Asn	Lys	Ala	Cys	Phe	Thr	Gly	His	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Val	Leu	Leu	Gly	Leu	Leu	Gly
1				5		

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Val Arg Ser Trp Gly Cys Gln Ala Leu Val Val Glu His Gly His Glu
 1 5 10 15
 Glu Ala Ala Arg Lys Gly Val Phe Arg Ile Phe Gly Pro Asn Arg Gln
 20 25 30
 Cys Phe Arg Asp His Leu Asp Val Ser Pro Ala Ser Asn Arg Ala Val
 35 40 45
 Cys Ser Asn Thr Thr Arg Thr Asn Asn Gly Leu Gln Glu Trp Gln His
 50 55 60
 Thr Gly
 65

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Val Gly Tyr Val Ser Gly Ser Gly Lys Ser Leu Leu Phe Pro Ala Ala
 1 5 10 15
 Ala Ala Ala Ser Arg Leu Gly Leu Ser Thr Trp Ser Val Val Pro Thr
 20 25 30
 Ser His His Gly Gln Tyr Glu
 35

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

400

Asp Gly Gly Arg Leu Ser Xaa Ala Gly Phe Arg Asn Glu Ile Pro Ser
 1 5 10 15
 Leu Ala Pro Pro Thr Cys Arg Lys Cys Ala His Ser Pro Pro Glu Gly
 20 25 30
 Arg Gln Gly Val Gly Ala Pro Gly Gln Ser Pro Pro Leu Ala Xaa Arg
 35 40 45
 Xaa Glu Gly Ala Xaa Pro Xaa His Lys Phe Thr Ser Arg Phe Ser Ala
 40 45 50
 Gly Asp Ala Leu Arg Thr Pro
 55 60

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Arg Gly Leu Asp Leu Asp Gln Glu Ser Thr Thr Leu Asp Lys Val Asp
 1 5 10 15
 Ser Trp Cys Leu Ser Leu Val Ala Gly Arg Leu Ala Val Asn Ser Leu
 20 25 30
 Gln Ala Val Gly Pro Ser Gly Arg Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

401

(B) LOCATION: 3..9493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

CG TGG GAG TCC GGG GCC CCG GAC CTC CCA CCG AGG TGG GGG GAA AGG	47
Trp Glu Ser Gly Ala Pro Asp Leu Pro Pro Arg Trp Gly Glu Arg	
1 5 10 15	
GGC CCT GGA CCG GCC GGG TGG AAG GCC CGG AAC CGG TCC ATC TTC CTC	95
Gly Pro Gly Pro Ala Gly Trp Lys Ala Arg Asn Arg Ser Ile Phe Leu	
20 25 30	
AAG GTT GAG GAA GGG GTA CGT CTA TCG GTC CGG TCG GTC CGA AAG GCG	143
Lys Val Glu Glu Gly Val Arg Leu Ser Val Arg Ser Val Arg Lys Ala	
35 40 45	
TCT GGA TGC CTA GTG TTA GGG TTC GTA GGT GGT AAA TCC CAG CTA GGC	191
Ser Gly Cys Leu Val Leu Gly Phe Val Gly Gly Lys Ser Gln Leu Gly	
50 55 60	
GTG AAA GCG CTA TAG GAT AGG CTT ATC CCG GTG ACC GCT GCC CCG GAA	239
Val Lys Ala Leu * Asp Arg Leu Ile Pro Val Thr Ala Ala Pro Glu	
65 70 75	
CCA GCC CCG CGG KTC TTT GGA CAC GGT CCA CAG GTT GGG GGT ACC GGT	287
Pro Ala Pro Arg Xaa Phe Gly His Gly Pro Gln Val Gly Gly Thr Gly	
80 85 90 95	
GTG AAT AAC CCC CCG ACT GAA GCG TCA GTC GTT AAA CGG AGA CGG TCT	335
Val Asn Asn Pro Pro Thr Glu Ala Ser Val Val Lys Arg Arg Arg Ser	
100 105 110	
CCT GAG ATC GCA ACG ACG CCC CAC GTA CGG GAA CGC CGC CAA AAC CTT	383
Pro Glu Ile Ala Thr Thr Pro His Val Arg Glu Arg Arg Gln Asn Leu	
115 120 125	
CGG GAC AGC TAT GCG GGT TGA CAA TCC CAG TGG GGG GCC GGG GAC CAG	431
Arg Asp Ser Tyr Ala Gly * Gln Ser Gln Trp Gly Ala Gly Asp Gln	
130 135 140	
CTG ATT ACT TGT CCT GCG AGT TCC TCT TGA GAC TGG CCG AAA GGC AGC	479
Leu Ile Thr Cys Pro Ala Ser Ser * Asp Trp Pro Lys Gly Ser	
145 150 155	
CAC GGG GCC ACC AAG GCG GCG CAG CGC TGC ATG CGG CAA GGG GAA AAA	527
His Gly Ala Thr Lys Ala Ala Gln Arg Cys Met Arg Gln Gly Glu Lys	
160 165 170 175	
TCC TTC GGG TGA CCC CTG GTG GCA ATC CCT TCC CTT AGG AGC ATG AGT	575
Ser Phe Gly * Pro Leu Val Ala Ile Pro Ser Leu Arg Ser Met Ser	
180 185 190	
GTG GTC GAC ACA TTC ACC ATG GCT TGG CTG TGG TTG CTG GTT TGC TTC	623
Val Val Asp Thr Phe Thr Met Ala Trp Leu Trp Leu Leu Val Cys Phe	
195 200 205	

402

CCC CTC GCG GGG GGG GTG CTC TTC AAC TCG CGG CAC CAG TGC TTC AAT	671
Pro Leu Ala Gly Gly Val Leu Phe Asn Ser Arg His Gln Cys Phe Asn	
210 215 220	
GGG GAC CAT TAT GTG CTT TCC AAT TGT TGT TCC CGA GAC GAG GTT TAC	719
Gly Asp His Tyr Val Leu Ser Asn Cys Cys Ser Arg Asp Glu Val Tyr	
225 230 235	
TTC TGT TTC GGG GAC GGA TGT CTG GTG GCT TAT GGC TGT ACT GTT TGC	767
Phe Cys Phe Gly Asp Gly Cys Leu Val Ala Tyr Gly Cys Thr Val Cys	
240 245 250 255	
ACA CAG TCT TGC TGG AAG CTC TAC CGG CCT GGG GTG GCT ACT CGG CCC	815
Thr Gln Ser Cys Trp Lys Leu Tyr Arg Pro Gly Val Ala Thr Arg Pro	
260 265 270	
GGG TCC GAA CCA GGT GAG CTG CTG GGG AGA TTT GGG AGT GTA ATT GGT	863
Gly Ser Glu Pro Gly Glu Leu Leu Gly Arg Phe Gly Ser Val Ile Gly	
275 280 285	
CCG GTG TCG GCT TCG GCT TAC ACC GCT GGA GTC CTC GGG TTG GGT GAA	911
Pro Val Ser Ala Ser Ala Tyr Thr Ala Gly Val Leu Gly Leu Gly Glu	
290 295 300	
CCT TAC AGT TTG GCC TTC TTG GGG ACG TTC CTC ACC AGT CGC CTC TCA	959
Pro Tyr Ser Leu Ala Phe Leu Gly Thr Phe Leu Thr Ser Arg Leu Ser	
305 310 315	
CGG ATT CCC AAC GTC ACC TGC GTG AAG GCT TGT GAC CTT GAG TTT ACC	1007
Arg Ile Pro Asn Val Thr Cys Val Lys Ala Cys Asp Leu Glu Phe Thr	
320 325 330 335	
TAC CCA GGC TTG TCC ATC GAT TTT GAC TGG GCG TTT ACC AAG ATC TTG	1055
Tyr Pro Gly Leu Ser Ile Asp Phe Asp Trp Ala Phe Thr Lys Ile Leu	
340 345 350	
CAG TTG CCG GCC AAG CTG TGG CGA GGC CTA ACG GCR GCW CCG GTC TTG	1103
Gln Leu Pro Ala Lys Leu Trp Arg Gly Leu Thr Xaa Xaa Pro Val Leu	
355 360 365	
AGC CTC CTC GTG ATC CTC ATG CTG GTC CTC GAG CAG CGC CTC CTG ATA	1151
Ser Leu Leu Val Ile Leu Met Leu Val Leu Glu Gln Arg Leu Leu Ile	
370 375 380	
GCC TTC CTA CTG CTT TTG GTA GTG GGC GAG GCT CAG AGG GGG ATG TTC	1199
Ala Phe Leu Leu Leu Leu Val Val Gly Glu Ala Gln Arg Gly Met Phe	
385 390 395	
GAC AAC TGC GTG TGT GGT TAC TGG GGG GGC AAG AGG CCC CCG TCG GTG	1247
Asp Asn Cys Val Cys Gly Tyr Trp Gly Gly Lys Arg Pro Pro Ser Val	
400 405 410 415	
ACC CCG CTG TAC CGT GGC AAC GGT ACT GTG GTG TGT GAC TGT GAT TTT	1295
Thr Pro Leu Tyr Arg Gly Asn Gly Thr Val Val Cys Asp Cys Asp Phe	
420 425 430	
GGA AAA ATG CAT TGG GCC CCC CCC TTG TGT TCC GGY CTG GTG TGG CGG	1343

403

Gly Lys Met His Trp Ala Pro Pro Leu Cys Ser Xaa Leu Val Trp Arg	
435 440 445	
GAC GGT CAT AGG AGG GGC ACC GTG CGC GAC CTC CCC CCG GTT TGC CCC	1391
Asp Gly His Arg Arg Gly Thr Val Arg Asp Leu Pro Pro Val Cys Pro	
450 455 460	
CGG GAG GTT CTC GGC ACG GTG ACA GTC ATG TGT CAG TGG GGT TCT GCC	1439
Arg Glu Val Leu Gly Thr Val Thr Val Met Cys Gln Trp Gly Ser Ala	
465 470 475	
TAC TGG ATT TGG AGA TTT GGG GAC TGG GTT GCA TTG TAC GAC GAG CTA	1487
Tyr Trp Ile Trp Arg Phe Gly Asp Trp Val Ala Leu Tyr Asp Glu Leu	
480 485 490 495	
CCA CGA TCA GCT CTC TGT ACT TTC TTC TCA GGT CAT GGT CCA CAA CCT	1535
Pro Arg Ser Ala Leu Cys Thr Phe Phe Ser Gly His Gly Pro Gln Pro	
500 505 510	
AAA GAT CTC TCA GTC TTG AAT CCA TCC GGG GCA CCT TGT GCT TCT TGC	1583
Lys Asp Leu Ser Val Leu Asn Pro Ser Gly Ala Pro Cys Ala Ser Cys	
515 520 525	
GTC GTT GAC CAG AGG CCG CTG AAA TGT GGT TCC TGC GTC CGC GAC TGC	1631
Val Val Asp Gln Arg Pro Leu Lys Cys Gly Ser Cys Val Arg Asp Cys	
530 535 540	
TGG GAG ACG GGG GGT CCT GGG TTC GAT GAG TGC GGT GTC GGT ACT CGG	1679
Trp Glu Thr Gly Gly Pro Gly Phe Asp Glu Cys Gly Val Gly Thr Arg	
545 550 555	
ATG ACG AAG CAC CTC GAG GCC GTC CTG GTT GAT GGA GGT GTG GAG TCC	1727
Met Thr Lys His Leu Glu Ala Val Leu Val Asp Gly Gly Val Glu Ser	
560 565 570 575	
AAG GTG ACA ACG CCC AAG GGT GAG CGC CCC AAA TAC ATA GGT CAG CAC	1775
Lys Val Thr Thr Pro Lys Gly Glu Arg Pro Lys Tyr Ile Gly Gln His	
580 585 590	
GGT GTG GGA ACC TAC TAC GGC GCT GTC CGT AGC CTC AAC ATC AGT TAC	1823
Gly Val Gly Thr Tyr Tyr Gly Ala Val Arg Ser Leu Asn Ile Ser Tyr	
595 600 605	
CTA GTG ACT GAG GTG GGG GGC TAT TGG CAT GCG CTG AAG TGC CCG TGC	1871
Leu Val Thr Glu Val Gly Gly Tyr Trp His Ala Leu Lys Cys Pro Cys	
610 615 620	
GAC TTT GTG CCC CGA GTG CTC CCA GAA AGA ATT CCA GGT AGG CCT GTG	1919
Asp Phe Val Pro Arg Val Leu Pro Glu Arg Ile Pro Gly Arg Pro Val	
625 630 635	
AAT GCA TGT CTA GCT GGG AAG TCT CCG CAC CCG TTC GCA AGT TGG GCT	1967
Asn Ala Cys Leu Ala Gly Lys Ser Pro His Pro Phe Ala Ser Trp Ala	
640 645 650 655	
CCC GGT GGG TTT TAC GCC CCC GTG TTC ACC AAG TGC AAC TGG CCG AAG	2015
Pro Gly Gly Phe Tyr Ala Pro Val Phe Thr Lys Cys Asn Trp Pro Lys	

404

660	665	670	
ACC TCC GGA GTG GAT GTG TGT CCT GGG TTT GCT TTC GAT TTC CCT GGT Thr Ser Gly Val Asp Val Cys Pro Gly Phe Ala Phe Asp Phe Pro Gly 675 680 685			2063
GAT CAC AAC GGC TTC ATC CAT GTT AAA GGC AAC AGA CAG CAG GTT TAC Asp His Asn Gly Phe Ile His Val Lys Gly Asn Arg Gln Gln Val Tyr 690 695 700			2111
AGT GGT CAG CGA AGG TCT TCG CCG GCT TGG TTG CTT ACT GAC ATG GTC Ser Gly Gln Arg Arg Ser Ser Pro Ala Trp Leu Leu Thr Asp Met Val 705 710 715			2159
CTG GCC CTG TTG GTG GTG ATG AAG TTG GCT GAG GCT AGA GTT GTC CCC Leu Ala Leu Leu Val Val Met Lys Leu Ala Glu Ala Arg Val Val Pro 720 725 730 735			2207
CTG TTT ATG CTG GCA ATG TGG TGG TGG TTG AAT GGA GCA TCT GCT GCC Leu Phe Met Leu Ala Met Trp Trp Trp Leu Asn Gly Ala Ser Ala Ala 740 745 750			2255
ACT ATT GTC ATC ATA CAC CCT ACT GTC ACG AAG TCC ACT GAA AGT GTT Thr Ile Val Ile Ile His Pro Thr Val Thr Lys Ser Thr Glu Ser Val 755 760 765			2303
CCA TTG TGG ACT CCG CCC ACT GTT CCA ACT CCA TCT TGC CCG AAT TCT Pro Leu Trp Thr Pro Pro Thr Val Pro Thr Pro Ser Cys Pro Asn Ser 770 775 780			2351
ACC ACC GGA GTC GCG GAC TCT ACC TAC AAT GCT GGT TGC TAC ATG GTG Thr Thr Gly Val Ala Asp Ser Thr Tyr Asn Ala Gly Cys Tyr Met Val 785 790 795			2399
GCA GGC CTG GCG GCC GGG GCT CAG GCG GTC TGG GGT GCT GCC AAT GAT Ala Gly Leu Ala Ala Gly Ala Gln Ala Val Trp Gly Ala Ala Asn Asp 800 805 810 815			2447
GGT GCT CAG GCC GTC GTT GGT GGC ATC TGG CCC GCG TGG CTC AAG CTG Gly Ala Gln Ala Val Gly Gly Ile Trp Pro Ala Trp Leu Lys Leu 820 825 830			2495
CGA AGC TTC GCT GCC GGT CTG GCC TGG TTG TCA AAT GTT GGG GCT TAC Arg Ser Phe Ala Ala Gly Leu Ala Trp Leu Ser Asn Val Gly Ala Tyr 835 840 845			2543
TTG CCG GTC GTC GAG GCC GCV CTG GCT CCC GAG CTG GTG TGC ACC CCG Leu Pro Val Val Glu Ala Xaa Leu Ala Pro Glu Leu Val Cys Thr Pro 850 855 860			2591
GTG GTC GGC TGG GCA GCC CAG GAG TGG TGG TTC ACT GGT TGT CTG GGT Val Val Gly Trp Ala Ala Gln Glu Trp Trp Phe Thr Gly Cys Leu Gly 865 870 875			2639
GTG ATG TGT GTC GTG GCG TAC CTG AAT GTC CTG GGC TCT GTR AGG GCT Val Met Cys Val Val Ala Tyr Leu Asn Val Leu Gly Ser Xaa Arg Ala 880 885 890 895			2687

405

GCC GTG CTT GTG GCG ATG CAC TTC GCA AGG GGT GCT CTG CCG CTG GTA Ala Val Leu Val Ala Met His Phe Ala Arg Gly Ala Leu Pro Leu Val 900 905 910	2735
TTG GTG GTA GCT GCC GGG GTR ACC CGG GAG CGG CAC AGC GTC TTA GGG Leu Val Val Ala Ala Gly Xaa Thr Arg Glu Arg His Ser Val Leu Gly 915 920 925	2783
CTT GAG GTG TGC TTC GAT CTG GAT GGT GGA GAC TGG CCR GAC GCC AGT Leu Glu Val Cys Phe Asp Leu Asp Gly Gly Asp Trp Xaa Asp Ala Ser 930 935 940	2831
TGG TCT TGG GGT TTA GCA GGC GTG GTG AGC TGG GCC CTC CTG GTG GGG Trp Ser Trp Gly Leu Ala Gly Val Val Ser Trp Ala Leu Leu Val Gly 945 950 955	2879
GGT CTG ATG ACC CAC GGT GGC CGA TCA GCC AGA YTG ACT TGG TAY GCC Gly Leu Met Thr His Gly Gly Arg Ser Ala Arg Xaa Thr Trp Xaa Ala 960 965 970 975	2927
AGG TGG GCC GTC AAT TAY CAG AGG GTT CGY CGG TGG GTG AAC AAC TCA Arg Trp Ala Val Asn Xaa Gln Arg Val Xaa Arg Trp Val Asn Asn Ser 980 985 990	2975
CCG GTT GGA GCY TTT GGY CGT TGG MGG CGY GCC TGG AAA GCY TGG TTR Pro Val Gly Xaa Phe Xaa Arg Trp Xaa Xaa Ala Trp Lys Xaa Trp Xaa 995 1000 1005	3023
GTK GTG GCT TGG TTC TTC CCC CAG ACA GTT GCC ACA GTY TCC GTC ATC Xaa Val Ala Trp Phe Phe Pro Gln Thr Val Ala Thr Xaa Ser Val Ile 1010 1015 1020	3071
TTC ATA CTC TGT TTG AGC AGT TTA GAT GTC ATT GAT TTC ATC TTG GAR Phe Ile Leu Cys Leu Ser Ser Leu Asp Val Ile Asp Phe Ile Leu Xaa 1025 1030 1035	3119
GTA CTC TTG GTT AAC TCA CCA AAT CTC GCG CGC TTG GCG CGR GTG CTG Val Leu Leu Val Asn Ser Pro Asn Leu Ala Arg Leu Ala Xaa Val Leu 1040 1045 1050 1055	3167
GAC TCC TTA GCT CTH GCT GAG GAG CGG CTG GCC TGC TCT TGG CTG GTG Asp Ser Leu Ala Xaa Ala Glu Glu Arg Leu Ala Cys Ser Trp Leu Val 1060 1065 1070	3215
GGC GTC CTG CGC AAG CGG GGC GTC CTC CTC TAC GAG CAC GCY GGT CAC Gly Val Leu Arg Lys Arg Gly Val Leu Leu Tyr Glu His Xaa Gly His 1075 1080 1085	3263
ACT AGC AGG CGC GGT GCT GCC CGC TTG CGA GAG TGG GGY TTT GCG CTY Thr Ser Arg Arg Gly Ala Ala Arg Leu Arg Glu Trp Xaa Phe Ala Xaa 1090 1095 1100	3311
GAG CCK GTT AGY ATA ACC AAG GAA GAT TGY GCY ATT GTT CGG GAC TCT Glu Xaa Val Xaa Ile Thr Lys Glu Asp Xaa Xaa Ile Val Arg Asp Ser 1105 1110 1115	3359
GCT CGT GTG TTG GGC TGT GGA CAA TTG GTC CAT GGG AAA CCA GTG GTC	3407

406

Ala Arg Val Leu Gly Cys Gly Gln Leu Val His Gly Lys Pro Val Val	
1120 1125 1130 1135	
GCG AGG CGA GGC GAC GAG GTG TTG ATC GGC TGT GTG AAC AGT CGG TTC	3455
Ala Arg Arg Gly Asp Glu Val Leu Ile Gly Cys Val Asn Ser Arg Phe	
1140 1145 1150	
GAC CTT CCG CCT GGC TTT GTT CCC ACT GCT CCC GTG GTS CTT CAT CAR	3503
Asp Leu Pro Pro Gly Phe Val Pro Thr Ala Pro Val Xaa Leu His Xaa	
1155 1160 1165	
GCW GGC AAR GGR TTY TTY GGG GTT GTG AAG ACM TCC ATG ACA GGC AAG	3551
Xaa Gly Xaa Xaa Xaa Xaa Gly Val Val Lys Xaa Ser Met Thr Gly Lys	
1170 1175 1180	
GAC CCG TCC GAA CAC CAC GGR AAC GTG GTG GTC CTW GGG ACT TCA ACA	3599
Asp Pro Ser Glu His His Xaa Asn Val Val Val Xaa Gly Thr Ser Thr	
1185 1190 1195	
ACK CGT TCC ATG GGC TGC TGC GTG AAC GGA GTA GTG TAC ACR ACA TAC	3647
Xaa Arg Ser Met Gly Cys Cys Val Asn Gly Val Val Tyr Xaa Thr Tyr	
1200 1205 1210 1215	
CAT GGY ACC AAC GCC CGR CCK ATG GCG GGG CCK TTT GGK CCY GTC AAY	3695
His Xaa Thr Asn Ala Xaa Xaa Met Ala Gly Xaa Phe Xaa Xaa Val Xaa	
1220 1225 1230	
GCT CGG TGG TGG TCW GCG AGY GAC GAC GTC ACG GTY TAC CCG CTC CCW	3743
Ala Arg Trp Trp Xaa Ala Xaa Asp Asp Val Thr Xaa Tyr Pro Leu Xaa	
1235 1240 1245	
AAT GGY GCT TCT TGC CTY CAR GCW TGY AAG TGC CAA CCA ACT GGG GTG	3791
Asn Xaa Ala Ser Cys Xaa Xaa Xaa Xaa Lys Cys Gln Pro Thr Gly Val	
1250 1255 1260	
TGG GTG ATC CGG AAT GAC GGA GCT CTT TGC CAT GGA ACT CTC GGC AAG	3839
Trp Val Ile Arg Asn Asp Gly Ala Leu Cys His Gly Thr Leu Gly Lys	
1265 1270 1275	
GTG GTG GAT TTA GAT ATG CCC GCT GAG TTG TCA GAC TTT CGC GGG TCT	3887
Val Val Asp Leu Asp Met Pro Ala Glu Leu Ser Asp Phe Arg Gly Ser	
1280 1285 1290 1295	
TCT GGA TCA CCA ATC TTG TGC GAT GAG GGT CAT GCT GTT GGC ATG CTG	3935
Ser Gly Ser Pro Ile Leu Cys Asp Glu Gly His Ala Val Gly Met Leu	
1300 1305 1310	
ATT TCG GTG CTT CAT AGG GGG AGT AGG GTT TCC TCG GTG CGG TAT ACC	3983
Ile Ser Val Leu His Arg Gly Ser Arg Val Ser Ser Val Arg Tyr Thr	
1315 1320 1325	
AAA CCT TGG GAA ACT CTC CCT CGG GAG ATT GAG GCT CGA TCG GAG GCC	4031
Lys Pro Trp Glu Thr Leu Pro Arg Glu Ile Glu Ala Arg Ser Glu Ala	
1330 1335 1340	
CCC CCT GTG CCA GGA ACC ACT GGA TAC AGG GAG GCG CCA CTG TTC CTG	4079
Pro Pro Val Pro Gly Thr Thr Gly Tyr Arg Glu Ala Pro Leu Phe Leu	

407

1345	1350	1355	
CCC ACC GGA GCT GGC AAG TCG ACG CGC GTG CCG AAT GAG TAC GTC AAG			4127
Pro Thr Gly Ala Gly Lys Ser Thr Arg Val Pro Asn Glu Tyr Val Lys			
1360	1365	1370	1375
GCT GGA CAC AAR GTG CTT GTA CTA AAC CCA TCC ATT GCC ACA GTG AGG			4175
Ala Gly His Xaa Val Leu Val Leu Asn Pro Ser Ile Ala Thr Val Arg			
	1380	1385	1390
GCC ATG GGC CCT TAC ATG GAA AAG TTA ACC GGC AAA CAT CCG TCG GTG			4223
Ala Met Gly Pro Tyr Met Glu Lys Leu Thr Gly Lys His Pro Ser Val			
	1395	1400	1405
TAC TGT GGC CAT GAC ACT ACT GCA TAT TCC AGG ACT ACT GAC TCA TCT			4271
Tyr Cys Gly His Asp Thr Thr Ala Tyr Ser Arg Thr Thr Asp Ser Ser			
	1410	1415	1420
TTG ACC TAC TGT ACA TAC GGC AGG TTT ATG GCC AAT CCC AGG AAA TAC			4319
Leu Thr Tyr Cys Thr Tyr Gly Arg Phe Met Ala Asn Pro Arg Lys Tyr			
	1425	1430	1435
TTG CGG GGG AAC GAC GTC GTA ATT TGC GAC GAG TTG CAC GTC ACC GAC			4367
Leu Arg Gly Asn Asp Val Val Ile Cys Asp Glu Leu His Val Thr Asp			
	1440	1445	1450
CCG ACC TCA ATT TTG GGG ATG GGT CGG GCG AGG TTA CTC GCT CGC GAG			4415
Pro Thr Ser Ile Leu Gly Met Gly Arg Ala Arg Leu Leu Ala Arg Glu			
	1460	1465	1470
TGC GGC GTA CGC CTC CTG CTT TTC GCT ACG GCG ACC CCA CCG GTC TCT			4463
Cys Gly Val Arg Leu Leu Leu Phe Ala Thr Ala Thr Pro Pro Val Ser			
	1475	1480	1485
CCG ATG GCG AAG CAT GAA TCT ATT CAT GAG GAG ATG TTG GGC AGT GAG			4511
Pro Met Ala Lys His Glu Ser Ile His Glu Glu Met Leu Gly Ser Glu			
	1490	1495	1500
GGG GAG GTC CCC TTC TAT TGC CAA TTC CTC CCA CTG AGT AGG TAT GCT			4559
Gly Glu Val Pro Phe Tyr Cys Gln Phe Leu Pro Leu Ser Arg Tyr Ala			
	1505	1510	1515
ACT GGG AGA CAC CTG CTG TTT TGT CAT TCC AAG GTA GAR TGC ACT AGG			4607
Thr Gly Arg His Leu Leu Phe Cys His Ser Lys Val Xaa Cys Thr Arg			
	1520	1525	1530
TTA TCC TCA GCT TTG GCC AGC TTT GGT GTC AAC ACC GTT GTG TAC TTC			4655
Leu Ser Ser Ala Leu Ala Ser Phe Gly Val Asn Thr Val Val Tyr Phe			
	1540	1545	1550
AGA GGC AAA GAA ACT GAC ATT CCA ACT GGT GAC GTG TGC GTT TGC GCC			4703
Arg Gly Lys Glu Thr Asp Ile Pro Thr Gly Asp Val Cys Val Cys Ala			
	1555	1560	1565
ACA GAC GCA CTT TCC ACT GGT TAC ACT GGC AAT TTT GAC ACC GTA ACA			4751
Thr Asp Ala Leu Ser Thr Gly Tyr Thr Gly Asn Phe Asp Thr Val Thr			
	1570	1575	1580

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GAC TGT GGT TTA ATG GTT GAG GAG GTA GTG GAA GTG ACC CTG GAC CCG Asp Cys Gly Leu Met Val Glu Glu Val Val Glu Val Thr Leu Asp Pro 1585 1590 1595	4799
ACC ATC ACT ATC GGT GTG AAG ACC GTC CCG GCC CCT GCC GAA CTG AGG Thr Ile Thr Ile Gly Val Lys Thr Val Pro Ala Pro Ala Glu Leu Arg 1600 1605 1610 1615	4847
GCT CAG AGG CGT GGT AGG TGT GGC CGT GGG AAA GCG GGC ACT TAC TAT Ala Gln Arg Arg Gly Arg Cys Gly Arg Gly Lys Ala Gly Thr Tyr Tyr 1620 1625 1630	4895
CAG GCA TTG ATG TCT TCG GCG CCG GCG GGA ACS GTT CGG TCT GGG GCT Gln Ala Leu Met Ser Ser Ala Pro Ala Gly Xaa Val Arg Ser Gly Ala 1635 1640 1645	4943
CTC TGG GCA GCT GTT GAG GCT GGH GTC TCG TGG TAT GGC CTA GAG CCC Leu Trp Ala Ala Val Glu Ala Xaa Val Ser Trp Tyr Gly Leu Glu Pro 1650 1655 1660	4991
GAT GCT ATT GGA GAC CTG CTT AGG GCC TAC GAC TCG TGT CCT TAT ACT Asp Ala Ile Gly Asp Leu Leu Arg Ala Tyr Asp Ser Cys Pro Tyr Thr 1665 1670 1675	5039
GCT GCC ATC AGT GCG TCC ATC GGA GAG GCC ATT GCC TTT TTT ACT GGY Ala Ala Ile Ser Ala Ser Ile Gly Glu Ala Ile Ala Phe Phe Thr Xaa 1680 1685 1690 1695	5087
CTA GTG CCA ATG AGG AAT TAT CCT CAG GTG GTT TGG GCC AAG CAG AAG Leu Val Pro Met Arg Asn Tyr Pro Gln Val Val Trp Ala Lys Gln Lys 1700 1705 1710	5135
GGR CAC AAC TGG CCA CTC TTG GTG GGT GTG CAG AGG CAC ATG TGT GAG Xaa His Asn Trp Pro Leu Leu Val Gly Val Gln Arg His Met Cys Glu 1715 1720 1725	5183
GAC GCG GGC TGT GGT CCK CCC GCT AAT GGT CCC GAA TGG AGC GGC ATC Asp Ala Gly Cys Gly Xaa Pro Ala Asn Gly Pro Glu Trp Ser Gly Ile 1730 1735 1740	5231
AGG GGA AAA GGG CCT GTT CCC CTG TTG TGC CGA TGG GGT GGT GAC TTG Arg Gly Lys Gly Pro Val Pro Leu Leu Cys Arg Trp Gly Gly Asp Leu 1745 1750 1755	5279
CCT GAG TCG GTG GCT CCG CAT CAC TGG GTT GAT GAC CTA CAG GCC CGG Pro Glu Ser Val Ala Pro His His Trp Val Asp Asp Leu Gln Ala Arg 1760 1765 1770 1775	5327
CTC GGT GTG GCC GAG GGT TAC ACT CCC TGC ATT GCT GGA CCG GTG CTT Leu Gly Val Ala Glu Gly Tyr Thr Pro Cys Ile Ala Gly Pro Val Leu 1780 1785 1790	5375
TTG GTC GGT TTG GCG ATG GCG GGG GGG GCT ATC CTG GCA CAC TGG ACG Leu Val Gly Leu Ala Met Ala Gly Gly Ala Ile Leu Ala His Trp Thr 1795 1800 1805	5423
GGG TCT CTG GTT GTA GTG ACC AGT TGG GTT GTC AAT GGG AAC GGT AAC	5471

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Gly Ser Leu Val Val Val Thr Ser Trp Val Val Asn Gly Asn Gly Asn	
1810 1815 1820	
CCG CTG ATA CAA AGC GCC TCT AGG GGC GTG GCK ACY AGC GGT CCA TAC	5519
Pro Leu Ile Gln Ser Ala Ser Arg Gly Val Xaa Xaa Ser Gly Pro Tyr	
1825 1830 1835	
CCA GTA CCC CCA GAT GGT GGT GAA CGG TAC CCA TCA GAC ATC AAG CCA	5567
Pro Val Pro Pro Asp Gly Gly Glu Arg Tyr Pro Ser Asp Ile Lys Pro	
1840 1845 1850 1855	
ATY ACT GAG GCT GTG ACC ACC CTT GAG ACT GCG TGC GGY TGG GGC CCA	5615
Xaa Thr Glu Ala Val Thr Thr Leu Glu Thr Ala Cys Xaa Trp Gly Pro	
1860 1865 1870	
GCC GCG GCB AGT CTG GCT TAT GTG AAG GCC TGT GAA ACT GGA ACC ATG	5663
Ala Ala Xaa Ser Leu Ala Tyr Val Lys Ala Cys Glu Thr Gly Thr Met	
1875 1880 1885	
TTG GCT GAC AAR GCG AGT GCT GCG TGG CAG GCT TGG GCT GCA AAC AAC	5711
Leu Ala Asp Xaa Ala Ser Ala Ala Trp Gln Ala Trp Ala Ala Asn Asn	
1890 1895 1900	
TTT GTG CCT CCA CCA GCA TCA CAC TCA ACT TCC TTG TTR CAG AGC TTG	5759
Phe Val Pro Pro Pro Ala Ser His Ser Thr Ser Leu Xaa Gln Ser Leu	
1905 1910 1915	
GAY GCT GCG TTC ACT TCA GCT TGG GAT AGC GTG TTC ACT CAC GGC CGT	5807
Xaa Ala Ala Phe Thr Ser Ala Trp Asp Ser Val Phe Thr His Gly Arg	
1920 1925 1930 1935	
TCC TTG CTT GTT GGG TTC ACA GCT GCT TAC GGC GCT CGG CGG AAC CCA	5855
Ser Leu Leu Val Gly Phe Thr Ala Ala Tyr Gly Ala Arg Arg Asn Pro	
1940 1945 1950	
CCG CTG GGC GTC GGA GCC TCT TTC TTG CTG GGC ATG TCA TCG AGC CAC	5903
Pro Leu Gly Val Gly Ala Ser Phe Leu Leu Gly Met Ser Ser Ser His	
1955 1960 1965	
YTR ACT CAC GTC AGA CTT GCT GCT GCG TTG CTC CTC GGC GTC GGG GGT	5951
Xaa Thr His Val Arg Leu Ala Ala Ala Leu Leu Leu Gly Val Gly Gly	
1970 1975 1980	
ACC GTC CTA GGC ACG CCT GCT ACT GGG CTT GCT ATG GCG GGT GCC TAC	5999
Thr Val Leu Gly Thr Pro Ala Thr Gly Leu Ala Met Ala Gly Ala Tyr	
1985 1990 1995	
TTC GCK GGG GGC AGC GTT ACC GCT AAC TGG CTG AGT ATC ATT GTG GCT	6047
Phe Xaa Gly Gly Ser Val Thr Ala Asn Trp Leu Ser Ile Ile Val Ala	
2000 2005 2010 2015	
CTA ATC GGA GGC TGG GAG GGG GCR GTK AAC GCA GCC TCA CTC ACC TTC	6095
Leu Ile Gly Gly Trp Glu Gly Xaa Xaa Asn Ala Ala Ser Leu Thr Phe	
2020 2025 2030	
GAY CTC CTG GCK GGG AAG TTA CAA GCK AGY GAY GCT TGG TGC CTR GTC	6143
Xaa Leu Leu Xaa Gly Lys Leu Gln Xaa Xaa Xaa Ala Trp Cys Xaa Val	

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2035	2040	2045	
AGY TGC YTG GCC TCT CCG GGG GCT TCG GTG GCY GGT GTG GCD CTV GGY Xaa Cys Xaa Ala Ser Pro Gly Ala Ser Val Xaa Gly Val Xaa Xaa Xaa 2050 2055 2060			6191
CTD YTG CTV TGG TCT GTC AAR AAG GGT GTG GGW CAR GAY TGG GTT AAC Xaa Xaa Xaa Trp Ser Val Xaa Lys Gly Val Xaa Xaa Xaa Trp Val Asn 2065 2070 2075			6239
AGA YTG TTG ACG ATG ATG CCA CGC AGT TCG GTG ATG CCT GAC GAT TTC Arg Xaa Leu Thr Met Met Pro Arg Ser Ser Val Met Pro Asp Asp Phe 2080 2085 2090 2095			6287
TTC CTC AAA GAT GAG TTC GTC ACC AAG GTG TCT ACT GTC CTG CGA AAG Phe Leu Lys Asp Glu Phe Val Thr Lys Val Ser Thr Val Leu Arg Lys 2100 2105 2110			6335
TTG TCA TTG TCA AGA TGG ATC ATG ACT CTT GTG GAC AAG CGG GAG ATG Leu Ser Leu Ser Arg Trp Ile Met Thr Leu Val Asp Lys Arg Glu Met 2115 2120 2125			6383
GAG ATG GAG ACM CCC GCT TCT CAG ATT GTT TGG GAC TTG CTT GAC TGG Glu Met Glu Xaa Pro Ala Ser Gln Ile Val Trp Asp Leu Leu Asp Trp 2130 2135 2140			6431
TGC ATC CGG CTR GGT CGG TTC CTG TAC AAT AAA CTY ATG TTT GCT CTC Cys Ile Arg Xaa Gly Arg Phe Leu Tyr Asn Lys Xaa Met Phe Ala Leu 2145 2150 2155			6479
CCT AGG TTG CGC CTG CCG CTT ATC GGT TGC AGT ACC GGT TGG GGT GGC Pro Arg Leu Arg Leu Pro Leu Ile Gly Cys Ser Thr Gly Trp Gly Gly 2160 2165 2170 2175			6527
CCG TGG GAG GGC AAT GGT CAT TTG GAA ACA AGG TGT ACT TGT GGC TGT Pro Trp Glu Gly Asn Gly His Leu Glu Thr Arg Cys Thr Cys Gly Cys 2180 2185 2190			6575
GTG ATT ACC GGT GAT ATT CAC GAT GGT ATA TTG CAC GAC CTA CAT TAT Val Ile Thr Gly Asp Ile His Asp Gly Ile Leu His Asp Leu His Tyr 2195 2200 2205			6623
ACC TCC CTA CTG TGC AGA CAT TAC TAC AAG AGG ACA GTG CCT GTT GGC Thr Ser Leu Leu Cys Arg His Tyr Tyr Lys Arg Thr Val Pro Val Gly 2210 2215 2220			6671
GTC ATG GGC AAT GCT GAG GGA GCA GTC CCC CTT GTG CCT ACT GGC GGT Val Met Gly Asn Ala Glu Gly Ala Val Pro Leu Val Pro Thr Gly Gly 2225 2230 2235			6719
GGA ATC AGG ACT TAC CAA ATT GGG ACT TCT GAC TGG TTT GAG GCT GTG Gly Ile Arg Thr Tyr Gln Ile Gly Thr Ser Asp Trp Phe Glu Ala Val 2240 2245 2250 2255			6767
GTC GTG CAT GGG ACA ATC ACG GTG CAC GCC ACC AGT TGC TAT GAG TTG Val Val His Gly Thr Ile Thr Val His Ala Thr Ser Cys Tyr Glu Leu 2260 2265 2270			6815

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AAA GCT GCT GAC GTT CGG AGG GCG GTG CGA GCC GGC CCG ACT TAC GTT	6863
Lys Ala Ala Asp Val Arg Arg Ala Val Arg Ala Gly Pro Thr Tyr Val	
2275 2280 2285	
GGT GGC GTA CCT TGC AGC TGG AGC GCG CCG TGT ACT GCG CCT GCG CTC	6911
Gly Gly Val Pro Cys Ser Trp Ser Ala Pro Cys Thr Ala Pro Ala Leu	
2290 2295 2300	
GTT TAC AGG CTA GGC CAG GGC ATC AAA ATC GAT GGA GCG CGC CGA CTG	6959
Val Tyr Arg Leu Gly Gln Gly Ile Lys Ile Asp Gly Ala Arg Arg Leu	
2305 2310 2315	
TTG CCC TGT GAC TTA GCA CAG GGA GCG CGC CAC CCC CCG GTA TCT GGC	7007
Leu Pro Cys Asp Leu Ala Gln Gly Ala Arg His Pro Pro Val Ser Gly	
2320 2325 2330 2335	
AGT GTT GCC GGT AGT GGT TGG ACA GAT GAG GAC GAG AGG GAC TTG GTG	7055
Ser Val Ala Gly Ser Gly Trp Thr Asp Glu Asp Glu Arg Asp Leu Val	
2340 2345 2350	
GAA ACC AAG GCT GCC GCC ATC GAG GCC ATT GGG GCG GCC TTG CAC CTC	7103
Glu Thr Lys Ala Ala Ala Ile Glu Ala Ile Gly Ala Ala Leu His Leu	
2355 2360 2365	
CCT TCA CCG GAG GCT GCT CAG GCC GCT CTA GAG GCT TTG GAG GAG GCT	7151
Pro Ser Pro Glu Ala Ala Gln Ala Ala Leu Glu Ala Leu Glu Glu Ala	
2370 2375 2380	
GCC GTG TCC CTG TTG CCC CAT GTG CCC GTC ATT ATG GGT GAT GAC TGT	7199
Ala Val Ser Leu Leu Pro His Val Pro Val Ile Met Gly Asp Asp Cys	
2385 2390 2395	
TCA TGC CGG GAT GAG GCG TTC CAA GGC CAC TTC ATC CCA GAA CCC AAT	7247
Ser Cys Arg Asp Glu Ala Phe Gln Gly His Phe Ile Pro Glu Pro Asn	
2400 2405 2410 2415	
GTG ACA GAG GTA CCC ATT GAG CCC ACG GTC GGA GAC GTG GAG GCA CTC	7295
Val Thr Glu Val Pro Ile Glu Pro Thr Val Gly Asp Val Glu Ala Leu	
2420 2425 2430	
AAG CTG CGG GCT GCA GAC CTG ACC GCC AGG TTG CAA GAC TTG GAG GCC	7343
Lys Leu Arg Ala Ala Asp Leu Thr Ala Arg Leu Gln Asp Leu Glu Ala	
2435 2440 2445	
ATG GCT CTC GCC CGC GCT GAG TCA ATC GAG GAT GCT CGC GCA GCT TCG	7391
Met Ala Leu Ala Arg Ala Glu Ser Ile Glu Asp Ala Arg Ala Ala Ser	
2450 2455 2460	
ATG CCT TCG CTC ACC GAG GTG GAC TCA ATG CCA TCA TTG GAG TCG AGC	7439
Met Pro Ser Leu Thr Glu Val Asp Ser Met Pro Ser Leu Glu Ser Ser	
2465 2470 2475	
CCT TGC TCC TCC TTT GAA CAA ATC TCT TTA ACT GAA AGT GAC CCT GAG	7487
Pro Cys Ser Ser Phe Glu Gln Ile Ser Leu Thr Glu Ser Asp Pro Glu	
2480 2485 2490 2495	
ACT GTC GTC GAG GCT GGC TTA CCC TTG GAG TTC GTG AAC TCC AAC ACC	7535

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Thr Val Val Glu Ala Gly Leu Pro Leu Glu Ph Val Asn Ser Asn Thr	
2500 2505 2510	
GGG CCG TCT CCG GCT CGG AGG ATT GTC AGA ATC CGA CAG GCT TGC TGT	7583
Gly Pro Ser Pro Ala Arg Arg Ile Val Arg Ile Arg Gln Ala Cys Cys	
2515 2520 2525	
TGT GAC AGA TCC ACA ATG AAG GCC ATG CCG TTG TCG TTC ACT GTC GGG	7631
Cys Asp Arg Ser Thr Met Lys Ala Met Pro Leu Ser Phe Thr Val Gly	
2530 2535 2540	
GAG TGC CTC TTC GTT ACT CGC TAT GAC CCG GAC GGT CAC CAA CTG TTT	7679
Glu Cys Leu Phe Val Thr Arg Tyr Asp Pro Asp Gly His Gln Leu Phe	
2545 2550 2555	
GAC GAG CGA GGT CCG ATA GAG GTA TCT ACT CCT ATA TGT GAA GTG ATT	7727
Asp Glu Arg Gly Pro Ile Glu Val Ser Thr Pro Ile Cys Glu Val Ile	
2560 2565 2570 2575	
GGG GAC ATC AGG CTT CAG TGT GAC CAA ATT GAG GAA ACT CCA ACA TCT	7775
Gly Asp Ile Arg Leu Gln Cys Asp Gln Ile Glu Glu Thr Pro Thr Ser	
2580 2585 2590	
TAC TCT TAC ATC TGG TCA GGG GCG CCC TTG GGT ACT GGG AGA AGT GTC	7823
Tyr Ser Tyr Ile Trp Ser Gly Ala Pro Leu Gly Thr Gly Arg Ser Val	
2595 2600 2605	
CCC CAA CCC ATG ACG CGC CCT ATA GGG ACC CAT CTG ACT TGT GAC ACT	7871
Pro Gln Pro Met Thr Arg Pro Ile Gly Thr His Leu Thr Cys Asp Thr	
2610 2615 2620	
ACC AAA GTT TAT GTT ACT GAC CCT GAT CGG GCC GCT GAG CGG GCC GAG	7919
Thr Lys Val Tyr Val Thr Asp Pro Asp Arg Ala Ala Glu Arg Ala Glu	
2625 2630 2635	
AAG GTT ACA ATC TGG AGG GGT GAT AGG AAG TAT GAC AAG CAT TAT GAG	7967
Lys Val Thr Ile Trp Arg Gly Asp Arg Lys Tyr Asp Lys His Tyr Glu	
2640 2645 2650 2655	
GCT GTC GTT GAG GCT GTC CTG AAA AAG GCA GCC GCG ACG AAG TCT CAT	8015
Ala Val Val Glu Ala Val Leu Lys Lys Ala Ala Ala Thr Lys Ser His	
2660 2665 2670	
GGC TGG ACC TAT TCC CAG GCT ATA GCT AAA GTT AGG CGC CGA GCA GCC	8063
Gly Trp Thr Tyr Ser Gln Ala Ile Ala Lys Val Arg Arg Arg Ala Ala	
2675 2680 2685	
GCT GGA TAC GGC AGC AAG GTG ACC GCC TCC ACA TTG GCC ACT GGT TGG	8111
Ala Gly Tyr Gly Ser Lys Val Thr Ala Ser Thr Leu Ala Thr Gly Trp	
2690 2695 2700	
CCT CAC GTG GAG GAG ATG CTG GAC AAA ATA GCC AGG GGA CAG GAA GTT	8159
Pro His Val Glu Glu Met Leu Asp Lys Ile Ala Arg Gly Gln Glu Val	
2705 2710 2715	
CCT TTC ACT TTT GTG ACC AAG CGA GAG GTT TTC TTC TCC AAA ACT ACC	8207
Pro Phe Thr Phe Val Thr Lys Arg Glu Val Phe Phe Ser Lys Thr Thr	

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2720	2725	2730	2735	
CGT AAG CCC CCA AGA TTC ATA GTT TTC CCA CCT TTG GAC TTC AGG ATA				8255
Arg Lys Pro Pro Arg Phe Ile Val Phe Pro Pro Leu Asp Phe Arg Ile	2740	2745	2750	
GCT GAA AAG ATG ATT CTG GGT GAC CCC GGC ATC GTT GCA AAG TCA ATT				8303
Ala Glu Lys Met Ile Leu Gly Asp Pro Gly Ile Val Ala Lys Ser Ile	2755	2760	2765	
CTG GGT GAC GCT TAT CTG TTC CAG TAC ACG CCC AAT CAG AGG GTC AAA				8351
Leu Gly Asp Ala Tyr Leu Phe Gln Tyr Thr Pro Asn Gln Arg Val Lys	2770	2775	2780	
GCT CTG GTT AAG GCG TGG GAG GGG AAG TTG CAT CCC GCT GCG ATC ACT				8399
Ala Leu Val Lys Ala Trp Glu Gly Lys Leu His Pro Ala Ala Ile Thr	2785	2790	2795	
GTG GAC GCC ACT TGT TTC GAC TCA TCG ATT GAT GAG CAC GAC ATG CAG				8447
Val Asp Ala Thr Cys Phe Asp Ser Ser Ile Asp Glu His Asp Met Gln	2800	2805	2810 2815	
GTG GAG GCT TCG GTG TTT GCG GCG GCT AGT GAC AAC CCC TCA ATG GTA				8495
Val Glu Ala Ser Val Phe Ala Ala Ala Ser Asp Asn Pro Ser Met Val	2820	2825	2830	
CAT GCT TTG TGC AAG TAC TAC TCT GGT GGC CCT ATG GTT TCC CCA GAT				8543
His Ala Leu Cys Lys Tyr Tyr Ser Gly Gly Pro Met Val Ser Pro Asp	2835	2840	2845	
GGG GTT CCC TTG GGG TAC CGC CAG TGT AGG TCG TCG GGC GTG TTA ACA				8591
Gly Val Pro Leu Gly Tyr Arg Gln Cys Arg Ser Ser Gly Val Leu Thr	2850	2855	2860	
ACT AGC TCG GCG AAC AGC ATC ACT TGT TAC ATT AAG GTC AGC GCG GCC				8639
Thr Ser Ser Ala Asn Ser Ile Thr Cys Tyr Ile Lys Val Ser Ala Ala	2865	2870	2875	
TGC AGG CGG GTG GGG ATT AAG GCA CCA TCA TTC TTT ATA GCT GGA GAT				8687
Cys Arg Arg Val Gly Ile Lys Ala Pro Ser Phe Phe Ile Ala Gly Asp	2880 2885	2890	2895	
GAT TGC TTG ATC ATC TAT GAA AAT GAT GGA ACT GAT CCC TGC CCT GCT				8735
Asp Cys Leu Ile Ile Tyr Glu Asn Asp Gly Thr Asp Pro Cys Pro Ala	2900	2905	2910	
CTT AAG GCT GCC CTG GCC AAC TAT GGA TAC AGG TGT GAA CCA ACA AAG				8783
Leu Lys Ala Ala Leu Ala Asn Tyr Gly Tyr Arg Cys Glu Pro Thr Lys	2915	2920	2925	
CAT GCT TCA CTG GAC ACA GCT GAG TGT TGC TCG GCC TAC TTG GCT GAG				8831
His Ala Ser Leu Asp Thr Ala Glu Cys Cys Ser Ala Tyr Leu Ala Glu	2930	2935	2940	
TGC GTA GCT GGG GGT GCC AAG CGC TGG TGG TTG AGC ACG GAC ATG AGG				8879
Cys Val Ala Gly Gly Ala Lys Arg Trp Trp Leu Ser Thr Asp Met Arg	2945	2950	2955	

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AAG CCG CTC GCA AGG GCG TCT TCC GAA TAT TCG GAC CCA ATC GGC AGT	8927
Lys Pro Leu Ala Arg Ala Ser Ser Glu Tyr Ser Asp Pro Ile Gly Ser	
2960 2965 2970 2975	
GCT TTA GGG ACC ATC TTG ATG TAT CCC CGG CAT CCA ATC GTG CGG TAT	8975
Ala Leu Gly Thr Ile Leu Met Tyr Pro Arg His Pro Ile Val Arg Tyr	
2980 2985 2990	
GTT CTA ATA CCA CAC GTA CTA ATA ATG GCT TAC AGG AGT GGC AGC ACA	9023
Val Leu Ile Pro His Val Leu Ile Met Ala Tyr Arg Ser Gly Ser Thr	
2995 3000 3005	
CCG GAT GAG TTG GTT ATG TGT CAG GTT CAG GGA AAT CAT TAC TCT TTC	9071
Pro Asp Glu Leu Val Met Cys Gln Val Gln Gly Asn His Tyr Ser Phe	
3010 3015 3020	
CCG CTG CGG CTG CTG CCT CGC GTC TTG GTC TCT CTA CAT GGT CCG TGG	9119
Pro Leu Arg Leu Leu Pro Arg Val Leu Val Ser Leu His Gly Pro Trp	
3025 3030 3035	
TGC CTA CAA GTC ACC ACG GAC AGT ACG AAG ACT AGG ATG GAG GCA GGC	9167
Cys Leu Gln Val Thr Thr Asp Ser Thr Lys Thr Arg Met Glu Ala Gly	
3040 3045 3050 3055	
TCA GCS TTG CGG GAT TTA GGA ATG AAA TCC CTA GCC TGG CAC CGC CGA	9215
Ser Xaa Leu Arg Asp Leu Gly Met Lys Ser Leu Ala Trp His Arg Arg	
3060 3065 3070	
CGT GCC GGA AAT GTG CGC ACT CGC CTC CTG AGG GGA GGC AAG GAG TGG	9263
Arg Ala Gly Asn Val Arg Thr Arg Leu Leu Arg Gly Gly Lys Glu Trp	
3075 3080 3085	
GGG CAC CTG GCC AGA GCC CTC CTC TGG CAY CCA GGC TTG AAG GAG CAY	9311
Gly His Leu Ala Arg Ala Leu Leu Trp Xaa Pro Xaa Leu Lys Glu Xaa	
3090 3095 3100	
CCC CCR CCC ATA AAT TCA CTT CCA GGT TTT CAG CTG GCG ACG CCT TAC	9359
Pro Xaa Pro Ile Asn Ser Leu Pro Gly Phe Gln Leu Ala Thr Pro Tyr	
3105 3110 3115	
GAA CAC CAT GAA GAG GTC TTG ATC TCG ATC AAG AGT CGA CCA CCT TGG	9407
Glu His His Glu Glu Val Leu Ile Ser Ile Lys Ser Arg Pro Pro Trp	
3120 3125 3130 3135	
ATA AGG TGG ATT CTT GGT GCT TGT CTC TCG TTG CTG GCC GCC TTG CTG	9455
Ile Arg Trp Ile Leu Gly Ala Cys Leu Ser Leu Leu Ala Ala Leu Leu	
3140 3145 3150	
TGA ATT CGC TCC AGG CAG TAG GAC CTT CGG GTC GGG GG	9493
* Ile Arg Ser Arg Gln * Asp Leu Arg Val Gly	
3155 3160	

(2) INFORMATION FOR SEQ ID NO:386:

415

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

Trp Glu Ser Gly Ala Pro Asp Leu Pro Pro Arg Trp Gly Glu Arg Gly
 1             5             10             15
Pro Gly Pro Ala Gly Trp Lys Ala Arg Asn Arg Ser Ile Phe Leu Lys
          20             25             30
Val Glu Glu Gly Val Arg Leu Ser Val Arg Ser Val Arg Lys Ala Ser
          35             40             45
Gly Cys Leu Val Leu Gly Phe Val Gly Gly Lys Ser Gln Leu Gly Val
          50             55             60
Lys Ala Leu
          65
  
```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2972 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

Asp Arg Leu Ile Pro Val Thr Ala Ala Pro Glu Pro Ala Pro Arg Xaa
 1             5             10             15
Phe Gly His Gly Pro Gln Val Gly Gly Thr Gly Val Asn Asn Pro Pro
          20             25             30
Thr Glu Ala Ser Val Val Lys Arg Arg Arg Ser Pro Glu Ile Ala Thr
          35             40             45
Thr Pro His Val Arg Glu Arg Arg Gln Asn Leu Arg Asp Ser Tyr Ala
          50             55             60
  
```

(2) INFORMATION FOR SEQ ID NO:388:

416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Gln Ser Gln Trp Gly Ala Gly Asp Gln Leu Ile Thr Cys Pro Ala Ser
 1 5 10 15
 Ser Ser

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Asp Trp Pro Lys Gly Ser His Gly Ala Thr Lys Ala Ala Gln Arg Cys
 1 5 10 15
 Met Arg Gln Gly Glu Lys Ser Phe Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2973 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Pro Leu Val Ala Ile Pro Ser Leu Arg Ser Met Ser Val Val Asp Thr
 1 5 10 15
 Phe Thr Met Ala Trp Leu Trp Leu Leu Val Cys Phe Pro Leu Ala Gly
 20 25 30
 Gly Val Leu Phe Asn Ser Arg His Gln Cys Phe Asn Gly Asp His Tyr
 35 40 45

417

Val Leu Ser Asn Cys Cys Ser Arg Asp Glu Val Tyr Phe Cys Phe Gly
 50 55 60
 Asp Gly Cys Leu Val Ala Tyr Gly Cys Thr Val Cys Thr Gln Ser Cys
 65 70 75 80
 Trp Lys Leu Tyr Arg Pro Gly Val Ala Thr Arg Pro Gly Ser Glu Pro
 85 90 95
 Gly Glu Leu Leu Gly Arg Phe Gly Ser Val Ile Gly Pro Val Ser Ala
 100 105 110
 Ser Ala Tyr Thr Ala Gly Val Leu Gly Leu Gly Glu Pro Tyr Ser Leu
 115 120 125
 Ala Phe Leu Gly Thr Phe Leu Thr Ser Arg Leu Ser Arg Ile Pro Asn
 130 135 140
 Val Thr Cys Val Lys Ala Cys Asp Leu Glu Phe Thr Tyr Pro Gly Leu
 145 150 155 160
 Ser Ile Asp Phe Asp Trp Ala Phe Thr Lys Ile Leu Gln Leu Pro Ala
 165 170 175
 Lys Leu Trp Arg Gly Leu Thr Xaa Xaa Pro Val Leu Ser Leu Leu Val
 180 185 190
 Ile Leu Met Leu Val Leu Glu Gln Arg Leu Leu Ile Ala Phe Leu Leu
 195 200 205
 Leu Leu Val Val Gly Glu Ala Gln Arg Gly Met Phe Asp Asn Cys Val
 210 215 220
 Cys Gly Tyr Trp Gly Gly Lys Arg Pro Pro Ser Val Thr Pro Leu Tyr
 225 230 235 240
 Arg Gly Asn Gly Thr Val Val Cys Asp Cys Asp Phe Gly Lys Met His
 245 250 255
 Trp Ala Pro Pro Leu Cys Ser Xaa Leu Val Trp Arg Asp Gly His Arg
 260 265 270
 Arg Gly Thr Val Arg Asp Leu Pro Pro Val Cys Pro Arg Glu Val Leu
 275 280 285
 Gly Thr Val Thr Val Met Cys Gln Trp Gly Ser Ala Tyr Trp Ile Trp
 290 295 300
 Arg Phe Gly Asp Trp Val Ala Leu Tyr Asp Glu Leu Pro Arg Ser Ala
 305 310 315 320
 Leu Cys Thr Phe Phe Ser Gly His Gly Pro Gln Pro Lys Asp Leu Ser
 325 330 335
 Val Leu Asn Pro Ser Gly Ala Pro Cys Ala Ser Cys Val Val Asp Gln
 340 345 350

418

Arg Pro Leu Lys Cys Gly Ser Cys Val Arg Asp Cys Trp Glu Thr Gly
 355 360 365
 Gly Pro Gly Phe Asp Glu Cys Gly Val Gly Thr Arg Met Thr Lys His
 370 375 380
 Leu Glu Ala Val Leu Val Asp Gly Gly Val Glu Ser Lys Val Thr Thr
 385 390 395 400
 Pro Lys Gly Glu Arg Pro Lys Tyr Ile Gly Gln His Gly Val Gly Thr
 405 410 415
 Tyr Tyr Gly Ala Val Arg Ser Leu Asn Ile Ser Tyr Leu Val Thr Glu
 420 425 430
 Val Gly Gly Tyr Trp His Ala Leu Lys Cys Pro Cys Asp Phe Val Pro
 435 440 445
 Arg Val Leu Pro Glu Arg Ile Pro Gly Arg Pro Val Asn Ala Cys Leu
 450 455 460
 Ala Gly Lys Ser Pro His Pro Phe Ala Ser Trp Ala Pro Gly Gly Phe
 465 470 475 480
 Tyr Ala Pro Val Phe Thr Lys Cys Asn Trp Pro Lys Thr Ser Gly Val
 485 490 495
 Asp Val Cys Pro Gly Phe Ala Phe Asp Phe Pro Gly Asp His Asn Gly
 500 505 510
 Phe Ile His Val Lys Gly Asn Arg Gln Gln Val Tyr Ser Gly Gln Arg
 515 520 525
 Arg Ser Ser Pro Ala Trp Leu Leu Thr Asp Met Val Leu Ala Leu Leu
 530 535 540
 Val Val Met Lys Leu Ala Glu Ala Arg Val Val Pro Leu Phe Met Leu
 545 550 555 560
 Ala Met Trp Trp Trp Leu Asn Gly Ala Ser Ala Ala Thr Ile Val Ile
 565 570 575
 Ile His Pro Thr Val Thr Lys Ser Thr Glu Ser Val Pro Leu Trp Thr
 580 585 590
 Pro Pro Thr Val Pro Thr Pro Ser Cys Pro Asn Ser Thr Thr Gly Val
 595 600 605
 Ala Asp Ser Thr Tyr Asn Ala Gly Cys Tyr Met Val Ala Gly Leu Ala
 610 615 620
 Ala Gly Ala Gln Ala Val Trp Gly Ala Ala Asn Asp Gly Ala Gln Ala
 625 630 635 640
 Val Val Gly Gly Ile Trp Pro Ala Trp Leu Lys Leu Arg Ser Phe Ala
 645 650 655

419

Ala Gly Leu Ala Trp Leu Ser Asn Val Gly Ala Tyr Leu Pro Val Val
 660 665 670
 Glu Ala Xaa Leu Ala Pro Glu Leu Val Cys Thr Pro Val Val Gly Trp
 675 680 685
 Ala Ala Gln Glu Trp Trp Phe Thr Gly Cys Leu Gly Val Met Cys Val
 690 695 700
 Val Ala Tyr Leu Asn Val Leu Gly Ser Xaa Arg Ala Ala Val Leu Val
 705 710 715 720
 Ala Met His Phe Ala Arg Gly Ala Leu Pro Leu Val Leu Val Val Ala
 725 730 735
 Ala Gly Xaa Thr Arg Glu Arg His Ser Val Leu Gly Leu Glu Val Cys
 740 745 750
 Phe Asp Leu Asp Gly Gly Asp Trp Xaa Asp Ala Ser Trp Ser Trp Gly
 755 760 765
 Leu Ala Gly Val Val Ser Trp Ala Leu Leu Val Gly Gly Leu Met Thr
 770 775 780
 His Gly Gly Arg Ser Ala Arg Xaa Thr Trp Xaa Ala Arg Trp Ala Val
 785 790 795 800
 Asn Xaa Gln Arg Val Xaa Arg Trp Val Asn Asn Ser Pro Val Gly Xaa
 805 810 815
 Phe Xaa Arg Trp Xaa Xaa Ala Trp Lys Xaa Trp Xaa Xaa Val Ala Trp
 820 825 830
 Phe Phe Pro Gln Thr Val Ala Thr Xaa Ser Val Ile Phe Ile Leu Cys
 835 840 845
 Leu Ser Ser Leu Asp Val Ile Asp Phe Ile Leu Xaa Val Leu Leu Val
 850 855 860
 Asn Ser Pro Asn Leu Ala Arg Leu Ala Xaa Val Leu Asp Ser Leu Ala
 865 870 875 880
 Xaa Ala Glu Glu Arg Leu Ala Cys Ser Trp Leu Val Gly Val Leu Arg
 885 890 895
 Lys Arg Gly Val Leu Leu Tyr Glu His Xaa Gly His Thr Ser Arg Arg
 900 905 910
 Gly Ala Ala Arg Leu Arg Glu Trp Xaa Phe Ala Xaa Glu Xaa Val Xaa
 915 920 925
 Ile Thr Lys Glu Asp Xaa Xaa Ile Val Arg Asp Ser Ala Arg Val Leu
 930 935 940
 Gly Cys Gly Gln Leu Val His Gly Lys Pro Val Val Ala Arg Arg Gly
 945 950 955 960

420

Asp Glu Val Leu Ile Gly Cys Val Asn Ser Arg Phe Asp Leu Pro Pro
 965 970 975
 Gly Phe Val Pro Thr Ala Pro Val Xaa Leu His Xaa Xaa Gly Xaa Xaa
 980 985 990
 Xaa Xaa Gly Val Val Lys Xaa Ser Met Thr Gly Lys Asp Pro Ser Glu
 995 1000 1005
 His His Xaa Asn Val Val Val Xaa Gly Thr Ser Thr Xaa Arg Ser Met
 1010 1015 1020
 Gly Cys Cys Val Asn Gly Val Val Tyr Xaa Thr Tyr His Xaa Thr Asn
 1025 1030 1035 1040
 Ala Xaa Xaa Met Ala Gly Xaa Phe Xaa Xaa Val Xaa Ala Arg Trp Trp
 1045 1050 1055
 Xaa Ala Xaa Asp Asp Val Thr Xaa Tyr Pro Leu Xaa Asn Xaa Ala Ser
 1060 1065 1070
 Cys Xaa Xaa Xaa Xaa Lys Cys Gln Pro Thr Gly Val Trp Val Ile Arg
 1075 1080 1085
 Asn Asp Gly Ala Leu Cys His Gly Thr Leu Gly Lys Val Val Asp Leu
 1090 1095 1100
 Asp Met Pro Ala Glu Leu Ser Asp Phe Arg Gly Ser Ser Gly Ser Pro
 1105 1110 1115 1120
 Ile Leu Cys Asp Glu Gly His Ala Val Gly Met Leu Ile Ser Val Leu
 1125 1130 1135
 His Arg Gly Ser Arg Val Ser Ser Val Arg Tyr Thr Lys Pro Trp Glu
 1140 1145 1150
 Thr Leu Pro Arg Glu Ile Glu Ala Arg Ser Glu Ala Pro Pro Val Pro
 1155 1160 1165
 Gly Thr Thr Gly Tyr Arg Glu Ala Pro Leu Phe Leu Pro Thr Gly Ala
 1170 1175 1180
 Gly Lys Ser Thr Arg Val Pro Asn Glu Tyr Val Lys Ala Gly His Xaa
 1185 1190 1195 1200
 Val Leu Val Leu Asn Pro Ser Ile Ala Thr Val Arg Ala Met Gly Pro
 1205 1210 1215
 Tyr Met Glu Lys Leu Thr Gly Lys His Pro Ser Val Tyr Cys Gly His
 1220 1225 1230
 Asp Thr Thr Ala Tyr Ser Arg Thr Thr Asp Ser Ser Leu Thr Tyr Cys
 1235 1240 1245
 Thr Tyr Gly Arg Phe Met Ala Asn Pro Arg Lys Tyr Leu Arg Gly Asn
 1250 1255 1260

421

Asp Val Val Il Cys Asp Glu Leu His Val Thr Asp Pro Thr Ser Ile
 1265 1270 1275 1280
 Leu Gly Met Gly Arg Ala Arg Leu Leu Ala Arg Glu Cys Gly Val Arg
 1285 1290 1295
 Leu Leu Leu Phe Ala Thr Ala Thr Pro Pro Val Ser Pro Met Ala Lys
 1300 1305 1310
 His Glu Ser Ile His Glu Glu Met Leu Gly Ser Glu Gly Glu Val Pro
 1315 1320 1325
 Phe Tyr Cys Gln Phe Leu Pro Leu Ser Arg Tyr Ala Thr Gly Arg His
 1330 1335 1340
 Leu Leu Phe Cys His Ser Lys Val Xaa Cys Thr Arg Leu Ser Ser Ala
 1345 1350 1355 1360
 Leu Ala Ser Phe Gly Val Asn Thr Val Val Tyr Phe Arg Gly Lys Glu
 1365 1370 1375
 Thr Asp Ile Pro Thr Gly Asp Val Cys Val Cys Ala Thr Asp Ala Leu
 1380 1385 1390
 Ser Thr Gly Tyr Thr Gly Asn Phe Asp Thr Val Thr Asp Cys Gly Leu
 1395 1400 1405
 Met Val Glu Glu Val Val Glu Val Thr Leu Asp Pro Thr Ile Thr Ile
 1410 1415 1420
 Gly Val Lys Thr Val Pro Ala Pro Ala Glu Leu Arg Ala Gln Arg Arg
 1425 1430 1435 1440
 Gly Arg Cys Gly Arg Gly Lys Ala Gly Thr Tyr Tyr Gln Ala Leu Met
 1445 1450 1455
 Ser Ser Ala Pro Ala Gly Xaa Val Arg Ser Gly Ala Leu Trp Ala Ala
 1460 1465 1470
 Val Glu Ala Xaa Val Ser Trp Tyr Gly Leu Glu Pro Asp Ala Ile Gly
 1475 1480 1485
 Asp Leu Leu Arg Ala Tyr Asp Ser Cys Pro Tyr Thr Ala Ala Ile Ser
 1490 1495 1500
 Ala Ser Ile Gly Glu Ala Ile Ala Phe Phe Thr Xaa Leu Val Pro Met
 1505 1510 1515 1520
 Arg Asn Tyr Pro Gln Val Val Trp Ala Lys Gln Lys Xaa His Asn Trp
 1525 1530 1535
 Pro Leu Leu Val Gly Val Gln Arg His Met Cys Glu Asp Ala Gly Cys
 1540 1545 1550
 Gly Xaa Pro Ala Asn Gly Pro Glu Trp Ser Gly Ile Arg Gly Lys Gly
 1555 1560 1565

422

Pro Val Pro Leu Leu Cys Arg Trp Gly Gly Asp Leu Pro Glu Ser Val
 1570 1575 1580
 Ala Pro His His Trp Val Asp Asp Leu Gln Ala Arg Leu Gly Val Ala
 1585 1590 1595 1600
 Glu Gly Tyr Thr Pro Cys Ile Ala Gly Pro Val Leu Leu Val Gly Leu
 1605 1610 1615
 Ala Met Ala Gly Gly Ala Ile Leu Ala His Trp Thr Gly Ser Leu Val
 1620 1625 1630
 Val Val Thr Ser Trp Val Val Asn Gly Asn Gly Asn Pro Leu Ile Gln
 1635 1640 1645
 Ser Ala Ser Arg Gly Val Xaa Xaa Ser Gly Pro Tyr Pro Val Pro Pro
 1650 1655 1660
 Asp Gly Gly Glu Arg Tyr Pro Ser Asp Ile Lys Pro Xaa Thr Glu Ala
 1665 1670 1675 1680
 Val Thr Thr Leu Glu Thr Ala Cys Xaa Trp Gly Pro Ala Ala Xaa Ser
 1685 1690 1695
 Leu Ala Tyr Val Lys Ala Cys Glu Thr Gly Thr Met Leu Ala Asp Xaa
 1700 1705 1710
 Ala Ser Ala Ala Trp Gln Ala Trp Ala Ala Asn Asn Phe Val Pro Pro
 1715 1720 1725
 Pro Ala Ser His Ser Thr Ser Leu Xaa Gln Ser Leu Xaa Ala Ala Phe
 1730 1735 1740
 Thr Ser Ala Trp Asp Ser Val Phe Thr His Gly Arg Ser Leu Leu Val
 1745 1750 1755 1760
 Gly Phe Thr Ala Ala Tyr Gly Ala Arg Arg Asn Pro Pro Leu Gly Val
 1765 1770 1775
 Gly Ala Ser Phe Leu Leu Gly Met Ser Ser Ser His Xaa Thr His Val
 1780 1785 1790
 Arg Leu Ala Ala Ala Leu Leu Leu Gly Val Gly Gly Thr Val Leu Gly
 1795 1800 1805
 Thr Pro Ala Thr Gly Leu Ala Met Ala Gly Ala Tyr Phe Xaa Gly Gly
 1810 1815 1820
 Ser Val Thr Ala Asn Trp Leu Ser Ile Ile Val Ala Leu Ile Gly Gly
 1825 1830 1835 1840
 Trp Glu Gly Xaa Xaa Asn Ala Ala Ser Leu Thr Phe Xaa Leu Leu Xaa
 1845 1850 1855
 Gly Lys Leu Gln Xaa Xaa Xaa Ala Trp Cys Xaa Val Xaa Cys Xaa Ala
 1860 1865 1870

423

Ser Pro Gly Ala Ser Val Xaa Gly Val Xaa Xaa Xaa Xaa Xaa Xaa Trp
 1875 1880 1885

Ser Val Xaa Lys Gly Val Xaa Xaa Xaa Trp Val Asn Arg Xaa Leu Thr
 1890 1895 1900

Met Met Pro Arg Ser Ser Val Met Pro Asp Asp Phe Phe Leu Lys Asp
 1905 1910 1915 1920

Glu Phe Val Thr Lys Val Ser Thr Val Leu Arg Lys Leu Ser Leu Ser
 1925 1930 1935

Arg Trp Ile Met Thr Leu Val Asp Lys Arg Glu Met Glu Met Glu Xaa
 1940 1945 1950

Pro Ala Ser Gln Ile Val Trp Asp Leu Leu Asp Trp Cys Ile Arg Xaa
 1955 1960 1965

Gly Arg Phe Leu Tyr Asn Lys Xaa Met Phe Ala Leu Pro Arg Leu Arg
 1970 1975 1980

Leu Pro Leu Ile Gly Cys Ser Thr Gly Trp Gly Gly Pro Trp Glu Gly
 1985 1990 1995 2000

Asn Gly His Leu Glu Thr Arg Cys Thr Cys Gly Cys Val Ile Thr Gly
 2005 2010 2015

Asp Ile His Asp Gly Ile Leu His Asp Leu His Tyr Thr Ser Leu Leu
 2020 2025 2030

Cys Arg His Tyr Tyr Lys Arg Thr Val Pro Val Gly Val Met Gly Asn
 2035 2040 2045

Ala Glu Gly Ala Val Pro Leu Val Pro Thr Gly Gly Gly Ile Arg Thr
 2050 2055 2060

Tyr Gln Ile Gly Thr Ser Asp Trp Phe Glu Ala Val Val Val His Gly
 2065 2070 2075 2080

Thr Ile Thr Val His Ala Thr Ser Cys Tyr Glu Leu Lys Ala Ala Asp
 2085 2090 2095

Val Arg Arg Ala Val Arg Ala Gly Pro Thr Tyr Val Gly Gly Val Pro
 2100 2105 2110

Cys Ser Trp Ser Ala Pro Cys Thr Ala Pro Ala Leu Val Tyr Arg Leu
 2115 2120 2125

Gly Gln Gly Ile Lys Ile Asp Gly Ala Arg Arg Leu Leu Pro Cys Asp
 2130 2135 2140

Leu Ala Gln Gly Ala Arg His Pro Pro Val Ser Gly Ser Val Ala Gly
 2145 2150 2155 2160

Ser Gly Trp Thr Asp Glu Asp Glu Arg Asp Leu Val Glu Thr Lys Ala
 2165 2170 2175

424

Ala Ala Ile Glu Ala Ile Gly Ala Ala Leu His Leu Pro Ser Pro Glu
2180 2185 2190

Ala Ala Gln Ala Ala Leu Glu Ala Leu Glu Glu Ala Ala Val Ser Leu
2195 2200 2205

Leu Pro His Val Pro Val Ile Met Gly Asp Asp Cys Ser Cys Arg Asp
2210 2215 2220

Glu Ala Phe Gln Gly His Phe Ile Pro Glu Pro Asn Val Thr Glu Val
2225 2230 2235 2240

Pro Ile Glu Pro Thr Val Gly Asp Val Glu Ala Leu Lys Leu Arg Ala
2245 2250 2255

Ala Asp Leu Thr Ala Arg Leu Gln Asp Leu Glu Ala Met Ala Leu Ala
2260 2265 2270

Arg Ala Glu Ser Ile Glu Asp Ala Arg Ala Ala Ser Met Pro Ser Leu
2275 2280 2285

Thr Glu Val Asp Ser Met Pro Ser Leu Glu Ser Ser Pro Cys Ser Ser
2290 2295 2300

Phe Glu Gln Ile Ser Leu Thr Glu Ser Asp Pro Glu Thr Val Val Glu
2305 2310 2315 2320

Ala Gly Leu Pro Leu Glu Phe Val Asn Ser Asn Thr Gly Pro Ser Pro
2325 2330 2335

Ala Arg Arg Ile Val Arg Ile Arg Gln Ala Cys Cys Cys Asp Arg Ser
2340 2345 2350

Thr Met Lys Ala Met Pro Leu Ser Phe Thr Val Gly Glu Cys Leu Phe
2355 2360 2365

Val Thr Arg Tyr Asp Pro Asp Gly His Gln Leu Phe Asp Glu Arg Gly
2370 2375 2380

Pro Ile Glu Val Ser Thr Pro Ile Cys Glu Val Ile Gly Asp Ile Arg
2385 2390 2395 2400

Leu Gln Cys Asp Gln Ile Glu Glu Thr Pro Thr Ser Tyr Ser Tyr Ile
2405 2410 2415

Trp Ser Gly Ala Pro Leu Gly Thr Gly Arg Ser Val Pro Gln Pro Met
2420 2425 2430

Thr Arg Pro Ile Gly Thr His Leu Thr Cys Asp Thr Thr Lys Val Tyr
2435 2440 2445

Val Thr Asp Pro Asp Arg Ala Ala Glu Arg Ala Glu Lys Val Thr Ile
2450 2455 2460

Trp Arg Gly Asp Arg Lys Tyr Asp Lys His Tyr Glu Ala Val Val Glu
2465 2470 2475 2480

425

Ala Val Leu Lys Lys Ala Ala Ala Thr Lys Ser His Gly Trp Thr Tyr
2485 2490 2495

Ser Gln Ala Ile Ala Lys Val Arg Arg Arg Ala Ala Ala Gly Tyr Gly
2500 2505 2510

Ser Lys Val Thr Ala Ser Thr Leu Ala Thr Gly Trp Pro His Val Glu
2515 2520 2525

Glu Met Leu Asp Lys Ile Ala Arg Gly Gln Glu Val Pro Phe Thr Phe
2530 2535 2540

Val Thr Lys Arg Glu Val Phe Phe Ser Lys Thr Thr Arg Lys Pro Pro
2545 2550 2555 2560

Arg Phe Ile Val Phe Pro Pro Leu Asp Phe Arg Ile Ala Glu Lys Met
2565 2570 2575

Ile Leu Gly Asp Pro Gly Ile Val Ala Lys Ser Ile Leu Gly Asp Ala
2580 2585 2590

Tyr Leu Phe Gln Tyr Thr Pro Asn Gln Arg Val Lys Ala Leu Val Lys
2595 2600 2605

Ala Trp Glu Gly Lys Leu His Pro Ala Ala Ile Thr Val Asp Ala Thr
2610 2615 2620

Cys Phe Asp Ser Ser Ile Asp Glu His Asp Met Gln Val Glu Ala Ser
2625 2630 2635 2640

Val Phe Ala Ala Ala Ser Asp Asn Pro Ser Met Val His Ala Leu Cys
2645 2650 2655

Lys Tyr Tyr Ser Gly Gly Pro Met Val Ser Pro Asp Gly Val Pro Leu
2660 2665 2670

Gly Tyr Arg Gln Cys Arg Ser Ser Gly Val Leu Thr Thr Ser Ser Ala
2675 2680 2685

Asn Ser Ile Thr Cys Tyr Ile Lys Val Ser Ala Ala Cys Arg Arg Val
2690 2695 2700

Gly Ile Lys Ala Pro Ser Phe Phe Ile Ala Gly Asp Asp Cys Leu Ile
2705 2710 2715 2720

Ile Tyr Glu Asn Asp Gly Thr Asp Pro Cys Pro Ala Leu Lys Ala Ala
2725 2730 2735

Leu Ala Asn Tyr Gly Tyr Arg Cys Glu Pro Thr Lys His Ala Ser Leu
2740 2745 2750

Asp Thr Ala Glu Cys Cys Ser Ala Tyr Leu Ala Glu Cys Val Ala Gly
2755 2760 2765

Gly Ala Lys Arg Trp Trp Leu Ser Thr Asp Met Arg Lys Pro Leu Ala
2770 2775 2780

426

Arg Ala S r Ser Glu Tyr Ser Asp Pro Ile Gly Ser Ala Leu Gly Thr
 2785 2790 2795 2800
 Ile Leu Met Tyr Pro Arg His Pro Ile Val Arg Tyr Val Leu Ile Pro
 2805 2810 2815
 His Val Leu Ile Met Ala Tyr Arg Ser Gly Ser Thr Pro Asp Glu Leu
 2820 2825 2830
 Val Met Cys Gln Val Gln Gly Asn His Tyr Ser Phe Pro Leu Arg Leu
 2835 2840 2845
 Leu Pro Arg Val Leu Val Ser Leu His Gly Pro Trp Cys Leu Gln Val
 2850 2855 2860
 Thr Thr Asp Ser Thr Lys Thr Arg Met Glu Ala Gly Ser Xaa Leu Arg
 2865 2870 2875 2880
 Asp Leu Gly Met Lys Ser Leu Ala Trp His Arg Arg Arg Ala Gly Asn
 2885 2890 2895
 Val Arg Thr Arg Leu Leu Arg Gly Gly Lys Glu Trp Gly His Leu Ala
 2900 2905 2910
 Arg Ala Leu Leu Trp Xaa Pro Xaa Leu Lys Glu Xaa Pro Xaa Pro Ile
 2915 2920 2925
 Asn Ser Leu Pro Gly Phe Gln Leu Ala Thr Pro Tyr Glu His His Glu
 2930 2935 2940
 Glu Val Leu Ile Ser Ile Lys Ser Arg Pro Pro Trp Ile Arg Trp Ile
 2945 2950 2955 2960
 Leu Gly Ala Cys Leu Ser Leu Leu Ala Ala Leu Leu
 2965 2970

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Ile Arg Ser Arg Gln
 1 5

427

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Asp Leu Arg Val Gly
1 5

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ACCACAAACA CTCCAGTTTG TTACACTCCG CTAGGAATGC TCCTGGAGCA CCCCCCTAG	60
CAGGGCGTGG GGGATTTCCT CTGCCCCTCT GCAGAAGGGT GGAGCCAACC ACCTTAGTAT	120
GTAGGCGGCG GGAATCATGA CGCTCGCGTG ATGACAAGCG CCAAGCTTGA CTTGGATGGC	180
CCTGATGGGC GTTCATGGGT TCGGTGGTGG TGGCGCTTTA GGCAGCCTCC ACGCCCACCA	240
CCTCCCAGAT AGAGCGGCGG CACTGTAGGG AAGACCGGGG ACCGGTCACT ACCAAGGACG	300
CAGACCTCTT TTTGAGTATC ACGCCTCCGG AAGTAGTTGG GCAAGCCCAC CTATATGTGT	360
TGGGATGGTT GGGGTTAGCC ATCCATACCG TACTGCCTGA TAGGGTCCTT GCGAGGGGAT	420
CTGGGAGTCT CGTAGACCGT AGCACATGCC TGTTATTTCT ACTCAAACAA GTCCTGTACC	480
TGCGCCCAAG ACGCGCAAGA ACAAGCAGAC GCAGGCTTCA TATCCTGTGT CCATTAAAC	540
ATCTGTTGAA AGGGGACAAC GAGCAAAGCG CAAAGTCCAG CGCGATGCTC GGCCTCGTAA	600
TTACAAAATT GCTGGTATCC ATGATGGCTT GCAGACATTG GCTCAGGCTG CTTTGCCAGC	660

TCATGGTTGG GGACGCCAAG ACCCTCGCCA TAAGTCTCGC AATCTTGGAA TCCTTCTGGA 720
TTACCCTTTG GGGTGGATTG GTGATGTTAC AACTCACACA CCTCTAGTAG GCCCCGTGGT 780
GGCAGGAGCG GTCGTTGAC CAGTCTGCCA GATAGTACGC TTGCTGGAGG ATGGAGTCAA 840
CTGGGCTACT GGTGTTTCG GTGTCCACCT TTTTGTGGTA TGTCTGCTAT CTTTGGCCTG 900
TCCCTGTAGT GGGGCGCGGG TCACTGACCC AGACACAAAT ACCACAATCC TGACCAATTG 960
CTGCCAGCGT AATCAGGTTA TCTATTGTTT TCCTTCCACT TGCCTACACG AGCCTGGTTG 1020
TGTGATCTGC GCGGACGAGT GCTGGGTTCC CGCCAATCCG TACATCTCAC ACCCTTCCAA 1080
TTGGACTGGC ACGGACTCCT TCTTGGCTGA CCACATTGAT TTTGTTATGG GCGCTCTTGT 1140
GACCTGTGAC GCCCTTGACA TTGGTGAGTT GTGTGGTGCG TGTGTATTAG TCGGTGACTG 1200
GCTTGTGAGG CACTGGCTTA TTCACATAGA CCTCAATGAA ACTGGTACTT GTTACCTGGA 1260
AGTGCCCACT GGAATAGATC CTGGGTTCTT AGGGTTTATC GGGTGGATGG CCGGCAAGGT 1320
CGAGGCTGTC ATCTTCTTGA CCAAAGTGGC TTCACAAGTA CCATACGCTA TTGCGACTAT 1380
GTTTAGCAGT GTACACTACC TGGCGGTTGG CGCTCTGATC TACTATGCCT CTCGGGGCAA 1440
GTGGTATCAG TTGCTCCTAG CGCTTATGCT TTACATAGAA GCGACCTCTG GAAACCCTAT 1500
CAGGGTGCCC ACTGGATGCT CAATAGCTGA GTTTTGCTCG CCTTTGATGA TACCATGTCC 1560
TGCCACTCT TATTTGAGTG AGAATGTGTC AGAAGTCATT TGTTACAGTC CAAAGTGGAC 1620
CAGGCCTGTC ACTCTAGAGT ATAACAATC CATATCTTGG TACCCCTATA CAATCCCTGG 1680
TGCGAGGGGA TGTATGGTTA AATTCAAAAA TAACACATGG GGTGCTGCC GTATTGCGAA 1740
TGTGCCATCG TACTGCACTA TGGGCACTGA TGCAGTGTGG AACGACACTC GCAACACTTA 1800
CGAAGCATGC GGTGTAACAC CATGGCTAAC AACCAGCATGG CACAACGGCT CAGCCCTGAA 1860
ATTGGCTATA TTACAATACC CTGGGTCTAA AGAAATGTTT AAACCTCATA ATTGGATGTC 1920
AGGCCATTTG TATTTTGAGG GATCAGATAC CCCTATAGTT TACTTTTATG ACCCTGTGAA 1980
TTCCACTCTC CTACCACCGG AGAGGTGGGC TAGGTTGCCC GGTACCCAC CTGTGGTACG 2040
TGGTCTTGG TTACAGGTTT CGCAAGGGTT TTACAGTGAT GTGAAAGACC TAGCCACAGG 2100
ATTGATCACC AAAGACAAAG CCTGGAAAAA TTATCAGGTC TTATATTCCG CCACGGGTGC 2160
TTTGTCTCTT ACGGGAGTTA CCACCAAGGC CGTGGTGCTA ATTCTGTTGG GGTGTGTGG 2220
CAGCAAGTAT CTTATTTTAG CCTACCTCTG TTAATTGTCC CTTTGTGTTG GCGCGCTTC 2280
TGGTTACCCT TTGCGTCCTG TGCTCCCATC CCAGTCGTAT CTCCAAGCTG GCTGGGATGT 2340
TTTGTCTAAA GCTCAAGTAG CTCCTTTTGC TTTGATTTTC TTCATCTGTT GCTATCTCCG 2400

CTGCAGGCTA CGTTATGCTG CCCTTTTAGG GTTTGTGCCC ATGGCTGCGG GCTTGCCCCCT 2460
AACTTTCTTT GTTGCAGCAG CTGCTGCCCCA ACCAGATTAT GACTGGTGGG TGCGACTGCT 2520
AGTGGCAGGG TTAGTTTTGT GGGCCGCGCG TGACCGTGGT CCACGTATAG CTCTGCTTGT 2580
AGGTCCTTGG CCTCTGGTAG CGCTTTTAAC CCTCTTGCAT TTGGCTACGC CTGCTTCAGC 2640
TTTTGACACC GAGATAATTG GAGGGCTGAC AATACCACCT GTAGTAGCAT TAGTTGTCAT 2700
GTCTCGTTTT GGCTTCTTTG CTCACCTGTT ACCTCGCTGT GCTTTAGTTA ACTCCTATCT 2760
TTGGCAACGT TGGGAGAATT GGTTTTGGAA CGTTACACTA AGACCGGAGA GGTTCCTCCT 2820
TGTGCTGCTT TGTTCCTCCG GTGCGACATA TGACACGCTG GTGACTTTCT GTGTGTGTCA 2880
CGTAGCTCTT CTATGTTTAA CATCCAGTGC AGCATCGTTC TTTGGGACTG ACTCTAGGGT 2940
TAGGGCCCAT AGAATGTTGG TCGCTCTCGG AAAGTGTCAT GCTTGGTATT CTCATTATGT 3000
TCTTAAGTTT TTCCTCTTAG TGTTCGTGA GAATGGTGTG TTTTCTATA AGCACTTGCA 3060
TGGTGATGTC TTGCCTAATG ATTTTGCCTC GAAACTACCA TTGCAAGAGC CATTTTTCCC 3120
TTTTGAAGGC AAGGCAAGGG TCTATAGGAA TGAAGGAAGA CGCTTGGCGT GTGGGGACAC 3180
GGTTGATGGT TTGCCCCTTG TTGCGCTCT CGGCGACCTT GTTTTCGCAG GGTTAGCTAT 3240
GCCGCCAGAT GGGTGGGCCA TTACCGCACC TTTTACGCTG CAGTGTCTCT CTGAACGTGG 3300
CACGCTGTCA GCGATGGCAG TGGTCATGAC TGGTATAGAC CCCCGAACCT GGACTGGAAC 3360
TATCTTCAGA TTAGGATCTC TGGCCACTAG CTACATGGGA TTTGTTTGTG ACAACGTGTT 3420
GTATACTGCT CACCATGGCA GCAAGGGGCG CCGGTTGGCT CATCCACAG GCTCCATACA 3480
CCCAATAACC GTTGACGCGG CTAATGACCA GGACATCTAT CAACCACCAT GTGGAGCTGG 3540
GTCCCTTACT CGGTGCTCTT GCGGGGAGAC CAAGGGGTAT CTGGTAACAC GACTGGGGTC 3600
ATTGGTTGAG GTCAACAAAT CCGATGACCC TTATTGGTGT GTGTGCGGGG CCCTTCCCAT 3660
GGCTGTTGCC AAGGGTTCTT CAGGTGCCCC GATTCTGTGC TCCTCCGGGC ATGTTATTGG 3720
GATGTTACC GCTGCTAGAA ATTCTGGCGG TTCAGTCAGC CAGATTAGGG TTAGGCCGTT 3780
GGTGTGTGCT GGATACCATC CCCAGTACAC AGCACATGCC ACTCTTGATA CAAAACCTAC 3840
TGTGCCTAAC GAGTATTCAG TGCAAATTTT AATTGCCCCC ACTGGCAGCG GCAAGTCAAC 3900
CAAATTACCA CTTTCTTACA TGCAGGAGAA GTATGAGGTC TTGGTCCTAA ATCCCAGTGT 3960
GGCTACAACA GCATCAATGC CAAAGTACAT GCACGCGACG TACGGCGTGA ATCCAAATTG 4020
CTATTTTAAT GGCAAATGTA CCAACACAGG GGCTTCACTT ACGTACAGCA CATATGGCAT 4080
GTACCTGACC GGAGCATGTT CCCGGAAC TAACGTCATC ATTTGTGACG AATGCCATGC 4140

TACCGATGCA ACCACCGTGT TGGGCATTGG AAAGGTTCTA ACCGAAGCTC CATCCAAAAA	4200
TGTTAGGCTA GTGGTTCTTG CCACGGCTAC CCCCCCTGGA GTAATCCCTA CACCACATGC	4260
CAACATAACT GAGATTCAAT TAACCGATGA AGGCACTATC CCCTTTCATG GAAAAAAGAT	4320
TAAGGAGGAA AATCTGAAGA AAGGGAGACA CCTTATCTTT GAGGCTACCA AAAAAGACTG	4380
TGATGAGCTT GCTAACGAGT TAGCTCGAAA GGGAATAACA GCTGTCTCTT ACTATAGGGG	4440
ATGTGACATC TCAAAAATCC CTGAGGGCGA CTGTGTAGTA GTTGCCACTG ATGCCTTG TG	4500
TACAGGGTAC ACTGGTGACT TTGATTCCGT GTATGACTGC AGCCTCATGG TAGAAGGCAC	4560
ATGCCATGTT GACCTTGACC CTACTTTCAC CATGGGTGTT CGTGTGTGCG GGGTCTCAGC	4620
AATAGTTAAA GGCCAGCGTA GGGGCCGCAC AGGCCGTGGG AGAGCTGGCA TATACTACTA	4680
TGTAGACGGG AGTTGTACCC CTTGCGGTAT GGTTCCTGAA TGCAACATTG TTGAAGCCTT	4740
CGACGCAGCC AAGGCATGGT ATGTTTTGTC ATCAACAGAA GCTCAAACTA TTCTGGACAC	4800
CTATCGCACC CAACCTGGGT TACCTGCGAT AGGAGCAAAT TTGGACGAGT GGGCTGATCT	4860
CTTTTCTATG GTCAACCCCG AACCTTCATT TGTCATACT GCAAAAAGAA CTGCTGACAA	4920
TTATGTTTTG TTGACTGCAG CCCAACTACA ACTGTGTCAT CAGTATGGCT ATGCTGCTCC	4980
CAATGACGCA CCACGGTGGC AGGGAGCCCG GCTTGGGAAA AAACCTTG TG GGGTTCTGTG	5040
GCGCTTGGAC GCGCTGACG CCTGTCCTGG CCCAGAGCCC AGCGAGGTGA CCAGATACCA	5100
AATGTGCTTC ACTGAAGTCA ATACTTCTGG GACAGCCGCA CTCGCTGTTG GCGTTGGAGT	5160
GGCTATGGCT TATCTAGCCA TTGACACTTT TGGCGCCACT TGTGTGCGGC GTTGCTGGTC	5220
TATTACATCA GTCCCTACCG GTGCTACTGT CGCCCCAGTG GTTGACGAAG AAGAAATCGT	5280
GGAGGAGTGT GCATCATTC A TCCCTTGGA GGCCATGGTT GCTGCAATCG ATAAGCTGAA	5340
GAGTACAATA ACCACAATA GTCCTTTCAC ATTGGAAACC GCCCTTGAAA AACTTAACAC	5400
CTTTCTTGGG CCTCATGCAG CTACAATCCT TGCTATCATA GAGTATTGCT GTGGCTTAGT	5460
CACTTTACCT GACAATCCCT TTGCATCATG CGTGTGCTT TTCATTGCGG GTATTACTAC	5520
CCCCTACCT CACAAGATCA AAATGTTCTT GTCATTATTT GGAGGCGCAA TTGCGTCCAA	5580
GCTTACAGAC GCTAGAGGCG CACTGGCGTT CATGATGGCC GGGGCTGCGG GAACAGCTCT	5640
TGGTACATGG ACATCGGTGG GTTTTGTCTT TGACATGCTA GGCGGCTATG CTGCCGCTC	5700
ATCCACTGCT TGCTTGACAT TTAAATGCTT GATGGGTGAG TGGCCCACTA TGGATCAGCT	5760
TGCTGGTTTA GTCTACTCCG CGTTCAATCC GGCCGCAGGA GTTGTGGGCG TCTTGTGACG	5820
TTGTGCAATG TTTGCTTTGA CAACAGCAGG GCCAGATCAC TGGCCCAACA GACTTCTTAC	5880

TATGCTTGCT AGGAGCAACA CTGTATGTAA TGAGTACTTT ATTGCCACTC GTGACATCCG 5940
CAGGAAGATA CTGGGCATTC TGGAGGCATC TACCCCCTGG AGTGTTCATAT CAGCTTGTCAT 6000
CCGTTGGCTC CACACCCCGA CGGAGGATGA TTGCGGCCTC ATTGCTTGGG GTCTAGAGAT 6060
TTGGCAGTAT GTGTGCAATT TCTTTGTGAT TTGCTTTAAT GTCCTTAAAG CTGGAGTTCA 6120
GAGCATGGTT AACATTCCCTG GTTGTCCCTT CTACAGCTGC CAGAAGGGGT ACAAGGGCCC 6180
CTGGATTGGA TCAGGTATGC TCCAAGCACG CTGTCCATGC GGTGCTGAAC TCATCTTTTC 6240
TGTTGAGAAT GGTTTTGCAA AACTTTACAA AGGACCCAGA ACTTGTTCAA ATTACTGGAG 6300
AGGGGCTGTT CCAGTCAACG CTAGGCTGTG TGGGTCGGCT AGACCGGACC CAACTGATTG 6360
GACTAGTCTT GTCGTCAATT ATGGCGTTAG GGACTACTGT AAATATGAGA AATTGGGAGA 6420
TCACATTTTT GTTACAGCAG TATCCTCTCC AAATGTCTGT TTCACCCAGG TGCCCCCAAC 6480
CTTGAGAGCT GCAGTGGCCG TGGACGGCGT ACAGGTTTCA TGTATCTAG GTGAGCCCAA 6540
AACTCCTTGG ACGACATCTG CTGCTGTGA CCGTCCGGAC GGTAAGGGTA AACTGTAA 6600
GCTTCCCTTC CGCGTTGACG GTCACACACC TGGTGTGCGC ATGCAACTTA ATTTGCGTGA 6660
TGCACTTGAG ACAAAAGACT GTAATTCCAT AAACAACACT CCTAGTGATG AAGCCGCAGT 6720
GTCCGCTCTT GTTTTCAAAC AGGAGTTGCG GCGTACAAAC CAATTGCTTG AGGCAATTC 6780
AGCTGGCGTT GACACCACCA AACTGCCAGC CCCCTCCATC GAAGAGGTAG TGGTAAGAAA 6840
GCGCCAGTTC CGGGCAAGAA CTGGTTCGCT TACCTTGCCT CCCCCTCCGA GATCCGTCCC 6900
AGGAGTGTC TGTCTGAAA GCCTGCAACG AAGTGACCCG TTAGAAGGTC CTTCAAACCT 6960
CCCTTCTTCA CCACCTGTTT TACAGTTGGC CATGCCGATG CCCCTGTTGG GAGCAGGTGA 7020
GTGTAACCCT TCACTGCAA TTGGATGTGC AATGACCGAA ACAGGCGGAG GCCCTGATGA 7080
TTTACCCAGT TACCCTCCCA AAAAGGAGGT CTCTGAATGG TCAGACGGAA GTTGGTCAAC 7140
GACTACAACC GCTTCCAGCT ACGTTACTGG CCCCCGTAC CCTAAGATAC GGGGAAAGGA 7200
TTCCACTCAG TCAGCCCCCG CCAAACGGCC TACAAAAAAG AAGTTGGGAA AGAGTGAGTT 7260
TTCGTGCAGC ATGAGCTACA CTGGACCGA CGTGATTAGC TTCAAACTG CTTCTAAAGT 7320
TCTGTCTGCA ACTCGGGCCA TCACTAGTGG TTTCTTCAA CAAAGATCAT TGGTGTATGT 7380
GACTGAGCCG CGGGATGCGG AGCTTAGAAA ACAAAAAGTC ACTATTAATA GACAACCTCT 7440
GTTCCCCCA TCATACCACA AGCAAGTGAG ATTGGCTAAG GAAAAAGCTT CAAAAGTTGT 7500
CGGTGTCATG TGGGACTATG ATGAAGTAGC AGCTCACACG CCCTCTAAGT CTGCTAAGTC 7560
CCACATCACT GGCCTTCGGG GCACTGATGT TCGTTCTGGA GCAGCCCGCA AGGCTGTTCT 7620

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GGACTTGCAG AAGTGTGTCG AGGCAGGTGA GATACCGAGT CATTATCGGC AAAGTGTGAT	7680
AGTTCCAAAG GAGGAGGTCT TCGTGAAGAC CCCCCAGAAA CCAACAAAGA AACCCCCAAG	7740
GCTTATCTCG TACCCCCACC TTGAAATGAG ATGTGTTGAG AAGATGTACT ACGGTCAGGT	7800
TGCTCCTGAC GTAGTTAAAG CTGTCATGGG AGATGCGTAC GGGTTTGTCTG ACCCACGTAC	7860
CCGTGTCAAG CGTCTGTTGT CGATGTGGTC ACCCGATGCA GTCGGAGCCA CATGCCGATAC	7920
AGTGTGTTTT GACAGTACCA TCACACCCGA GGATATCATG GTGGAGACAG ACATCTACTC	7980
AGCAGCTAAA CTCAGTGACC AACACCGAGC TGGCATTAC ACCATTGCCA GGCAGTTATA	8040
CGCTGGAGGA CCGATGATCG CTTATGATGG CCGAGAGATC GGATATCGTA GGTGTAGGTC	8100
TTCCGGCGTC TATACTACCT CAAGTTCCAA CAGTTTGACC TGCTGGCTGA AGGTAAATGC	8160
TGCAGCCGAA CAGGCTGGCA TGAAGAACCC TCGCTTCCTT ATTTGCGGCG ATGATTGCAC	8220
CGTAATTTGG AAGAGCGCCG GAGCAGATGC AGACAAACAA GCAATGCGTG TCTTTGCTAG	8280
CTGGATGAAG GTGATGGGTG CACCACAAGA TTGTGTGCCT CAACCCAAAT ACAGTTTGA	8340
AGAATTAACA TCATGCTCAT CAAATGTTAC CTCTGGAATT ACCAAAAGTG GCAAGCCTTA	8400
CTACTTTCTT ACAAGAGATC CTCGTATCCC CTTGGCAGG TGCTCTGCCG AGGGTCTGGG	8460
ATACAACCCC AGTGCTGCGT GGATTGGGTA TCTAATACAT CACTACCCAT GTTTGTGGGT	8520
TAGCCGTGTG TTGGCTGTCC ATTTTCATGA GCAGATGCTC TTTGAGGACA AACTTCCCGA	8580
GACTGTGACC TTTGACTGGT ATGGGAAAAA TTATACGGTG CCTGTAGAAG ATCTGCCCAG	8640
CATCATTGCT GGTGTGCACG GTATTGAGGC TTTCTCGGTG GTGCGCTACA CCAACGCTGA	8700
GATCCTCAGA GTTTCCCAAT CACTAACAGA CATGACCATG CCCCCCTGC GAGCCTGGCG	8760
AAAGAAAGCC AGGGCGGTCC TCGCCAGCGC CAAGAGGCGT GGCGGAGCAC ACGCAAAATT	8820
GGCTCGCTTC CTTCTCTGGC ATGCTACATC TAGACCTCTA CCAGATTGGG ATAAGACGAG	8880
CGTGGCTCGG TACACCACTT TCAATTATTG TGATGTTTAC TCCCCGAGG GGGATGTGTT	8940
TGTTACACCA CAGAGAAGAT TGCAGAAGTT TCTTGTAAG TATTTGGCTG TCATTGTTTT	9000
TGCCCTAGGG CTCATTGCTG TTGACTAGC CATCAGCTGA ACCCCCCAAT TCAAAATTAA	9060
TTAACAGTTT TTTTTTTTTT TTTTTTTTTT TTTTAGGGCA GCGGCAACAG GGGAGACCCC	9120
GGGCTTAACG ACCCCGCGAT GTG	9143

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GATCAGGTAT GCTCCAAGCA CGCTGTCCAT GCGGTGCTGA ACTCATCTTT TCTGTTGAGA	60
ATGGTTTTTGC AAAACTTTAC AAAGGACCCA GAACTTGTTT AAATTACTGG AGAGGGGCTG	120
TTCCAGTCAA CGCTAGGCTG TGTGGGTCGG CTAGACCGGA CCCAACTGAT TGGACTAGTC	180
TTGTCGTCAA TTATGGCGTT AGGGACTACT GTAAATATGA GAAATTGGGA GATC	234

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GATCACATTT TTGTTACAGC AGTATCCTCT CCAAATGTCT GTTTCACCCA GGTGCCCCCA	60
ACCTTGAGAG CTGCAGTGGC CGTGGACCGC GTACAGGTTC AGYGTTATCT AGGTGAGCCC	120
AAAACTCCTT GGACGACATC TGCTTGCTGT TACGGTCCTG ACGGTAAGGG TAAAACGTGTT	180
AAGCTTCCCT TCCGCGTTGA CGGACACACA CCTGGTGGTC GCATGCAACT TAATTTGCGT	240
GATCGACTTG AGGCAAATGA CTGTAATTCC ATAAACAACA CTCCTAGTGA TGAAGCCGCA	300
GTGTCCGCTC TTGTTTTCAA ACAGGAGTTG CGGCGTACAA ACCAATTGCT TGAGGCAATT	360
TCAGCTGGCG TTGACACCAC CAACTGCCA GCCCCCTCCC AGATCGAAGA GGTAGTGGTA	420
AGAAAGCGCC AGTTCCGGGC AAGAACTGGT TCGCTTACCT TGCCTCCCCC TCCGAGATC	479

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9143 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: 5'UTR
 (B) LOCATION: 1..445

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 446..9037

(ix) FEATURE:

(A) NAME/KEY: 3'UTR
 (B) LOCATION: 9038..9143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ACCACAAACA CTCCAGTTTG TTACACTCCG CTAGGAATGC TCCTGGAGCA CCCCCCTAG	60
CAGGGCGTGG GGGATTTCCT CTGCCCCGTCT GCAGAAGGGT GGAGCCAACC ACCTTAGTAT	120
GTAGGCGGCG GGAATCATGA CGCTCGCGTG ATGACAAGCG CCAAGCTTGA CTTGGATGGC	180
CCTGATGGGC GTTCATGGGT TCGGTGGTGG TGGCGCTTTA GGCAGCCTCC ACGCCCACCA	240
CCTCCCAGAT AGAGCGGCGG CACTGTAGGG AAGACCGGGG ACCGGTCACT ACCAAGGACG	300
CAGACCTCTT TTTGAGTATC ACGCCTCCGG AAGTAGTTGG GCAAGCCCAC CTATATGTGT	360
TGGGATGGTT GGGGTTAGCC ATCCATACCG TACTGCCTGA TAGGGTCCTT GCGAGGGGAT	420
CTGGGAGTCT CGTAGACCGT AGCAC ATG CCT GTT ATT TCT ACT CAA ACA AGT	472
Met Pro Val Ile Ser Thr Gln Thr Ser	
1 5	
CCT GTA CCT GCG CCC AGA ACG CGC AAG AAC AAG CAG ACG CAG GCT TCA	520
Pro Val Pro Ala Pro Arg Thr Arg Lys Asn Lys Gln Thr Gln Ala Ser	
10 15 20 25	
TAT CCT GTG TCC ATT AAA ACA TCT GTT GAA AGG GGA CAA CGA GCA AAG	568
Tyr Pro Val Ser Ile Lys Thr Ser Val Glu Arg Gly Gln Arg Ala Lys	
30 35 40	
CGC AAA GTC CAG CGC GAT GCT CGG CCT CGT AAT TAC AAA ATT GCT GGT	616
Arg Lys Val Gln Arg Asp Ala Arg Pro Arg Asn Tyr Lys Ile Ala Gly	
45 50 55	
ATC CAT GAT GGC TTG CAG ACA TTG GCT CAG GCT GCT TTG CCA GCT CAT	664
Ile His Asp Gly Leu Gln Thr Leu Ala Gln Ala Ala Leu Pro Ala His	
60 65 70	
GGT TGG GGA CGC CAA GAC CCT CGC CAT AAG TCT CGC AAT CTT GGA ATC	712
Gly Trp Gly Arg Gln Asp Pro Arg His Lys Ser Arg Asn Leu Gly Ile	
75 80 85	
CTT CTG GAT TAC CCT TTG GGG TGG ATT GGT GAT GTT ACA ACT CAC ACA	760

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Leu Leu Asp Tyr Pro Leu Gly Trp Ile Gly Asp Val Thr Thr His Thr	
90 95 100 105	
CCT CTA GTA GGC CCG CTG GTG GCA GGA GCG GTC GTT CGA CCA GTC TGC	808
Pro Leu Val Gly Pro Leu Val Ala Gly Ala Val Val Arg Pro Val Cys	
110 115 120	
CAG ATA GTA CGC TTG CTG GAG GAT GGA GTC AAC TGG GCT ACT GGT TGG	856
Gln Ile Val Arg Leu Leu Glu Asp Gly Val Asn Trp Ala Thr Gly Trp	
125 130 135	
TTC GGT GTC CAC CTT TTT GTG GTA TGT CTG CTA TCT TTG GCC TGT CCC	904
Phe Gly Val His Leu Phe Val Val Cys Leu Leu Ser Leu Ala Cys Pro	
140 145 150	
TGT AGT GGG GCG CGG GTC ACT GAC CCA GAC ACA AAT ACC ACA ATC CTG	952
Cys Ser Gly Ala Arg Val Thr Asp Pro Asp Thr Asn Thr Thr Ile Leu	
155 160 165	
ACC AAT TGC TGC CAG CGT AAT CAG GTT ATC TAT TGT TCT CCT TCC ACT	1000
Thr Asn Cys Cys Gln Arg Asn Gln Val Ile Tyr Cys Ser Pro Ser Thr	
170 175 180 185	
TGC CTA CAC GAG CCT GGT TGT GTG ATC TGC GCG GAC GAG TGC TGG GTT	1048
Cys Leu His Glu Pro Gly Cys Val Ile Cys Ala Asp Glu Cys Trp Val	
190 195 200	
CCC GCC AAT CCG TAC ATC TCA CAC CCT TCC AAT TGG ACT GGC ACG GAC	1096
Pro Ala Asn Pro Tyr Ile Ser His Pro Ser Asn Trp Thr Gly Thr Asp	
205 210 215	
TCC TTC TTG GCT GAC CAC ATT GAT TTT GTT ATG GGC GCT CTT GTG ACC	1144
Ser Phe Leu Ala Asp His Ile Asp Phe Val Met Gly Ala Leu Val Thr	
220 225 230	
TGT GAC GCC CTT GAC ATT GGT GAG TTG TGT GGT GCG TGT GTA TTA GTC	1192
Cys Asp Ala Leu Asp Ile Gly Glu Leu Cys Gly Ala Cys Val Leu Val	
235 240 245	
GGT GAC TGG CTT GTC AGG CAC TGG CTT ATT CAC ATA GAC CTC AAT GAA	1240
Gly Asp Trp Leu Val Arg His Trp Leu Ile His Ile Asp Leu Asn Glu	
250 255 260 265	
ACT GGT ACT TGT TAC CTG GAA GTG CCC ACT GGA ATA GAT CCT GGG TTC	1288
Thr Gly Thr Cys Tyr Leu Glu Val Pro Thr Gly Ile Asp Pro Gly Phe	
270 275 280	
CTA GGG TTT ATC GGG TGG ATG GCC GGC AAG GTC GAG GCT GTC ATC TTC	1336
Leu Gly Phe Ile Gly Trp Met Ala Gly Lys Val Glu Ala Val Ile Phe	
285 290 295	
TTG ACC AAA CTG GCT TCA CAA GTA CCA TAC GCT ATT GCG ACT ATG TTT	1384
Leu Thr Lys Leu Ala Ser Gln Val Pro Tyr Ala Ile Ala Thr Met Phe	
300 305 310	
AGC AGT GTA CAC TAC CTG GCG GTT GGC GCT CTG ATC TAC TAT GCC TCT	1432
Ser Ser Val His Tyr Leu Ala Val Gly Ala Leu Ile Tyr Tyr Ala Ser	

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315	320	325	
CGG GGC AAG TGG TAT CAG TTG CTC CTA GCG CTT ATG CTT TAC ATA GAA Arg Gly Lys Trp Tyr Gln Leu Leu Leu Ala Leu Met Leu Tyr Ile Glu 330 335 340 345			1480
GCG ACC TCT GGA AAC CCT ATC AGG GTG CCC ACT GGA TGC TCA ATA GCT Ala Thr Ser Gly Asn Pro Ile Arg Val Pro Thr Gly Cys Ser Ile Ala 350 355 360			1528
GAG TTT TGC TCG CCT TTG ATG ATA CCA TGT CCT TGC CAC TCT TAT TTG Glu Phe Cys Ser Pro Leu Met Ile Pro Cys Pro Cys His Ser Tyr Leu 365 370 375			1576
AGT GAG AAT GTG TCA GAA GTC ATT TGT TAC AGT CCA AAG TGG ACC AGG Ser Glu Asn Val Ser Glu Val Ile Cys Tyr Ser Pro Lys Trp Thr Arg 380 385 390			1624
CCT GTC ACT CTA GAG TAT AAC AAC TCC ATA TCT TGG TAC CCC TAT ACA Pro Val Thr Leu Glu Tyr Asn Asn Ser Ile Ser Trp Tyr Pro Tyr Thr 395 400 405			1672
ATC CCT GGT GCG AGG GGA TGT ATG GTT AAA TTC AAA AAT AAC ACA TGG Ile Pro Gly Ala Arg Gly Cys Met Val Lys Phe Lys Asn Asn Thr Trp 410 415 420 425			1720
GGT TGC TGC CGT ATT CGC AAT GTG CCA TCG TAC TGC ACT ATG GGC ACT Gly Cys Cys Arg Ile Arg Asn Val Pro Ser Tyr Cys Thr Met Gly Thr 430 435 440			1768
GAT GCA GTG TGG AAC GAC ACT CGC AAC ACT TAC GAA GCA TGC GGT GTA Asp Ala Val Trp Asn Asp Thr Arg Asn Thr Tyr Glu Ala Cys Gly Val 445 450 455			1816
ACA CCA TGG CTA ACA ACC GCA TGG CAC AAC GGC TCA GCC CTG AAA TTG Thr Pro Trp Leu Thr Thr Ala Trp His Asn Gly Ser Ala Leu Lys Leu 460 465 470			1864
GCT ATA TTA CAA TAC CCT GGG TCT AAA GAA ATG TTT AAA CCT CAT AAT Ala Ile Leu Gln Tyr Pro Gly Ser Lys Glu Met Phe Lys Pro His Asn 475 480 485			1912
TGG ATG TCA GGC CAT TTG TAT TTT GAG GGA TCA GAT ACC CCT ATA GTT Trp Met Ser Gly His Leu Tyr Phe Glu Gly Ser Asp Thr Pro Ile Val 490 495 500 505			1960
TAC TTT TAT GAC CCT GTG AAT TCC ACT CTC CTA CCA CCG GAG AGG TGG Tyr Phe Tyr Asp Pro Val Asn Ser Thr Leu Leu Pro Pro Glu Arg Trp 510 515 520			2008
GCT AGG TTG CCC GGT ACC CCA CCT GTG GTA CGT GGT TCT TGG TTA CAG Ala Arg Leu Pro Gly Thr Pro Pro Val Val Arg Gly Ser Trp Leu Gln 525 530 535			2056
GTT CCG CAA GGG TTT TAC AGT GAT GTG AAA GAC CTA GCC ACA GGA TTG Val Pro Gln Gly Phe Tyr Ser Asp Val Lys Asp Leu Ala Thr Gly Leu 540 545 550			2104

437

ATC ACC AAA GAC AAA GCC TGG AAA AAT TAT CAG GTC TTA TAT TCC GCC Ile Thr Lys Asp Lys Ala Trp Lys Asn Tyr Gln Val Leu Tyr Ser Ala 555 560 565	2152
ACG GGT GCT TTG TCT CTT ACG GGA GTT ACC ACC AAG GCC GTG GTG CTA Thr Gly Ala Leu Ser Leu Thr Gly Val Thr Thr Lys Ala Val Val Leu 570 575 580 585	2200
ATT CTG TTG GGG TTG TGT GGC AGC AAG TAT CTT ATT TTA GCC TAC CTC Ile Leu Leu Gly Leu Cys Gly Ser Lys Tyr Leu Ile Leu Ala Tyr Leu 590 595 600	2248
TGT TAC TTG TCC CTT TGT TTT GGG CGC GCT TCT GGT TAC CCT TTG CGT Cys Tyr Leu Ser Leu Cys Phe Gly Arg Ala Ser Gly Tyr Pro Leu Arg 605 610 615	2296
CCT GTG CTC CCA TCC CAG TCG TAT CTC CAA GCT GGC TGG GAT GTT TTG Pro Val Leu Pro Ser Gln Ser Tyr Leu Gln Ala Gly Trp Asp Val Leu 620 625 630	2344
TCT AAA GCT CAA GTA GCT CCT TTT GCT TTG ATT TTC TTC ATC TGT TGC Ser Lys Ala Gln Val Ala Pro Phe Ala Leu Ile Phe Phe Ile Cys Cys 635 640 645	2392
TAT CTC CGC TGC AGG CTA CGT TAT GCT GCC CTT TTA GGG TTT GTG CCC Tyr Leu Arg Cys Arg Leu Arg Tyr Ala Ala Leu Leu Gly Phe Val Pro 650 655 660 665	2440
ATG GCT GCG GGC TTG CCC CTA ACT TTC TTT GTT GCA GCA GCT GCT GCC Met Ala Ala Gly Leu Pro Leu Thr Phe Val Ala Ala Ala Ala Ala 670 675 680	2488
CAA CCA GAT TAT GAC TGG TGG GTG CGA CTG CTA GTG GCA GGG TTA GTT Gln Pro Asp Tyr Asp Trp Trp Val Arg Leu Leu Val Ala Gly Leu Val 685 690 695	2536
TTG TGG GCC GGC CGT GAC CGT GGT CCA CGT ATA GCT CTG CTT GTA GGT Leu Trp Ala Gly Arg Asp Arg Gly Pro Arg Ile Ala Leu Leu Val Gly 700 705 710	2584
CCT TGG CCT CTG GTA GCG CTT TTA ACC CTC TTG CAT TTG GCT ACG CCT Pro Trp Pro Leu Val Ala Leu Leu Thr Leu Leu His Leu Ala Thr Pro 715 720 725	2632
GCT TCA GCT TTT GAC ACC GAG ATA ATT GGA GGG CTG ACA ATA CCA CCT Ala Ser Ala Phe Asp Thr Glu Ile Ile Gly Gly Leu Thr Ile Pro Pro 730 735 740 745	2680
GTA GTA GCA TTA GTT GTC ATG TCT CGT TTT GGC TTC TTT GCT CAC TTG Val Val Ala Leu Val Val Met Ser Arg Phe Gly Phe Phe Ala His Leu 750 755 760	2728
TTA CCT CGC TGT GCT TTA GTT AAC TCC TAT CTT TGG CAA CGT TGG GAG Leu Pro Arg Cys Ala Leu Val Asn Ser Tyr Leu Trp Gln Arg Trp Glu 765 770 775	2776
AAT TGG TTT TGG AAC GTT ACA CTA AGA CCG GAG AGG TTT CTC CTT GTG	2824

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Asn	Trp	Phe	Trp	Asn	Val	Thr	Leu	Arg	Pro	Glu	Arg	Phe	Leu	Leu	Val	
		780					785					790				
CTG	GTT	TGT	TTC	CCC	GGT	GCG	ACA	TAT	GAC	ACG	CTG	GTG	ACT	TTC	TGT	2872
Leu	Val	Cys	Phe	Pro	Gly	Ala	Thr	Tyr	Asp	Thr	Leu	Val	Thr	Phe	Cys	
		795				800					805					
GTG	TGT	CAC	GTA	GCT	CTT	CTA	TGT	TTA	ACA	TCC	AGT	GCA	GCA	TCG	TTC	2920
Val	Cys	His	Val	Ala	Leu	Leu	Cys	Leu	Thr	Ser	Ser	Ala	Ala	Ser	Phe	
810					815					820					825	
TTT	GGG	ACT	GAC	TCT	AGG	GTT	AGG	GCC	CAT	AGA	ATG	TTG	GTG	CGT	CTC	2968
Phe	Gly	Thr	Asp	Ser	Arg	Val	Arg	Ala	His	Arg	Met	Leu	Val	Arg	Leu	
				830					835					840		
GGA	AAG	TGT	CAT	GCT	TGG	TAT	TCT	CAT	TAT	GTT	CTT	AAG	TTT	TTC	CTC	3016
Gly	Lys	Cys	His	Ala	Trp	Tyr	Ser	His	Tyr	Val	Leu	Lys	Phe	Phe	Leu	
			845					850					855			
TTA	GTG	TTT	GGT	GAG	AAT	GGT	GTG	TTT	TTC	TAT	AAG	CAC	TTG	CAT	GGT	3064
Leu	Val	Phe	Gly	Glu	Asn	Gly	Val	Phe	Phe	Tyr	Lys	His	Leu	His	Gly	
		860					865						870			
GAT	GTC	TTG	CCT	AAT	GAT	TTT	GCC	TCG	AAA	CTA	CCA	TTG	CAA	GAG	CCA	3112
Asp	Val	Leu	Pro	Asn	Asp	Phe	Ala	Ser	Lys	Leu	Pro	Leu	Gln	Glu	Pro	
		875				880					885					
TTT	TTC	CCT	TTT	GAA	GGC	AAG	GCA	AGG	GTC	TAT	AGG	AAT	GAA	GGA	AGA	3160
Phe	Phe	Pro	Phe	Glu	Gly	Lys	Ala	Arg	Val	Tyr	Arg	Asn	Glu	Gly	Arg	
890					895				900						905	
CGC	TTG	GCG	TGT	GGG	GAC	ACG	GTT	GAT	GGT	TTG	CCC	GTT	GTT	GCG	CGT	3208
Arg	Leu	Ala	Cys	Gly	Asp	Thr	Val	Asp	Gly	Leu	Pro	Val	Val	Ala	Arg	
				910					915					920		
CTC	GGC	GAC	CTT	GTT	TTC	GCA	GGG	TTA	GCT	ATG	CCG	CCA	GAT	GGG	TGG	3256
Leu	Gly	Asp	Leu	Val	Phe	Ala	Gly	Leu	Ala	Met	Pro	Pro	Asp	Gly	Trp	
			925					930						935		
GCC	ATT	ACC	GCA	CCT	TTT	ACG	CTG	CAG	TGT	CTC	TCT	GAA	CGT	GGC	ACG	3304
Ala	Ile	Thr	Ala	Pro	Phe	Thr	Leu	Gln	Cys	Leu	Ser	Glu	Arg	Gly	Thr	
		940					945						950			
CTG	TCA	GCG	ATG	GCA	GTG	GTC	ATG	ACT	GGT	ATA	GAC	CCC	CGA	ACT	TGG	3352
Leu	Ser	Ala	Met	Ala	Val	Val	Met	Thr	Gly	Ile	Asp	Pro	Arg	Thr	Trp	
		955				960					965					
ACT	GGA	ACT	ATC	TTC	AGA	TTA	GGA	TCT	CTG	GCC	ACT	AGC	TAC	ATG	GGA	3400
Thr	Gly	Thr	Ile	Phe	Arg	Leu	Gly	Ser	Leu	Ala	Thr	Ser	Tyr	Met	Gly	
970					975				980					985		
TTT	GTT	TGT	GAC	AAC	GTG	TTG	TAT	ACT	GCT	CAC	CAT	GGC	AGC	AAG	GGG	3448
Phe	Val	Cys	Asp	Asn	Val	Leu	Tyr	Thr	Ala	His	His	Gly	Ser	Lys	Gly	
				990					995					1000		
CGC	CGG	TTG	GCT	CAT	CCC	ACA	GGC	TCC	ATA	CAC	CCA	ATA	ACC	GTT	GAC	3496
Arg	Arg	Leu	Ala	His	Pro	Thr	Gly	Ser	Ile	His	Pro	Ile	Thr	Val	Asp	

439

1005	1010	1015	
GCG GCT AAT GAC CAG GAC ATC TAT CAA CCA CCA TGT GGA GCT GGG TCC Ala Ala Asn Asp Gln Asp Ile Tyr Gln Pro Pro Cys Gly Ala Gly Ser 1020 1025 1030			3544
CTT ACT CGG TGC TCT TGC GGG GAG ACC AAG GGG TAT CTG GTA ACA CGA Leu Thr Arg Cys Ser Cys Gly Glu Thr Lys Gly Tyr Leu Val Thr Arg 1035 1040 1045			3592
CTG GGG TCA TTG GTT GAG GTC AAC AAA TCC GAT GAC CCT TAT TGG TGT Leu Gly Ser Leu Val Glu Val Asn Lys Ser Asp Asp Pro Tyr Trp Cys 1050 1055 1060 1065			3640
GTG TGC GGG GCC CTT CCC ATG GCT GTT GCC AAG GGT TCT TCA GGT GCC Val Cys Gly Ala Leu Pro Met Ala Val Ala Lys Gly Ser Ser Gly Ala 1070 1075 1080			3688
CCG ATT CTG TGC TCC TCC GGG CAT GTT ATT GGG ATG TTC ACC GCT GCT Pro Ile Leu Cys Ser Ser Gly His Val Ile Gly Met Phe Thr Ala Ala 1085 1090 1095			3736
AGA AAT TCT GGC GGT TCA GTC AGC CAG ATT AGG GTT AGG CCG TTG GTG Arg Asn Ser Gly Gly Ser Val Ser Gln Ile Arg Val Arg Pro Leu Val 1100 1105 1110			3784
TGT GCT GGA TAC CAT CCC CAG TAC ACA GCA CAT GCC ACT CTT GAT ACA Cys Ala Gly Tyr His Pro Gln Tyr Thr Ala His Ala Thr Leu Asp Thr 1115 1120 1125			3832
AAA CCT ACT GTG CCT AAC GAG TAT TCA GTG CAA ATT TTA ATT GCC CCC Lys Pro Thr Val Pro Asn Glu Tyr Ser Val Gln Ile Leu Ile Ala Pro 1130 1135 1140 1145			3880
ACT GGC AGC GGC AAG TCA ACC AAA TTA CCA CTT TCT TAC ATG CAG GAG Thr Gly Ser Gly Lys Ser Thr Lys Leu Pro Leu Ser Tyr Met Gln Glu 1150 1155 1160			3928
AAG TAT GAG GTC TTG GTC CTA AAT CCC AGT GTG GCT ACA ACA GCA TCA Lys Tyr Glu Val Leu Val Leu Asn Pro Ser Val Ala Thr Thr Ala Ser 1165 1170 1175			3976
ATG CCA AAG TAC ATG CAC GCG ACG TAC GGC GTG AAT CCA AAT TGC TAT Met Pro Lys Tyr Met His Ala Thr Tyr Gly Val Asn Pro Asn Cys Tyr 1180 1185 1190			4024
TTT AAT GGC AAA TGT ACC AAC ACA GGG GCT TCA CTT ACG TAC AGC ACA Phe Asn Gly Lys Cys Thr Asn Thr Gly Ala Ser Leu Thr Tyr Ser Thr 1195 1200 1205			4072
TAT GGC ATG TAC CTG ACC GGA GCA TGT TCC CGG AAC TAT GAC GTC ATC Tyr Gly Met Tyr Leu Thr Gly Ala Cys Ser Arg Asn Tyr Asp Val Ile 1210 1215 1220 1225			4120
ATT TGT GAC GAA TGC CAT GCT ACC GAT GCA ACC ACC GTG TTG GGC ATT Ile Cys Asp Glu Cys His Ala Thr Asp Ala Thr Thr Val Leu Gly Ile 1230 1235 1240			4168

440

GGA AAG GTT CTA ACC GAA GCT CCA TCC AAA AAT GTT AGG CTA GTG GTT Gly Lys Val Leu Thr Glu Ala Pro Ser Lys Asn Val Arg Leu Val Val 1245 1250 1255	4216
CTT GCC ACG GCT ACC CCC CCT GGA GTA ATC CCT ACA CCA CAT GCC AAC Leu Ala Thr Ala Thr Pro Pro Gly Val Ile Pro Thr Pro His Ala Asn 1260 1265 1270	4264
ATA ACT GAG ATT CAA TTA ACC GAT GAA GGC ACT ATC CCC TTT CAT GGA Ile Thr Glu Ile Gln Leu Thr Asp Glu Gly Thr Ile Pro Phe His Gly 1275 1280 1285	4312
AAA AAG ATT AAG GAG GAA AAT CTG AAG AAA GGG AGA CAC CTT ATC TTT Lys Lys Ile Lys Glu Glu Asn Leu Lys Lys Gly Arg His Leu Ile Phe 1290 1295 1300 1305	4360
GAG GCT ACC AAA AAA CAC TGT GAT GAG CTT GCT AAC GAG TTA GCT CGA Glu Ala Thr Lys Lys His Cys Asp Glu Leu Ala Asn Glu Leu Ala Arg 1310 1315 1320	4408
AAG GGA ATA ACA GCT GTC TCT TAC TAT AGG GGA TGT GAC ATC TCA AAA Lys Gly Ile Thr Ala Val Ser Tyr Tyr Arg Gly Cys Asp Ile Ser Lys 1325 1330 1335	4456
ATC CCT GAG GGC GAC TGT GTA GTA GTT GCC ACT GAT GCC TTG TGT ACA Ile Pro Glu Gly Asp Cys Val Val Val Ala Thr Asp Ala Leu Cys Thr 1340 1345 1350	4504
GGG TAC ACT GGT GAC TTT GAT TCC GTG TAT GAC TGC AGC CTC ATG GTA Gly Tyr Thr Gly Asp Phe Asp Ser Val Tyr Asp Cys Ser Leu Met Val 1355 1360 1365	4552
GAA GGC ACA TGC CAT GTT GAC CTT GAC CCT ACT TTC ACC ATG GGT GTT Glu Gly Thr Cys His Val Asp Leu Asp Pro Thr Phe Thr Met Gly Val 1370 1375 1380 1385	4600
CGT GTG TGC GGG GTC TCA GCA ATA GTT AAA GGC CAG CGT AGG GGC CGC Arg Val Cys Gly Val Ser Ala Ile Val Lys Gly Gln Arg Arg Gly Arg 1390 1395 1400	4648
ACA GGC CGT GGG AGA GCT GGC ATA TAC TAC TAT GTA GAC GGG AGT TGT Thr Gly Arg Gly Arg Ala Gly Ile Tyr Tyr Tyr Val Asp Gly Ser Cys 1405 1410 1415	4696
ACC CCT TCG GGT ATG GTT CCT GAA TGC AAC ATT GTT GAA GCC TTC GAC Thr Pro Ser Gly Met Val Pro Glu Cys Asn Ile Val Glu Ala Phe Asp 1420 1425 1430	4744
GCA GCC AAG GCA TGG TAT GGT TTG TCA TCA ACA GAA GCT CAA ACT ATT Ala Ala Lys Ala Trp Tyr Gly Leu Ser Ser Thr Glu Ala Gln Thr Ile 1435 1440 1445	4792
CTG GAC ACC TAT CGC ACC CAA CCT GGG TTA CCT GCG ATA GGA GCA AAT Leu Asp Thr Tyr Arg Thr Gln Pro Gly Leu Pro Ala Ile Gly Ala Asn 1450 1455 1460 1465	4840
TTG GAC GAG TGG GCT GAT CTC TTT TCT ATG GTC AAC CCC GAA CCT TCA	4888

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Leu Asp Glu Trp	Ala Asp Leu Ph	Ser Met Val Asn Pro Glu Pro Ser	
1470	1475	1480	
TTT GTC AAT ACT GCA AAA AGA ACT GCT GAC AAT TAT GTT TTG TTG ACT			4936
Phe Val Asn Thr Ala Lys Arg Thr Ala Asp Asn Tyr Val Leu Leu Thr			
1485	1490	1495	
GCA GCC CAA CTA CAA CTG TGT CAT CAG TAT GGC TAT GCT GCT CCC AAT			4984
Ala Ala Gln Leu Gln Leu Cys His Gln Tyr Gly Tyr Ala Ala Pro Asn			
1500	1505	1510	
GAC GCA CCA CGG TGG CAG GGA GCC CGG CTT GGG AAA AAA CCT TGT GGG			5032
Asp Ala Pro Arg Trp Gln Gly Ala Arg Leu Gly Lys Lys Pro Cys Gly			
1515	1520	1525	
GTT CTG TGG CGC TTG GAC GGC GCT GAC GCC TGT CCT GGC CCA GAG CCC			5080
Val Leu Trp Arg Leu Asp Gly Ala Asp Ala Cys Pro Gly Pro Glu Pro			
1530	1535	1540	1545
AGC GAG GTG ACC AGA TAC CAA ATG TGC TTC ACT GAA GTC AAT ACT TCT			5128
Ser Glu Val Thr Arg Tyr Gln Met Cys Phe Thr Glu Val Asn Thr Ser			
1550	1555	1560	
GGG ACA GCC GCA CTC GCT GTT GGC GTT GGA GTG GCT ATG GCT TAT CTA			5176
Gly Thr Ala Ala Leu Ala Val Gly Val Gly Val Ala Met Ala Tyr Leu			
1565	1570	1575	
GCC ATT GAC ACT TTT GGC GCC ACT TGT GTG CGG CGT TGC TGG TCT ATT			5224
Ala Ile Asp Thr Phe Gly Ala Thr Cys Val Arg Arg Cys Trp Ser Ile			
1580	1585	1590	
ACA TCA GTC CCT ACC GGT GCT ACT GTC GCC CCA GTG GTT GAC GAA GAA			5272
Thr Ser Val Pro Thr Gly Ala Thr Val Ala Pro Val Val Asp Glu Glu			
1595	1600	1605	
GAA ATC GTG GAG GAG TGT GCA TCA TTC ATT CCC TTG GAG GCC ATG GTT			5320
Glu Ile Val Glu Glu Cys Ala Ser Phe Ile Pro Leu Glu Ala Met Val			
1610	1615	1620	1625
GCT GCA ATC GAT AAG CTG AAG AGT ACA ATA ACC ACA ACT AGT CCT TTC			5368
Ala Ala Ile Asp Lys Leu Lys Ser Thr Ile Thr Thr Thr Ser Pro Phe			
1630	1635	1640	
ACA TTG GAA ACC GCC CTT GAA AAA CTT AAC ACC TTT CTT GGG CCT CAT			5416
Thr Leu Glu Thr Ala Leu Glu Lys Leu Asn Thr Phe Leu Gly Pro His			
1645	1650	1655	
GCA GCT ACA ATC CTT GCT ATC ATA GAG TAT TGC TGT GGC TTA GTC ACT			5464
Ala Ala Thr Ile Leu Ala Ile Ile Glu Tyr Cys Cys Gly Leu Val Thr			
1660	1665	1670	
TTA CCT GAC AAT CCC TTT GCA TCA TGC GTG TTT GCT TTC ATT GCG GGT			5512
Leu Pro Asp Asn Pro Phe Ala Ser Cys Val Phe Ala Phe Ile Ala Gly			
1675	1680	1685	
ATT ACT ACC CCA CTA CCT CAC AAG ATC AAA ATG TTC CTG TCA TTA TTT			5560
Ile Thr Thr Pro Leu Pro His Lys Ile Lys Met Phe Leu Ser Leu Phe			

442

1690	1695	1700	1705	
GGA GGC GCA ATT GCG TCC AAG CTT ACA GAC GCT AGA GGC GCA CTG GCG				5608
Gly Gly Ala Ile Ala Ser Lys Leu Thr Asp Ala Arg Gly Ala Leu Ala				
1710		1715	1720	
TTC ATG ATG GCC GGG GCT GCG GGA ACA GCT CTT GGT ACA TGG ACA TCG				5656
Phe Met Met Ala Gly Ala Ala Gly Thr Ala Leu Gly Thr Trp Thr Ser				
1725		1730	1735	
GTG GGT TTT GTC TTT GAC ATG CTA GGC GGC TAT GCT GCC GCC TCA TCC				5704
Val Gly Phe Val Phe Asp Met Leu Gly Gly Tyr Ala Ala Ala Ser Ser				
1740		1745	1750	
ACT GCT TGC TTG ACA TTT AAA TGC TTG ATG GGT GAG TGG CCC ACT ATG				5752
Thr Ala Cys Leu Thr Phe Lys Cys Leu Met Gly Glu Trp Pro Thr Met				
1755		1760	1765	
GAT CAG CTT GCT GGT TTA GTC TAC TCC GCG TTC AAT CCG GCC GCA GGA				5800
Asp Gln Leu Ala Gly Leu Val Tyr Ser Ala Phe Asn Pro Ala Ala Gly				
1770		1775	1780	1785
GTT GTG GGC GTC TTG TCA GCT TGT GCA ATG TTT GCT TTG ACA ACA GCA				5848
Val Val Gly Val Leu Ser Ala Cys Ala Met Phe Ala Leu Thr Thr Ala				
1790		1795	1800	
GGG CCA GAT CAC TGG CCC AAC AGA CTT CTT ACT ATG CTT GCT AGG AGC				5896
Gly Pro Asp His Trp Pro Asn Arg Leu Leu Thr Met Leu Ala Arg Ser				
1805		1810	1815	
AAC ACT GTA TGT AAT GAG TAC TTT ATT GCC ACT CGT GAC ATC CGC AGG				5944
Asn Thr Val Cys Asn Glu Tyr Phe Ile Ala Thr Arg Asp Ile Arg Arg				
1820		1825	1830	
AAG ATA CTG GGC ATT CTG GAG GCA TCT ACC CCC TGG AGT GTC ATA TCA				5992
Lys Ile Leu Gly Ile Leu Glu Ala Ser Thr Pro Trp Ser Val Ile Ser				
1835		1840	1845	
GCT TGC ATC CGT TGG CTC CAC ACC CCG ACG GAG GAT GAT TGC GGC CTC				6040
Ala Cys Ile Arg Trp Leu His Thr Pro Thr Glu Asp Asp Cys Gly Leu				
1850		1855	1860	1865
ATT GCT TGG GGT CTA GAG ATT TGG CAG TAT GTG TGC AAT TTC TTT GTG				6088
Ile Ala Trp Gly Leu Glu Ile Trp Gln Tyr Val Cys Asn Phe Phe Val				
1870		1875	1880	
ATT TGC TTT AAT GTC CTT AAA GCT GGA GTT CAG AGC ATG GTT AAC ATT				6136
Ile Cys Phe Asn Val Leu Lys Ala Gly Val Gln Ser Met Val Asn Ile				
1885		1890	1895	
CCT GGT TGT CCT TTC TAC AGC TGC CAG AAG GGG TAC AAG GGC CCC TGG				6184
Pro Gly Cys Pro Phe Tyr Ser Cys Gln Lys Gly Tyr Lys Gly Pro Trp				
1900		1905	1910	
ATT GGA TCA GGT ATG CTC CAA GCA CGC TGT CCA TGC GGT GCT GAA CTC				6232
Ile Gly Ser Gly Met Leu Gln Ala Arg Cys Pro Cys Gly Ala Glu Leu				
1915		1920	1925	

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ATC TTT TCT GTT GAG AAT GGT TTT GCA AAA CTT TAC AAA GGA CCC AGA Ile Phe Ser Val Glu Asn Gly Phe Ala Lys Leu Tyr Lys Gly Pro Arg 1930 1935 1940 1945	6280
ACT TGT TCA AAT TAC TGG AGA GGG GCT GTT CCA GTC AAC GCT AGG CTG Thr Cys Ser Asn Tyr Trp Arg Gly Ala Val Pro Val Asn Ala Arg Leu 1950 1955 1960	6328
TGT GGG TCG GCT AGA CCG GAC CCA ACT GAT TGG ACT AGT CTT GTC GTC Cys Gly Ser Ala Arg Pro Asp Pro Thr Asp Trp Thr Ser Leu Val Val 1965 1970 1975	6376
AAT TAT GGC GTT AGG GAC TAC TGT AAA TAT GAG AAA TTG GGA GAT CAC Asn Tyr Gly Val Arg Asp Tyr Cys Lys Tyr Glu Lys Leu Gly Asp His 1980 1985 1990	6424
ATT TTT GTT ACA GCA GTA TCC TCT CCA AAT GTC TGT TTC ACC CAG GTG Ile Phe Val Thr Ala Val Ser Ser Pro Asn Val Cys Phe Thr Gln Val 1995 2000 2005	6472
CCC CCA ACC TTG AGA GCT GCA GTG GCC GTG GAC GGC GTA CAG GTT CAG Pro Pro Thr Leu Arg Ala Ala Val Ala Val Asp Gly Val Gln Val Gln 2010 2015 2020 2025	6520
TGT TAT CTA GGT GAG CCC AAA ACT CCT TGG ACG ACA TCT GCT TGC TGT Cys Tyr Leu Gly Glu Pro Lys Thr Pro Trp Thr Thr Ser Ala Cys Cys 2030 2035 2040	6568
TAC GGT CCG GAC GGT AAG GGT AAA ACT GTT AAG CTT CCC TTC CGC GTT Tyr Gly Pro Asp Gly Lys Gly Lys Thr Val Lys Leu Pro Phe Arg Val 2045 2050 2055	6616
GAC GGT CAC ACA CCT GGT GTG CGC ATG CAA CTT AAT TTG CGT GAT GCA Asp Gly His Thr Pro Gly Val Arg Met Gln Leu Asn Leu Arg Asp Ala 2060 2065 2070	6664
CTT GAG ACA AAT GAC TGT AAT TCC ATA AAC AAC ACT CCT AGT GAT GAA Leu Glu Thr Asn Asp Cys Asn Ser Ile Asn Asn Thr Pro Ser Asp Glu 2075 2080 2085	6712
GCC GCA GTG TCC GCT CTT GTT TTC AAA CAG GAG TTG CGG CGT ACA AAC Ala Ala Val Ser Ala Leu Val Phe Lys Gln Glu Leu Arg Arg Thr Asn 2090 2095 2100 2105	6760
CAA TTG CTT GAG GCA ATT TCA GCT GGC GTT GAC ACC ACC AAA CTG CCA Gln Leu Leu Glu Ala Ile Ser Ala Gly Val Asp Thr Thr Lys Leu Pro 2110 2115 2120	6808
GCC CCC TCC ATC GAA GAG GTA GTG GTA AGA AAG CGC CAG TTC CGG GCA Ala Pro Ser Ile Glu Glu Val Val Val Arg Lys Arg Gln Phe Arg Ala 2125 2130 2135	6856
AGA ACT GGT TCG CTT ACC TTG CCT CCC CCT CCG AGA TCC GTC CCA GGA Arg Thr Gly Ser Leu Thr Leu Pro Pro Pro Pro Arg Ser Val Pro Gly 2140 2145 2150	6904
GTG TCA TGT CCT GAA AGC CTG CAA CGA AGT GAC CCG TTA GAA GGT CCT	6952

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Val Ser Cys Pro Glu Ser Leu Gln Arg Ser Asp Pro Leu Glu Gly Pro	
2155 2160 2165	
TCA AAC CTC CCT TCT TCA CCA CCT GTT CTA CAG TTG GCC ATG CCG ATG	7000
Ser Asn Leu Pro Ser Ser Pro Pro Val Leu Gln Leu Ala Met Pro Met	
2170 2175 2180 2185	
CCC CTG TTG GGA GCA GGT GAG TGT AAC CCT TTC ACT GCA ATT GGA TGT	7048
Pro Leu Leu Gly Ala Gly Glu Cys Asn Pro Phe Thr Ala Ile Gly Cys	
2190 2195 2200	
GCA ATG ACC GAA ACA GGC GGA GGC CCT GAT GAT TTA CCC AGT TAC CCT	7096
Ala Met Thr Glu Thr Gly Gly Gly Pro Asp Asp Leu Pro Ser Tyr Pro	
2205 2210 2215	
CCC AAA AAG GAG GTC TCT GAA TGG TCA GAC GGA AGT TGG TCA ACG ACT	7144
Pro Lys Lys Glu Val Ser Glu Trp Ser Asp Gly Ser Trp Ser Thr Thr	
2220 2225 2230	
ACA ACC GCT TCC AGC TAC GTT ACT GGC CCC CCG TAC CCT AAG ATA CGG	7192
Thr Thr Ala Ser Ser Tyr Val Thr Gly Pro Pro Tyr Pro Lys Ile Arg	
2235 2240 2245	
GGA AAG GAT TCC ACT CAG TCA GCC CCC GCC AAA CGG CCT ACA AAA AAG	7240
Gly Lys Asp Ser Thr Gln Ser Ala Pro Ala Lys Arg Pro Thr Lys Lys	
2250 2255 2260 2265	
AAG TTG GGA AAG AGT GAG TTT TCG TGC AGC ATG AGC TAC ACT TGG ACC	7288
Lys Leu Gly Lys Ser Glu Phe Ser Cys Ser Met Ser Tyr Thr Trp Thr	
2270 2275 2280	
GAC GTG ATT AGC TTC AAA ACT GCT TCT AAA GTT CTG TCT GCA ACT CGG	7336
Asp Val Ile Ser Phe Lys Thr Ala Ser Lys Val Leu Ser Ala Thr Arg	
2285 2290 2295	
GCC ATC ACT AGT GGT TTC CTC AAA CAA AGA TCA TTG GTG TAT GTG ACT	7384
Ala Ile Thr Ser Gly Phe Leu Lys Gln Arg Ser Leu Val Tyr Val Thr	
2300 2305 2310	
GAG CCG CGG GAT GCG GAG CTT AGA AAA CAA AAA GTC ACT ATT AAT AGA	7432
Glu Pro Arg Asp Ala Glu Leu Arg Lys Gln Lys Val Thr Ile Asn Arg	
2315 2320 2325	
CAA CCT CTG TTC CCC CCA TCA TAC CAC AAG CAA GTG AGA TTG GCT AAG	7480
Gln Pro Leu Phe Pro Pro Ser Tyr His Lys Gln Val Arg Leu Ala Lys	
2330 2335 2340 2345	
GAA AAA GCT TCA AAA GTT GTC GGT GTC ATG TGG GAC TAT GAT GAA GTA	7528
Glu Lys Ala Ser Lys Val Val Gly Val Met Trp Asp Tyr Asp Glu Val	
2350 2355 2360	
GCA GCT CAC ACG CCC TCT AAG TCT GCT AAG TCC CAC ATC ACT GGC CTT	7576
Ala Ala His Thr Pro Ser Lys Ser Ala Lys Ser His Il Thr Gly Leu	
2365 2370 2375	
CGG GGC ACT GAT GTT CGT TCT GGA GCA GCC CGC AAG GCT GTT CTG GAC	7624
Arg Gly Thr Asp Val Arg Ser Gly Ala Ala Arg Lys Ala Val Leu Asp	

445

2380	2385	2390	
TTG CAG AAG TGT GTC GAG GCA GGT GAG ATA CCG AGT CAT TAT CGG CAA Leu Gln Lys Cys Val Glu Ala Gly Glu Ile Pro Ser His Tyr Arg Gln 2395 2400 2405			7672
ACT GTG ATA GTT CCA AAG GAG GAG GTC TTC GTG AAG ACC CCC CAG AAA Thr Val Ile Val Pro Lys Glu Glu Val Phe Val Lys Thr Pro Gln Lys 2410 2415 2420 2425			7720
CCA ACA AAG AAA CCC CCA AGG CTT ATC TCG TAC CCC CAC CTT GAA ATG Pro Thr Lys Lys Pro Pro Arg Leu Ile Ser Tyr Pro His Leu Glu Met 2430 2435 2440			7768
AGA TGT GTT GAG AAG ATG TAC TAC GGT CAG GTT GCT CCT GAC GTA GTT Arg Cys Val Glu Lys Met Tyr Tyr Gly Gln Val Ala Pro Asp Val Val 2445 2450 2455			7816
AAA GCT GTC ATG GGA GAT GCG TAC GGG TTT GTC GAC CCA CGT ACC CGT Lys Ala Val Met Gly Asp Ala Tyr Gly Phe Val Asp Pro Arg Thr Arg 2460 2465 2470			7864
GTC AAG CGT CTG TTG TCG ATG TGG TCA CCC GAT GCA GTC GGA GCC ACA Val Lys Arg Leu Leu Ser Met Trp Ser Pro Asp Ala Val Gly Ala Thr 2475 2480 2485			7912
TGC GAT ACA GTG TGT TTT GAC AGT ACC ATC ACA CCC GAG GAT ATC ATG Cys Asp Thr Val Cys Phe Asp Ser Thr Ile Thr Pro Glu Asp Ile Met 2490 2495 2500 2505			7960
GTG GAG ACA GAC ATC TAC TCA GCA GCT AAA CTC AGT GAC CAA CAC CGA Val Glu Thr Asp Ile Tyr Ser Ala Ala Lys Leu Ser Asp Gln His Arg 2510 2515 2520			8008
GCT GGC ATT CAC ACC ATT GCG AGG CAG TTA TAC GCT GGA GGA CCG ATG Ala Gly Ile His Thr Ile Ala Arg Gln Leu Tyr Ala Gly Gly Pro Met 2525 2530 2535			8056
ATC GCT TAT GAT GGC CGA GAG ATC GGA TAT CGT AGG TGT AGG TCT TCC Ile Ala Tyr Asp Gly Arg Glu Ile Gly Tyr Arg Arg Cys Arg Ser Ser 2540 2545 2550			8104
GGC GTC TAT ACT ACC TCA AGT TCC AAC AGT TTG ACC TGC TGG CTG AAG Gly Val Tyr Thr Thr Ser Ser Ser Asn Ser Leu Thr Cys Trp Leu Lys 2555 2560 2565			8152
GTA AAT GCT GCA GCC GAA CAG GCT GGC ATG AAG AAC CCT CGC TTC CTT Val Asn Ala Ala Ala Glu Gln Ala Gly Met Lys Asn Pro Arg Phe Leu 2570 2575 2580 2585			8200
ATT TGC GGC GAT GAT TGC ACC GTA ATT TGG AAG AGC GCC GGA GCA GAT Ile Cys Gly Asp Asp Cys Thr Val Ile Trp Lys Ser Ala Gly Ala Asp 2590 2595 2600			8248
GCA GAC AAA CAA GCA ATG CGT GTC TTT GCT AGC TGG ATG AAG GTG ATG Ala Asp Lys Gln Ala Met Arg Val Phe Ala Ser Trp Met Lys Val Met 2605 2610 2615			8296

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GGT GCA CCA CAA GAT TGT GTG CCT CAA CCC AAA TAC AGT TTG GAA GAA	8344
Gly Ala Pro Gln Asp Cys Val Pro Gln Pro Lys Tyr Ser Leu Glu Glu	
2620 2625 2630	
TTA ACA TCA TGC TCA TCA AAT GTT ACC TCT GGA ATT ACC AAA AGT GGC	8392
Leu Thr Ser Cys Ser Ser Asn Val Thr Ser Gly Ile Thr Lys Ser Gly	
2635 2640 2645	
AAG CCT TAC TAC TTT CTT ACA AGA GAT CCT CGT ATC CCC CTT GGC AGG	8440
Lys Pro Tyr Tyr Phe Leu Thr Arg Asp Pro Arg Ile Pro Leu Gly Arg	
2650 2655 2660 2665	
TGC TCT GCC GAG GGT CTG GGA TAC AAC CCC AGT GCT GCG TGG ATT GGG	8488
Cys Ser Ala Glu Gly Leu Gly Tyr Asn Pro Ser Ala Ala Trp Ile Gly	
2670 2675 2680	
TAT CTA ATA CAT CAC TAC CCA TGT TTG TGG GTT AGC CGT GTG TTG GCT	8536
Tyr Leu Ile His His Tyr Pro Cys Leu Trp Val Ser Arg Val Leu Ala	
2685 2690 2695	
GTC CAT TTC ATG GAG CAG ATG CTC TTT GAG GAC AAA CTT CCC GAG ACT	8584
Val His Phe Met Glu Gln Met Leu Phe Glu Asp Lys Leu Pro Glu Thr	
2700 2705 2710	
GTG ACC TTT GAC TGG TAT GGG AAA AAT TAT ACG GTG CCT GTA GAA GAT	8632
Val Thr Phe Asp Trp Tyr Gly Lys Asn Tyr Thr Val Pro Val Glu Asp	
2715 2720 2725	
CTG CCC AGC ATC ATT GCT GGT GTG CAC GGT ATT GAG GCT TTC TCG GTG	8680
Leu Pro Ser Ile Ile Ala Gly Val His Gly Ile Glu Ala Phe Ser Val	
2730 2735 2740 2745	
GTG CGC TAC ACC AAC GCT GAG ATC CTC AGA GTT TCC CAA TCA CTA ACA	8728
Val Arg Tyr Thr Asn Ala Glu Ile Leu Arg Val Ser Gln Ser Leu Thr	
2750 2755 2760	
GAC ATG ACC ATG CCC CCC CTG CGA GCC TGG CGA AAG AAA GCC AGG GCG	8776
Asp Met Thr Met Pro Pro Leu Arg Ala Trp Arg Lys Lys Ala Arg Ala	
2765 2770 2775	
GTC CTC GCC AGC GCC AAG AGG CGT GGC GGA GCA CAC GCA AAA TTG GCT	8824
Val Leu Ala Ser Ala Lys Arg Arg Gly Gly Ala His Ala Lys Leu Ala	
2780 2785 2790	
CGC TTC CTT CTC TGG CAT GCT ACA TCT AGA CCT CTA CCA GAT TTG GAT	8872
Arg Phe Leu Leu Trp His Ala Thr Ser Arg Pro Leu Pro Asp Leu Asp	
2795 2800 2805	
AAG ACG AGC GTG GCT CGG TAC ACC ACT TTC AAT TAT TGT GAT GTT TAC	8920
Lys Thr Ser Val Ala Arg Tyr Thr Thr Phe Asn Tyr Cys Asp Val Tyr	
2810 2815 2820 2825	
TCC CCG GAG GGG GAT GTG TTT GTT ACA CCA CAG AGA AGA TTG CAG AAG	8968
Ser Pro Glu Gly Asp Val Phe Val Thr Pro Gln Arg Arg Leu Gln Lys	
2830 2835 2840	
TTT CTT GTG AAG TAT TTG GCT GTC ATT GTT TTT GCC CTA GGG CTC ATT	9016

447

Phe Leu Val Lys Tyr Leu Ala Val Ile Val Phe Ala Leu Gly Leu Ile
 2845 2850 2855

GCT GTT GGA CTA GCC ATC AGC TGAACCCCCA AATTCAAAAT TAATTAACAG 9067
 Ala Val Gly Leu Ala Ile Ser
 2860

TTTTTTTTTT TTTTTTTTTT TTTTTTTAGG GCAGCGGCAA CAGGGGAGAC CCCGGGCTTA 9127

ACGACCCCGC GATGTG 9143

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2864 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Pro Val Ile Ser Thr Gln Thr Ser Pro Val Pro Ala Pro Arg Thr
 1 5 10 15

Arg Lys Asn Lys Gln Thr Gln Ala Ser Tyr Pro Val Ser Ile Lys Thr
 20 25 30

Ser Val Glu Arg Gly Gln Arg Ala Lys Arg Lys Val Gln Arg Asp Ala
 35 40 45

Arg Pro Arg Asn Tyr Lys Ile Ala Gly Ile His Asp Gly Leu Gln Thr
 50 55 60

Leu Ala Gln Ala Ala Leu Pro Ala His Gly Trp Gly Arg Gln Asp Pro
 65 70 75 80

Arg His Lys Ser Arg Asn Leu Gly Ile Leu Leu Asp Tyr Pro Leu Gly
 85 90 95

Trp Ile Gly Asp Val Thr Thr His Thr Pro Leu Val Gly Pro Leu Val
 100 105 110

Ala Gly Ala Val Val Arg Pro Val Cys Gln Ile Val Arg Leu Leu Glu
 115 120 125

Asp Gly Val Asn Trp Ala Thr Gly Trp Phe Gly Val His Leu Phe Val
 130 135 140

Val Cys Leu Leu Ser Leu Ala Cys Pro Cys Ser Gly Ala Arg Val Thr
 145 150 155 160

Asp Pro Asp Thr Asn Thr Thr Ile Leu Thr Asn Cys Cys Gln Arg Asn
 165 170 175

Gln Val Ile Tyr Cys Ser Pro Ser Thr Cys Leu His Glu Pro Gly Cys

448

180	185	190
Val Ile Cys Ala Asp Glu Cys Trp	Val Pro Ala Asn	Pro Tyr Ile Ser
195	200	205
His Pro Ser Asn Trp Thr Gly Thr Asp Ser Phe Leu Ala Asp His Ile		220
210	215	
Asp Phe Val Met Gly Ala Leu Val Thr Cys Asp Ala Leu Asp Ile Gly		240
225	230	235
Glu Leu Cys Gly Ala Cys Val Leu Val Gly Asp Trp Leu Val Arg His		255
245	250	
Trp Leu Ile His Ile Asp Leu Asn Glu Thr Gly Thr Cys Tyr Leu Glu		270
260	265	
Val Pro Thr Gly Ile Asp Pro Gly Phe Leu Gly Phe Ile Gly Trp Met		285
275	280	
Ala Gly Lys Val Glu Ala Val Ile Phe Leu Thr Lys Leu Ala Ser Gln		300
290	295	
Val Pro Tyr Ala Ile Ala Thr Met Phe Ser Ser Val His Tyr Leu Ala		320
305	310	315
Val Gly Ala Leu Ile Tyr Tyr Ala Ser Arg Gly Lys Trp Tyr Gln Leu		335
325	330	
Leu Leu Ala Leu Met Leu Tyr Ile Glu Ala Thr Ser Gly Asn Pro Ile		350
340	345	
Arg Val Pro Thr Gly Cys Ser Ile Ala Glu Phe Cys Ser Pro Leu Met		365
355	360	
Ile Pro Cys Pro Cys His Ser Tyr Leu Ser Glu Asn Val Ser Glu Val		380
370	375	
Ile Cys Tyr Ser Pro Lys Trp Thr Arg Pro Val Thr Leu Glu Tyr Asn		400
385	390	395
Asn Ser Ile Ser Trp Tyr Pro Tyr Thr Ile Pro Gly Ala Arg Gly Cys		415
405	410	
Met Val Lys Phe Lys Asn Asn Thr Trp Gly Cys Cys Arg Ile Arg Asn		430
420	425	
Val Pro Ser Tyr Cys Thr Met Gly Thr Asp Ala Val Trp Asn Asp Thr		445
435	440	
Arg Asn Thr Tyr Glu Ala Cys Gly Val Thr Pro Trp Leu Thr Thr Ala		460
450	455	
Trp His Asn Gly Ser Ala Leu Lys Leu Ala Ile Leu Gln Tyr Pro Gly		480
465	470	475
Ser Lys Glu Met Phe Lys Pro His Asn Trp Met Ser Gly His Leu Tyr		

449

485

490

495

Phe Glu Gly Ser Asp Thr Pro Ile Val Tyr Phe Tyr Asp Pro Val Asn
 500 505 510

Ser Thr Leu Leu Pro Pro Glu Arg Trp Ala Arg Leu Pro Gly Thr Pro
 515 520 525

Pro Val Val Arg Gly Ser Trp Leu Gln Val Pro Gln Gly Phe Tyr Ser
 530 535 540

Asp Val Lys Asp Leu Ala Thr Gly Leu Ile Thr Lys Asp Lys Ala Trp
 545 550 555 560

Lys Asn Tyr Gln Val Leu Tyr Ser Ala Thr Gly Ala Leu Ser Leu Thr
 565 570 575

Gly Val Thr Thr Lys Ala Val Val Leu Ile Leu Leu Gly Leu Cys Gly
 580 585 590

Ser Lys Tyr Leu Ile Leu Ala Tyr Leu Cys Tyr Leu Ser Leu Cys Phe
 595 600 605

Gly Arg Ala Ser Gly Tyr Pro Leu Arg Pro Val Leu Pro Ser Gln Ser
 610 615 620

Tyr Leu Gln Ala Gly Trp Asp Val Leu Ser Lys Ala Gln Val Ala Pro
 625 630 635 640

Phe Ala Leu Ile Phe Phe Ile Cys Cys Tyr Leu Arg Cys Arg Leu Arg
 645 650 655

Tyr Ala Ala Leu Leu Gly Phe Val Pro Met Ala Ala Gly Leu Pro Leu
 660 665 670

Thr Phe Phe Val Ala Ala Ala Ala Gln Pro Asp Tyr Asp Trp Trp
 675 680 685

Val Arg Leu Leu Val Ala Gly Leu Val Leu Trp Ala Gly Arg Asp Arg
 690 695 700

Gly Pro Arg Ile Ala Leu Leu Val Gly Pro Trp Pro Leu Val Ala Leu
 705 710 715 720

Leu Thr Leu Leu His Leu Ala Thr Pro Ala Ser Ala Phe Asp Thr Glu
 725 730 735

Ile Ile Gly Gly Leu Thr Ile Pro Pro Val Val Ala Leu Val Val Met
 740 745 750

Ser Arg Phe Gly Phe Phe Ala His Leu Leu Pro Arg Cys Ala Leu Val
 755 760 765

Asn Ser Tyr Leu Trp Gln Arg Trp Glu Asn Trp Phe Trp Asn Val Thr
 770 775 780

Leu Arg Pro Glu Arg Phe Leu Leu Val Leu Val Cys Phe Pro Gly Ala

450

785	790	795	800
Thr Tyr Asp Thr Leu Val Thr Phe Cys Val Cys His Val Ala Leu Leu	805	810	815
Cys Leu Thr Ser Ser Ala Ala Ser Phe Phe Gly Thr Asp Ser Arg Val	820	825	830
Arg Ala His Arg Met Leu Val Arg Leu Gly Lys Cys His Ala Trp Tyr	835	840	845
Ser His Tyr Val Leu Lys Phe Phe Leu Leu Val Phe Gly Glu Asn Gly	850	855	860
Val Phe Phe Tyr Lys His Leu His Gly Asp Val Leu Pro Asn Asp Phe	865	870	875
Ala Ser Lys Leu Pro Leu Gln Glu Pro Phe Phe Pro Phe Glu Gly Lys	885	890	895
Ala Arg Val Tyr Arg Asn Glu Gly Arg Arg Leu Ala Cys Gly Asp Thr	900	905	910
Val Asp Gly Leu Pro Val Val Ala Arg Leu Gly Asp Leu Val Phe Ala	915	920	925
Gly Leu Ala Met Pro Pro Asp Gly Trp Ala Ile Thr Ala Pro Phe Thr	930	935	940
Leu Gln Cys Leu Ser Glu Arg Gly Thr Leu Ser Ala Met Ala Val Val	945	950	955
Met Thr Gly Ile Asp Pro Arg Thr Trp Thr Gly Thr Ile Phe Arg Leu	965	970	975
Gly Ser Leu Ala Thr Ser Tyr Met Gly Phe Val Cys Asp Asn Val Leu	980	985	990
Tyr Thr Ala His His Gly Ser Lys Gly Arg Arg Leu Ala His Pro Thr	995	1000	1005
Gly Ser Ile His Pro Ile Thr Val Asp Ala Ala Asn Asp Gln Asp Ile	1010	1015	1020
Tyr Gln Pro Pro Cys Gly Ala Gly Ser Leu Thr Arg Cys Ser Cys Gly	1025	1030	1035
Glu Thr Lys Gly Tyr Leu Val Thr Arg Leu Gly Ser Leu Val Glu Val	1045	1050	1055
Asn Lys Ser Asp Asp Pro Tyr Trp Cys Val Cys Gly Ala Leu Pro Met	1060	1065	1070
Ala Val Ala Lys Gly Ser Ser Gly Ala Pro Ile Leu Cys Ser Ser Gly	1075	1080	1085
His Val Ile Gly Met Phe Thr Ala Ala Arg Asn Ser Gly Gly Ser Val			

451

1090	1095	1100
Ser Gln Ile Arg Val Arg Pro Leu Val Cys Ala Gly Tyr His Pro Gln 1105	1110	1115 1120
Tyr Thr Ala His Ala Thr Leu Asp Thr Lys Pro Thr Val Pro Asn Glu 1125	1130	1135
Tyr Ser Val Gln Ile Leu Ile Ala Pro Thr Gly Ser Gly Lys Ser Thr 1140	1145	1150
Lys Leu Pro Leu Ser Tyr Met Gln Glu Lys Tyr Glu Val Leu Val Leu 1155	1160	1165
Asn Pro Ser Val Ala Thr Thr Ala Ser Met Pro Lys Tyr Met His Ala 1170	1175	1180
Thr Tyr Gly Val Asn Pro Asn Cys Tyr Phe Asn Gly Lys Cys Thr Asn 1185	1190	1195 1200
Thr Gly Ala Ser Leu Thr Tyr Ser Thr Tyr Gly Met Tyr Leu Thr Gly 1205	1210	1215
Ala Cys Ser Arg Asn Tyr Asp Val Ile Ile Cys Asp Glu Cys His Ala 1220	1225	1230
Thr Asp Ala Thr Thr Val Leu Gly Ile Gly Lys Val Leu Thr Glu Ala 1235	1240	1245
Pro Ser Lys Asn Val Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro 1250	1255	1260
Gly Val Ile Pro Thr Pro His Ala Asn Ile Thr Glu Ile Gln Leu Thr 1265	1270	1275 1280
Asp Glu Gly Thr Ile Pro Phe His Gly Lys Lys Ile Lys Glu Glu Asn 1285	1290	1295
Leu Lys Lys Gly Arg His Leu Ile Phe Glu Ala Thr Lys Lys His Cys 1300	1305	1310
Asp Glu Leu Ala Asn Glu Leu Ala Arg Lys Gly Ile Thr Ala Val Ser 1315	1320	1325
Tyr Tyr Arg Gly Cys Asp Ile Ser Lys Ile Pro Glu Gly Asp Cys Val 1330	1335	1340
Val Val Ala Thr Asp Ala Leu Cys Thr Gly Tyr Thr Gly Asp Phe Asp 1345	1350	1355 1360
Ser Val Tyr Asp Cys Ser Leu Met Val Glu Gly Thr Cys His Val Asp 1365	1370	1375
Leu Asp Pro Thr Phe Thr Met Gly Val Arg Val Cys Gly Val Ser Ala 1380	1385	1390
Ile Val Lys Gly Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Ala Gly		

452

1395	1400	1405
Ile Tyr Tyr Tyr Val Asp Gly Ser Cys Thr Pro Ser Gly Met Val Pro 1410	1415	1420
Glu Cys Asn Ile Val Glu Ala Phe Asp Ala Ala Lys Ala Trp Tyr Gly 1425	1430	1435 1440
Leu Ser Ser Thr Glu Ala Gln Thr Ile Leu Asp Thr Tyr Arg Thr Gln 1445	1450	1455
Pro Gly Leu Pro Ala Ile Gly Ala Asn Leu Asp Glu Trp Ala Asp Leu 1460	1465	1470
Phe Ser Met Val Asn Pro Glu Pro Ser Phe Val Asn Thr Ala Lys Arg 1475	1480	1485
Thr Ala Asp Asn Tyr Val Leu Leu Thr Ala Ala Gln Leu Gln Leu Cys 1490	1495	1500
His Gln Tyr Gly Tyr Ala Ala Pro Asn Asp Ala Pro Arg Trp Gln Gly 1505	1510	1515 1520
Ala Arg Leu Gly Lys Lys Pro Cys Gly Val Leu Trp Arg Leu Asp Gly 1525	1530	1535
Ala Asp Ala Cys Pro Gly Pro Glu Pro Ser Glu Val Thr Arg Tyr Gln 1540	1545	1550
Met Cys Phe Thr Glu Val Asn Thr Ser Gly Thr Ala Ala Leu Ala Val 1555	1560	1565
Gly Val Gly Val Ala Met Ala Tyr Leu Ala Ile Asp Thr Phe Gly Ala 1570	1575	1580
Thr Cys Val Arg Arg Cys Trp Ser Ile Thr Ser Val Pro Thr Gly Ala 1585	1590	1595 1600
Thr Val Ala Pro Val Val Asp Glu Glu Glu Ile Val Glu Glu Cys Ala 1605	1610	1615
Ser Phe Ile Pro Leu Glu Ala Met Val Ala Ala Ile Asp Lys Leu Lys 1620	1625	1630
Ser Thr Ile Thr Thr Thr Ser Pro Phe Thr Leu Glu Thr Ala Leu Glu 1635	1640	1645
Lys Leu Asn Thr Phe Leu Gly Pro His Ala Ala Thr Ile Leu Ala Ile 1650	1655	1660
Ile Glu Tyr Cys Cys Gly Leu Val Thr Leu Pro Asp Asn Pro Phe Ala 1665	1670	1675 1680
Ser Cys Val Phe Ala Phe Ile Ala Gly Ile Thr Thr Pro Leu Pro His 1685	1690	1695
Lys Ile Lys Met Phe Leu Ser Leu Phe Gly Gly Ala Ile Ala Ser Lys		

453

1700	1705	1710
Leu Thr Asp Ala Arg Gly Ala Leu Ala Phe Met Met Ala Gly Ala Ala 1715	1720	1725
Gly Thr Ala Leu Gly Thr Trp Thr Ser Val Gly Phe Val Phe Asp Met 1730	1735	1740
Leu Gly Gly Tyr Ala Ala Ala Ser Ser Thr Ala Cys Leu Thr Phe Lys 1745	1750	1755 1760
Cys Leu Met Gly Glu Trp Pro Thr Met Asp Gln Leu Ala Gly Leu Val 1765	1770	1775
Tyr Ser Ala Phe Asn Pro Ala Ala Gly Val Val Gly Val Leu Ser Ala 1780	1785	1790
Cys Ala Met Phe Ala Leu Thr Thr Ala Gly Pro Asp His Trp Pro Asn 1795	1800	1805
Arg Leu Leu Thr Met Leu Ala Arg Ser Asn Thr Val Cys Asn Glu Tyr 1810	1815	1820
Phe Ile Ala Thr Arg Asp Ile Arg Arg Lys Ile Leu Gly Ile Leu Glu 1825	1830	1835 1840
Ala Ser Thr Pro Trp Ser Val Ile Ser Ala Cys Ile Arg Trp Leu His 1845	1850	1855
Thr Pro Thr Glu Asp Asp Cys Gly Leu Ile Ala Trp Gly Leu Glu Ile 1860	1865	1870
Trp Gln Tyr Val Cys Asn Phe Phe Val Ile Cys Phe Asn Val Leu Lys 1875	1880	1885
Ala Gly Val Gln Ser Met Val Asn Ile Pro Gly Cys Pro Phe Tyr Ser 1890	1895	1900
Cys Gln Lys Gly Tyr Lys Gly Pro Trp Ile Gly Ser Gly Met Leu Gln 1905	1910	1915 1920
Ala Arg Cys Pro Cys Gly Ala Glu Leu Ile Phe Ser Val Glu Asn Gly 1925	1930	1935
Phe Ala Lys Leu Tyr Lys Gly Pro Arg Thr Cys Ser Asn Tyr Trp Arg 1940	1945	1950
Gly Ala Val Pro Val Asn Ala Arg Leu Cys Gly Ser Ala Arg Pro Asp 1955	1960	1965
Pro Thr Asp Trp Thr Ser Leu Val Val Asn Tyr Gly Val Arg Asp Tyr 1970	1975	1980
Cys Lys Tyr Glu Lys Leu Gly Asp His Ile Phe Val Thr Ala Val Ser 1985	1990	1995 2000
Ser Pro Asn Val Cys Phe Thr Gln Val Pro Pro Thr Leu Arg Ala Ala		

454

2005					2010					2015						
Val	Ala	Val	Asp	Gly	Val	Gln	Val	Gln	Cys	Tyr	Leu	Gly	Glu	Pro	Lys	
2020					2025					2030						
Thr	Pro	Trp	Thr	Thr	Ser	Ala	Cys	Cys	Tyr	Gly	Pro	Asp	Gly	Lys	Gly	
2035					2040					2045						
Lys	Thr	Val	Lys	Leu	Pro	Phe	Arg	Val	Asp	Gly	His	Thr	Pro	Gly	Val	
2050					2055					2060						
Arg	Met	Gln	Leu	Asn	Leu	Arg	Asp	Ala	Leu	Glu	Thr	Asn	Asp	Cys	Asn	
2065					2070					2075					2080	
Ser	Ile	Asn	Asn	Thr	Pro	Ser	Asp	Glu	Ala	Ala	Val	Ser	Ala	Leu	Val	
2085					2090					2095						
Phe	Lys	Gln	Glu	Leu	Arg	Arg	Thr	Asn	Gln	Leu	Leu	Glu	Ala	Ile	Ser	
2100					2105					2110						
Ala	Gly	Val	Asp	Thr	Thr	Lys	Leu	Pro	Ala	Pro	Ser	Ile	Glu	Glu	Val	
2115					2120					2125						
Val	Val	Arg	Lys	Arg	Gln	Phe	Arg	Ala	Arg	Thr	Gly	Ser	Leu	Thr	Leu	
2130					2135					2140						
Pro	Pro	Pro	Pro	Arg	Ser	Val	Pro	Gly	Val	Ser	Cys	Pro	Glu	Ser	Leu	
2145					2150					2155					2160	
Gln	Arg	Ser	Asp	Pro	Leu	Glu	Gly	Pro	Ser	Asn	Leu	Pro	Ser	Ser	Pro	
2165					2170					2175						
Pro	Val	Leu	Gln	Leu	Ala	Met	Pro	Met	Pro	Leu	Leu	Gly	Ala	Gly	Glu	
2180					2185					2190						
Cys	Asn	Pro	Phe	Thr	Ala	Ile	Gly	Cys	Ala	Met	Thr	Glu	Thr	Gly	Gly	
2195					2200					2205						
Gly	Pro	Asp	Asp	Leu	Pro	Ser	Tyr	Pro	Pro	Lys	Lys	Glu	Val	Ser	Glu	
2210					2215					2220						
Trp	Ser	Asp	Gly	Ser	Trp	Ser	Thr	Thr	Thr	Thr	Ala	Ser	Ser	Tyr	Val	
2225					2230					2235					2240	
Thr	Gly	Pro	Pro	Tyr	Pro	Lys	Ile	Arg	Gly	Lys	Asp	Ser	Thr	Gln	Ser	
2245					2250					2255						
Ala	Pro	Ala	Lys	Arg	Pro	Thr	Lys	Lys	Lys	Leu	Gly	Lys	Ser	Glu	Phe	
2260					2265					2270						
Ser	Cys	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Asp	Val	Ile	Ser	Phe	Lys	Thr	
2275					2280					2285						
Ala	Ser	Lys	Val	Leu	Ser	Ala	Thr	Arg	Ala	Ile	Thr	Ser	Gly	Phe	Leu	
2290					2295					2300						
Lys	Gln	Arg	Ser	Leu	Val	Tyr	Val	Thr	Glu	Pro	Arg	Asp	Ala	Glu	Leu	

455

2305	2310	2315	2320
Arg Lys Gln Lys Val Thr Ile Asn Arg Gln Pro Leu Phe Pro Pro Ser	2325	2330	2335
Tyr His Lys Gln Val Arg Leu Ala Lys Glu Lys Ala Ser Lys Val Val	2340	2345	2350
Gly Val Met Trp Asp Tyr Asp Glu Val Ala Ala His Thr Pro Ser Lys	2355	2360	2365
Ser Ala Lys Ser His Ile Thr Gly Leu Arg Gly Thr Asp Val Arg Ser	2370	2375	2380
Gly Ala Ala Arg Lys Ala Val Leu Asp Leu Gln Lys Cys Val Glu Ala	2385	2390	2395 2400
Gly Glu Ile Pro Ser His Tyr Arg Gln Thr Val Ile Val Pro Lys Glu	2405	2410	2415
Glu Val Phe Val Lys Thr Pro Gln Lys Pro Thr Lys Lys Pro Pro Arg	2420	2425	2430
Leu Ile Ser Tyr Pro His Leu Glu Met Arg Cys Val Glu Lys Met Tyr	2435	2440	2445
Tyr Gly Gln Val Ala Pro Asp Val Val Lys Ala Val Met Gly Asp Ala	2450	2455	2460
Tyr Gly Phe Val Asp Pro Arg Thr Arg Val Lys Arg Leu Leu Ser Met	2465	2470	2475 2480
Trp Ser Pro Asp Ala Val Gly Ala Thr Cys Asp Thr Val Cys Phe Asp	2485	2490	2495
Ser Thr Ile Thr Pro Glu Asp Ile Met Val Glu Thr Asp Ile Tyr Ser	2500	2505	2510
Ala Ala Lys Leu Ser Asp Gln His Arg Ala Gly Ile His Thr Ile Ala	2515	2520	2525
Arg Gln Leu Tyr Ala Gly Gly Pro Met Ile Ala Tyr Asp Gly Arg Glu	2530	2535	2540
Ile Gly Tyr Arg Arg Cys Arg Ser Ser Gly Val Tyr Thr Thr Ser Ser	2545	2550	2555 2560
Ser Asn Ser Leu Thr Cys Trp Leu Lys Val Asn Ala Ala Ala Glu Gln	2565	2570	2575
Ala Gly Met Lys Asn Pro Arg Phe Leu Ile Cys Gly Asp Asp Cys Thr	2580	2585	2590
Val Ile Trp Lys Ser Ala Gly Ala Asp Ala Asp Lys Gln Ala Met Arg	2595	2600	2605
Val Phe Ala Ser Trp Met Lys Val Met Gly Ala Pro Gln Asp Cys Val			

456

2610	2615	2620
Pro Gln Pro Lys Tyr Ser Leu Glu Glu Leu Thr Ser Cys Ser Ser Asn		
2625	2630	2635 2640
Val Thr Ser Gly Ile Thr Lys Ser Gly Lys Pro Tyr Tyr Phe Leu Thr		
	2645	2650 2655
Arg Asp Pro Arg Ile Pro Leu Gly Arg Cys Ser Ala Glu Gly Leu Gly		
	2660	2665 2670
Tyr Asn Pro Ser Ala Ala Trp Ile Gly Tyr Leu Ile His His Tyr Pro		
	2675	2680 2685
Cys Leu Trp Val Ser Arg Val Leu Ala Val His Phe Met Glu Gln Met		
	2690	2695 2700
Leu Phe Glu Asp Lys Leu Pro Glu Thr Val Thr Phe Asp Trp Tyr Gly		
	2705	2710 2715 2720
Lys Asn Tyr Thr Val Pro Val Glu Asp Leu Pro Ser Ile Ile Ala Gly		
	2725	2730 2735
Val His Gly Ile Glu Ala Phe Ser Val Val Arg Tyr Thr Asn Ala Glu		
	2740	2745 2750
Ile Leu Arg Val Ser Gln Ser Leu Thr Asp Met Thr Met Pro Pro Leu		
	2755	2760 2765
Arg Ala Trp Arg Lys Lys Ala Arg Ala Val Leu Ala Ser Ala Lys Arg		
	2770	2775 2780
Arg Gly Gly Ala His Ala Lys Leu Ala Arg Phe Leu Leu Trp His Ala		
	2785	2790 2795 2800
Thr Ser Arg Pro Leu Pro Asp Leu Asp Lys Thr Ser Val Ala Arg Tyr		
	2805	2810 2815
Thr Thr Phe Asn Tyr Cys Asp Val Tyr Ser Pro Glu Gly Asp Val Phe		
	2820	2825 2830
Val Thr Pro Gln Arg Arg Leu Gln Lys Phe Leu Val Lys Tyr Leu Ala		
	2835	2840 2845
Val Ile Val Phe Ala Leu Gly Leu Ile Ala Val Gly Leu Ala Ile Ser		
	2850	2855 2860

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

457

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
1           5           10           15
Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile
20           25           30
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
35           40           45
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
50           55           60
Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly
65           70           75           80
Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe
85           90           95
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala
100          105          110
Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
115          120          125
Ile Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met
130          135          140
Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
145          150          155          160
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
165          170          175
Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly
180          185          190
Arg Thr Gly Arg Gly Lys Pro Gly
195          200

```

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399;

[illegible]

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9034 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..9034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

AAA	GGT	GGT	GGA	TGG	GTG	ATG	ACA	GGG	TTG	GTA	GGT	CGT	AAA	TCC	CGG	
Lys	Gly	Gly	Gly	Trp	Val	Met	Thr	Gly	Leu	Val	Gly	Arg	Lys	Ser	Arg	48
1				5					10					15		
TCA	TCC	TGG	TAG	CCA	CTA	TAG	GTG	GGT	CTT	AAG	GGG	AGG	CTA	CGG	TCC	
Ser	Ser	Trp	*	Pro	Leu	*	Val	Gly	Leu	Lys	Gly	Arg	Leu	Arg	Ser	96
			20					25					30			
CTC	TTG	CGC	ATA	TGG	AGG	AAA	AGC	GCA	CGG	TCC	ACA	GGT	GTT	GGT	CCT	
Leu	Leu	Arg	Ile	Trp	Arg	Lys	Ser	Ala	Arg	Ser	Thr	Gly	Val	Gly	Pro	144
		35					40					45				
ACC	GGT	GTA	ATA	AGG	ACC	CGG	CGC	TAG	GCA	CGC	CGT	TAA	ACC	GAG	CCC	192

459

Thr Gly Val Ile Arg Thr Arg Arg * Ala Arg Arg * Thr Glu Pro	
50 55 60	
GTT ACT CCC CTG GGC AAA CGA CGC CCA CGT ACG GTC CAC GTC GCC CTT	240
Val Thr Pro Leu Gly Lys Arg Arg Pro Arg Thr Val His Val Ala Leu	
65 70 75 80	
CAA TGT CTC TCT TGA CCA ATA GGC GTA CGG CGA GTT GAC AAG GAC CAG	288
Gln Cys Leu Ser * Pro Ile Gly Val Arg Arg Val Asp Lys Asp Gln	
85 90 95	
TGG GGG CCG GGC GGG AGG GGG AAG GAC CCC CAC CGC TGC CCT TCC CGG	336
Trp Gly Pro Gly Gly Arg Gly Lys Asp Pro His Arg Cys Pro Ser Arg	
100 105 110	
GGA GGC GGG AAA TGC ATG GGG CCA CCC AGC TCC GCG GCG GCC TAC AGC	384
Gly Gly Gly Lys Cys Met Gly Pro Pro Ser Ser Ala Ala Ala Tyr Ser	
115 120 125	
CGG GGT AGC CCA AGA ACT TCG GGT GAG GGC GGG TGG CAT TTC TTT TCC	432
Arg Gly Ser Pro Arg Thr Ser Gly Glu Gly Gly Trp His Phe Phe Ser	
130 135 140	
TAT ACC GAT CAT GGC AGT CCT TCT GCT CCT ACT CGT GGT GGA GCC GGG	480
Tyr Thr Asp His Gly Ser Pro Ser Ala Pro Thr Arg Gly Gly Ala Gly	
145 150 155 160	
GCT ATT TTA GCC CCG GCC ACC CAT GCT TGT AGC GCG AAA GGG CAA TAT	528
Ala Ile Leu Ala Pro Ala Thr His Ala Cys Ser Ala Lys Gly Gln Tyr	
165 170 175	
TTS CTC ACA AAC TGT TGC GCC CTG GAG GAC ATA GGC TTC TGC CTG GAG	576
Xaa Leu Thr Asn Cys Cys Ala Leu Glu Asp Ile Gly Phe Cys Leu Glu	
180 185 190	
GGC GGA TGC CTG GTG GCT CTG GGG TGC ACC ATT TGC ACC GAC CGC TGC	624
Gly Gly Cys Leu Val Ala Leu Gly Cys Thr Ile Cys Thr Asp Arg Cys	
195 200 205	
TGG CCA CTG TAT CAG GCG GGT TTG GCC GTG CGG CCC GGC AAG TCC GCC	672
Trp Pro Leu Tyr Gln Ala Gly Leu Ala Val Arg Pro Gly Lys Ser Ala	
210 215 220	
GCC CAG TTG GTG GGG GAA CTC GGT AGT CTC TAC GGG CCC TTG TCG GTC	720
Ala Gln Leu Val Gly Glu Leu Gly Ser Leu Tyr Gly Pro Leu Ser Val	
225 230 235 240	
TCG GCT TAT GTG GCC GGG ATC CTG GGG CTT GGG GAG GTC TAC TCG GGG	768
Ser Ala Tyr Val Ala Gly Ile Leu Gly Leu Gly Glu Val Tyr Ser Gly	
245 250 255	
GTC CTC ACC GTC GGG GTG GCG TTG ACG CGC AGG GTC TAC CCG GTC CCG	816
Val Leu Thr Val Gly Val Ala Leu Thr Arg Arg Val Tyr Pro Val Pro	
260 265 270	
AAC CTG ACG TGT GCA GTA GAG TGT CAG TTG AAG TGG GAA AGT GAG TTT	864
Asn Leu Thr Cys Ala Val Glu Cys Glu Leu Lys Trp Glu Ser Glu Phe	

460

275	280	285	
TGG AGA TGG ACT GAA CAG CTG GCC TCA AAC TAC TGG ATT CTG GAA TAC Trp Arg Trp Thr Glu Gln Leu Ala Ser Asn Tyr Trp Ile Leu Glu Tyr 290 295 300			912
CTC TGG AAG GTG CCT TTC GAC TTT TGG CGG GGA GTG ATG AGC CTT ACT Leu Trp Lys Val Pro Phe Asp Phe Trp Arg Gly Val Met Ser Leu Thr 305 310 315 320			960
CCT CTC TTG GTG TGC GTG GCG GCC CTC CTC CTG CTG GAG CAG CGT ATT Pro Leu Leu Val Cys Val Ala Ala Leu Leu Leu Leu Glu Gln Arg Ile 325 330 335			1008
GTC ATG GTC TTC CTC CTG GTC ACT ATG GCG GGC ATG TCG CAA GGC GCG Val Met Val Phe Leu Leu Val Thr Met Ala Gly Met Ser Gln Gly Ala 340 345 350			1056
CCC GCC TCA AGT GTT GGG GTC ACG GCC TTT CGA GGC GGG TTT GAC TTG Pro Ala Ser Ser Val Gly Val Thr Ala Phe Arg Gly Gly Phe Asp Leu 355 360 365			1104
GCA GTC TTG TTC TTG CAG GTC GAA CGG GTC CCG CGT GCC GAC AGG GAG Ala Val Leu Phe Leu Gln Val Glu Arg Val Pro Arg Ala Asp Arg Glu 370 375 380			1152
AGG GTT TGG GAA CGT GGG AAC GTC ACA CTT TTG TGT GAC TGC CCC AAC Arg Val Trp Glu Arg Gly Asn Val Thr Leu Leu Cys Asp Cys Pro Asn 385 390 395 400			1200
GGT CCT TGG GTG TGG GTC CCG GCC CTT TGC CAG GCA ATC GGA TGG GGC Gly Pro Trp Val Trp Val Pro Ala Leu Cys Gln Ala Ile Gly Trp Gly 405 410 415			1248
GAC CCT ATC ACT CAT TGG AGC CAC GGA CAA AAT CAG TGG CCC CTT TCT Asp Pro Ile Thr His Trp Ser His Gly Gln Asn Gln Trp Pro Leu Ser 420 425 430			1296
TGT CCC CAA TTT GTC TAC GGC GCC GTT TCA GTG ACC TGC GTG TGG GGT Cys Pro Gln Phe Val Tyr Gly Ala Val Ser Val Thr Cys Val Trp Gly 435 440 445			1344
TCT GTG TCT TGG TTT GCT TCC ACT GGG GGT CGC GAC TCC AAG GTT GAT Ser Val Ser Trp Phe Ala Ser Thr Gly Gly Arg Asp Ser Lys Val Asp 450 455 460			1392
GTG TGG AGT TTG GTT CCA GTT GGC TCT GCC AGC TGC ACC ATA GCC GCA Val Trp Ser Leu Val Pro Val Gly Ser Ala Ser Cys Thr Ile Ala Ala 465 470 475 480			1440
CTG GGA TCT TCG GAT CGC GAC ACA GTG GTT GAG CTC TCC GAG TGG GGA Leu Gly Ser Ser Asp Arg Asp Thr Val Val Glu Leu Ser Glu Trp Gly 485 490 495			1488
ATT CCC TGC GCC ACT TGT ATC CTG GAC AGG CGG CCT GCC TCG TGT GGC Ile Pro Cys Ala Thr Cys Ile Leu Asp Arg Arg Pro Ala Ser Cys Gly 500 505 510			1536

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ACC TGT GTG AGG GAC TGC TGG CCC GAG ACC GGG TCG GTA CGT TTC CCA Thr Cys Val Arg Asp Cys Trp Pro Glu Thr Gly Ser Val Arg Phe Pro 515 520 525	1584
TTC CAC AGG TGT GGC GCG GGA CCG AGG CTG ACC AGA GAC CTT GAG GCT Phe His Arg Cys Gly Ala Gly Pro Arg Leu Thr Arg Asp Leu Glu Ala 530 535 540	1632
GTG CCC TTC GTC AAT AGG ACA ACT CCC TTC ACC ATA AGG GGG CCC CTG Val Pro Phe Val Asn Arg Thr Thr Pro Phe Thr Ile Arg Gly Pro Leu 545 550 555 560	1680
GGC AAC CAG GGG CGA GGC AAC CCG GTG CGG TCG CCC TTG GGT TTT GGG Gly Asn Gln Gly Arg Gly Asn Pro Val Arg Ser Pro Leu Gly Phe Gly 565 570 575	1728
TCC TAC ACC ATG ACC AAG ATC CGA GAC TCC TTA CAC TTG GTG AAA TGT Ser Tyr Thr Met Thr Lys Ile Arg Asp Ser Leu His Leu Val Lys Cys 580 585 590	1776
CCC ACC CCA GCC ATT GAG CCT CCC ACC GGA ACG TTT GGG TTC TTC CCA Pro Thr Pro Ala Ile Glu Pro Pro Thr Gly Thr Phe Gly Phe Phe Pro 595 600 605	1824
GGA GTC CCC CCC CTT AAC AAC TGC ATG CTT CTC GGC ACT GAG GTG TCA Gly Val Pro Pro Leu Asn Asn Cys Met Leu Leu Gly Thr Glu Val Ser 610 615 620	1872
GAG GTA TTG GGT GGG GCG GGC CTC ACT GGG GGG TTT TAC GAA CCT CTG Glu Val Leu Gly Gly Ala Gly Leu Thr Gly Gly Phe Tyr Glu Pro Leu 625 630 635 640	1920
GTG CGG CGG TGT TCA GAG CTG ATG GGT CGG CGG AAT CCG GTC TGC CCG Val Arg Arg Cys Ser Glu Leu Met Gly Arg Arg Asn Pro Val Cys Pro 645 650 655	1968
GGG TTT GCA TGG CTC TCT TCG GGA CGG CCT GAT GGG TTC ATA CAT GTT Gly Phe Ala Trp Leu Ser Ser Gly Arg Pro Asp Gly Phe Ile His Val 660 665 670	2016
CAG GGC CAC TTG CAG GAG GTG GAT GCG GGC AAC TTC ATT CCG CCC CCA Gln Gly His Leu Gln Glu Val Asp Ala Gly Asn Phe Ile Pro Pro Pro 675 680 685	2064
CGC TGG TTG CTC TTG GAC TTT GTA TTT GTC CTG TTA TAC CTG ATG AAG Arg Trp Leu Leu Leu Asp Phe Val Phe Val Leu Leu Tyr Leu Met Lys 690 695 700	2112
CTG GCA GAG GCA CGG TTG GTC CCG CTG ATC CTC CTC CTG CTA TGG TGG Leu Ala Glu Ala Arg Leu Val Pro Leu Ile Leu Leu Leu Leu Trp Trp 705 710 715 720	2160
TGG GTG AAC CAG TTG GCG GTC CTT GKT GTG SCG GCT GCK CRC GCC GCC Trp Val Asn Gln Leu Ala Val Leu Xaa Val Xaa Ala Xaa Xaa Ala Ala 725 730 735	2208
GTG GCT GGA GAG GTG TTT GCG GGC CCT GCC TTG TCC TGG TGT CTG GGC	2256

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Val Ala Gly Glu Val Phe Ala Gly Pro Ala Leu Ser Trp Cys Leu Gly	
740 745 750	
CTA CCC TTC GTG AGT ATG ATC CTG GGG CTA GCA AAC CTG GTG TTG TAC	2304
Leu Pro Phe Val Ser Met Ile Leu Gly Leu Ala Asn Leu Val Leu Tyr	
755 760 765	
TTC CGC TGG ATG GGT CCT CAA CGC CTG ATG TTC CTC GTG TTG TGG AAG	2352
Phe Arg Trp Met Gly Pro Gln Arg Leu Met Phe Leu Val Leu Trp Lys	
770 775 780	
CTC GCT CGG GGG GCT TTC CCG CTG GCA TTA CTG ATG GGG ATT TCC GCC	2400
Leu Ala Arg Gly Ala Phe Pro Leu Ala Leu Leu Met Gly Ile Ser Ala	
785 790 795 800	
ACT CGC GGC CGC ACC TCT GTG CTT GGC GCC GAA TTC TGC TTT GAT GTC	2448
Thr Arg Gly Arg Thr Ser Val Leu Gly Ala Glu Phe Cys Phe Asp Val	
805 810 815	
ACC TTT GAA GTG GAC ACG TCA GTC TTG GGT TGG GTG GTT GCT AGT GTG	2496
Thr Phe Glu Val Asp Thr Ser Val Leu Gly Trp Val Val Ala Ser Val	
820 825 830	
GTG GCT TGG GCC ATA GCG CTC CTG AGC TCT ATG AGC GCG GGG GGG TGG	2544
Val Ala Trp Ala Ile Ala Leu Leu Ser Ser Met Ser Ala Gly Gly Trp	
835 840 845	
AAG CAC AAA GCC ATA ATC TAT AGG ACG TGG TGT AAA GGG TAC CAG GCG	2592
Lys His Lys Ala Ile Ile Tyr Arg Thr Trp Cys Lys Gly Tyr Gln Xaa	
850 855 860	
CTT CGC CAG CGC GTG GTG CGT AGC CCC CTC GGG GAG GGG CGG CCC ACC	2640
Leu Arg Gln Arg Val Val Arg Ser Pro Leu Gly Glu Gly Arg Pro Thr	
865 870 875 880	
AAG CCG CTG ACG ATA GCC TGG TGT CTG GCC TCT TAC ATC TGG CCG GAC	2688
Lys Pro Leu Thr Ile Ala Trp Cys Leu Ala Ser Tyr Ile Trp Pro Asp	
885 890 895	
GCT GTG ATG TTG GTG GTT GTG GCC ATG GTC CTC CTC TTC GGC CTT TTC	2736
Ala Val Met Leu Val Val Val Ala Met Val Leu Leu Phe Gly Leu Phe	
900 905 910	
GAC GCG CTC GAT TGG GCC TTG GAG GAG CTC CTT GTG TCG CGG CCT TCG	2784
Asp Ala Leu Asp Trp Ala Leu Glu Leu Leu Val Ser Arg Pro Ser	
915 920 925	
TTG CGT CGT TTG GCA AGG GTG GTG GAG TGT TGT GTG ATG GCG GGC GAG	2832
Leu Arg Arg Leu Ala Arg Val Val Glu Cys Cys Val Met Ala Gly Glu	
930 935 940	
AAG GCC ACT ACC GTC CGG CTT GTG TCC AAG ATG TGC GCG AGA GGC GCC	2880
Lys Ala Thr Thr Val Arg Leu Val Ser Lys Met Cys Ala Arg Gly Ala	
945 950 955 960	
TAC CTG TTT GAC CAC ATG GGG TCG TTC TCG CGC GCG GTC AAG GAG CGC	2928
Tyr Leu Phe Asp His Met Gly Ser Phe Ser Arg Ala Val Lys Glu Arg	

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965	970	975	
TTG CTG GAG TGG GAC GCG GCT TTG GAG MCC CTG TCA TTC ACT AGG ACG Leu Leu Glu Trp Asp Ala Ala Leu Glu Xaa Leu Ser Phe Thr Arg Thr 980 985 990			2976
GAC TGT CGC ATC ATA CGA GAC GCC GCC AGG ACC CTG AGC TGC GGC CAA Asp Cys Arg Ile Ile Arg Asp Ala Ala Arg Thr Leu Ser Cys Gly Gln 995 1000 1005			3024
TGC GTC ATG GGC TTG CCC GTG GTG GCT AGG CGC GGC GAT GAG GTC CTG Cys Val Met Gly Leu Pro Val Val Ala Arg Arg Gly Asp Glu Val Leu 1010 1015 1020			3072
ATT GGG GTC TTT CAG GAT GTG AAC CAC TTG CCT CCG GGG TTT GYT CCT Ile Gly Val Phe Gln Asp Val Asn His Leu Pro Pro Gly Phe Xaa Pro 1025 1030 1035 1040			3120
ACA GCG CCT GTT GTC ATC CGT CGG TGC GGA AAG GGC TTC CTC GGG GTC Thr Ala Pro Val Val Ile Arg Arg Cys Gly Lys Gly Phe Leu Gly Val 1045 1050 1055			3168
ACT AAG GCT GCC TTG ACT GGT CGG GAT CCT GAC TTA CAC CCA GGA AAC Thr Lys Ala Ala Leu Thr Gly Arg Asp Pro Asp Leu His Pro Gly Asn 1060 1065 1070			3216
GTC ATG GTT TTG GGG ACG GCT ACC TCG CGC AGC ATG GGA ACG TGC TTA Val Met Val Leu Gly Thr Ala Thr Ser Arg Ser Met Gly Thr Cys Leu 1075 1080 1085			3264
AAC GGG TTG CTG TTC ACG ACA TTC CAT GGG GCT TCT TCC CGA ACC ATT Asn Gly Leu Leu Phe Thr Thr Phe His Gly Ala Ser Ser Arg Thr Ile 1090 1095 1100			3312
GCG ACA CCT GTG GGG GCC CTT AAC CCA AGG TGG TGG TCG GCC AGT GAT Ala Thr Pro Val Gly Ala Leu Asn Pro Arg Trp Trp Ser Ala Ser Asp 1105 1110 1115 1120			3360
GAC GTC ACG GTC TAT CCC CTC CCC GAT GGA GCT AAC TCG TTG GTT CCC Asp Val Thr Val Tyr Pro Leu Pro Asp Gly Ala Asn Ser Leu Val Pro 1125 1130 1135			3408
TGC TCG TGT CAG GCT GAG TCC TGT TGG GTC ATY CGA TCC GAT GGG GCT Cys Ser Cys Gln Ala Glu Ser Cys Trp Val Xaa Arg Ser Asp Gly Ala 1140 1145 1150			3456
CTT TGC CAT GGC TTG AGC AAG GGG GAC AAG GTA GAA CTG GAC GTG GCC Leu Cys His Gly Leu Ser Lys Gly Asp Lys Val Glu Leu Asp Val Ala 1155 1160 1165			3504
ATG GAG GTT GCT GAC TTT CGT GGG TCG TCT GGG TCT CCT GTC CTA TGC Met Glu Val Ala Asp Phe Arg Gly Ser Ser Gly Ser Pro Val Leu Cys 1170 1175 1180			3552
GAC GAG GGG CAC GCT GTA GGA ATG CTC GTG TCC GTC CTT CAT TCG GGG Asp Glu Gly His Ala Val Gly Met Leu Val Ser Val Leu His Ser Gly 1185 1190 1195 1200			3600

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GGG AGG GTG ACC GCG GCT CGA TTC ACT CGG CCG TGG ACC CAA GTC CCA Gly Arg Val Thr Ala Ala Arg Phe Thr Arg Pro Trp Thr Gln Val Pro 1205 1210 1215	3648
ACA GAC GCC AAG ACT ACC ACT GAG CCA CCC CCG GTG CCA GCT AAA GGG Thr Asp Ala Lys Thr Thr Thr Glu Pro Pro Pro Val Pro Ala Lys Gly 1220 1225 1230	3696
GTT TTC AAA GAG GCT CCT CTT TTC ATG CCA ACA GGG GCG GGG AAA AGC Val Phe Lys Glu Ala Pro Leu Phe Met Pro Thr Gly Ala Gly Lys Ser 1235 1240 1245	3744
ACA CGC GTC CCT TTG GAG TAT GGA AAC ATG GGG CAC AAG GTC CTG ATT Thr Arg Val Pro Leu Glu Tyr Gly Asn Met Gly His Lys Val Leu Ile 1250 1255 1260	3792
CTC AAC CCG TCG GTT GCC ACT GTG AGG GCC ATG GGC CCT TAC ATG GAG Leu Asn Pro Ser Val Ala Thr Val Arg Ala Met Gly Pro Tyr Met Glu 1265 1270 1275 1280	3840
AGG CTG GCG GGG AAA CAT CCT AGC ATT TTC TGT GGA CAC GAC ACA ACA Arg Leu Ala Gly Lys His Pro Ser Ile Phe Cys Gly His Asp Thr Thr 1285 1290 1295	3888
GCT TTC ACA CGG ATC ACG GAC TCT CCA TTG ACG TAC TCT ACC TAT GGG Ala Phe Thr Arg Ile Thr Asp Ser Pro Leu Thr Tyr Ser Thr Tyr Gly 1300 1305 1310	3936
AGG TTT CTG GCC AAC CCG AGG CAG ATG CTG AGG GGA GTT TCC GTG GTC Arg Phe Leu Ala Asn Pro Arg Gln Met Leu Arg Gly Val Ser Val Val 1315 1320 1325	3984
ATC TGT GAT GAG TGC CAC AGT CAT GAC TCA ACT GTG TTG CTG GGT ATA Ile Cys Asp Glu Cys His Ser His Asp Ser Thr Val Leu Leu Gly Ile 1330 1335 1340	4032
GGC AGG GTC AGG GAC GTG GCG CGG GGG TGT GGA GTG CAA TTA GTG CTC Gly Arg Val Arg Asp Val Ala Arg Gly Cys Gly Val Gln Leu Val Leu 1345 1350 1355 1360	4080
TAC GCT ACT GCG ACT CCC CCG GGC TCG CCT ATG ACT CAG CAT CCA TCC Tyr Ala Thr Ala Thr Pro Pro Gly Ser Pro Met Thr Gln His Pro Ser 1365 1370 1375	4128
ATA ATT GAG ACA AAG CTG GAC GTT GGT GAG ATC CCC TTT TAT GGG CAT Ile Ile Glu Thr Lys Leu Asp Val Gly Glu Ile Pro Phe Tyr Gly His 1380 1385 1390	4176
GGT ATC CCC CTC GAG CGT ATG AGG ACT GGT CGC CAC CTT GTA TTC TGC Gly Ile Pro Leu Glu Arg Met Arg Thr Gly Arg His Leu Val Phe Cys 1395 1400 1405	4224
CAT TCC AAG GCG GAG TGC GAG AGA TTG GCC GGC CAG TTC TCC GCG CGG His Ser Lys Ala Glu Cys Glu Arg Leu Ala Gly Gln Phe Ser Ala Arg 1410 1415 1420	4272
GGG GTT AAT GCC ATC GCC TAT TAT AGG GGT AAG GAC AGT TCC ATC ATC	4320

465

Gly Val Asn Ala Ile Ala Tyr Tyr Arg Gly Lys Asp Ser Ser Ile Ile	
1425	1430 1435 1440
AAA GAC GGA GAC CTG GTG GTT TGT GCG ACA GAC GCG CTC TCT ACC GGG	4368
Lys Asp Gly Asp Leu Val Val Cys Ala Thr Asp Ala Leu Ser Thr Gly	
1445 1450 1455	
TAC ACA GGA AAC TTC GAT TCT GTC ACC GAC TGT GGG TTG GTG GTG GAG	4416
Tyr Thr Gly Asn Phe Asp Ser Val Thr Asp Cys Gly Leu Val Val Glu	
1460 1465 1470	
GAG GTC GTT GAG GTG ACC CTT GAT CCC ACC ATT ACC ATT TCC TTG CGG	4464
Glu Val Val Glu Val Thr Leu Asp Pro Thr Ile Thr Ile Ser Leu Arg	
1475 1480 1485	
ACT GTC CCT GCT TCG GCT GAA TTG TCG ATG CAG CGG CGC GGA CGC ACG	4512
Thr Val Pro Ala Ser Ala Glu Leu Ser Met Gln Arg Arg Gly Arg Thr	
1490 1495 1500	
GGG AGA GGT CGG TCG GGC CGC TAC TAC TAC GCT GGG GTC GGT AAG GCT	4560
Gly Arg Gly Arg Ser Gly Arg Tyr Tyr Tyr Ala Gly Val Gly Lys Ala	
1505 1510 1515 1520	
CCC GCG GGG GTG GTG CGG TCT GGT CCG GTC TGG TCG GCA GTG GAA GCT	4608
Pro Ala Gly Val Val Arg Ser Gly Pro Val Trp Ser Ala Val Glu Ala	
1525 1530 1535	
GGA GTG ACC TGG TAT GGA ATG GAA CCT GAC TTG ACA GCA AAC CTT CTG	4656
Gly Val Thr Trp Tyr Gly Met Glu Pro Asp Leu Thr Ala Asn Leu Leu	
1540 1545 1550	
AGA CTT TAC GAC GAC TGC CCT TAC ACC GCA GCC GTC GCA GCT GAC ATT	4704
Arg Leu Tyr Asp Asp Cys Pro Tyr Thr Ala Ala Val Ala Ala Asp Ile	
1555 1560 1565	
GGT GAA GCC GCG GTG TTC TTT GCG GGC CTC GCG CCC CTC AGG ATG CAT	4752
Gly Glu Ala Ala Val Phe Phe Ala Gly Leu Ala Pro Leu Arg Met His	
1570 1575 1580	
CCC GAT GTT AGC TGG GCA AAA GTT CCG GGC GTC AAT TGG CCC CTC CTG	4800
Pro Asp Val Ser Trp Ala Lys Val Arg Gly Val Asn Trp Pro Leu Leu	
1585 1590 1595 1600	
GTG GGT GTT CAG CGG ACG ATG TGT CGG GAA ACA CTG TCT CCC GGC CCG	4848
Val Gly Val Gln Arg Thr Met Cys Arg Glu Thr Leu Ser Pro Gly Pro	
1605 1610 1615	
TCG GAC GAC CCT CAG TGG GCA GGT CTG AAA GGC CCG AAT CCT GTC CCA	4896
Ser Asp Asp Pro Gln Trp Ala Gly Leu Lys Gly Pro Asn Pro Val Pro	
1620 1625 1630	
CTA CTG CTG AGG TGG GGC AAT GAT TTG CCA TCA AAA GTG GCC GGC CAC	4944
Leu Leu Leu Arg Trp Gly Asn Asp Leu Pro Ser Lys Val Ala Gly His	
1635 1640 1645	
CAC ATA GTT GAC GAT CTG GTC CGT CCG CTC GGT GTG GCG GAG GGA TAC	4992
His Ile Val Asp Asp Leu Val Arg Arg Leu Gly Val Ala Glu Gly Tyr	

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1650	1655	1660	
GTG CGC TGT GAT GCT GGR CCC ATC CTC ATG GTG GGC TTG GCC ATA GCG Val Arg Cys Asp Ala Xaa Pro Ile Leu Met Val Gly Leu Ala Ile Ala 1665	1670	1675	5040 1680
GGC GGC ATG ATC TAC GCC TCT TAC ACT GGG TCG CTA GTG GTG GTA ACA Gly Gly Met Ile Tyr Ala Ser Tyr Thr Gly Ser Leu Val Val Val Thr 1685	1690	1695	5088
GAC TGG GAT GTG AAG GGA GGT GGC AAT CCC CTT TAT AGG AGT GGT GAC Asp Trp Asp Val Lys Gly Gly Gly Asn Pro Leu Tyr Arg Ser Gly Asp 1700	1705	1710	5136
CAG GCC ACC CCT CAA CCC GTG GTG CAG GTC CCC CCG GTA GAC CAT CGG Gln Ala Thr Pro Gln Pro Val Val Gln Val Pro Pro Val Asp His Arg 1715	1720	1725	5184
CCG GGG GGG GAG TCT GCG CCA CGG GAT GCC AAG ACA GTG ACA GAT GCG Pro Gly Gly Glu Ser Ala Pro Arg Asp Ala Lys Thr Val Thr Asp Ala 1730	1735	1740	5232
GTG GCA GCC ATC CAG GTG AAC TGC GAT TGG TCT GTG ATG ACC CTG TCG Val Ala Ala Ile Gln Val Asn Cys Asp Trp Ser Val Met Thr Leu Ser 1745	1750	1755	5280 1760
ATC GGG GAA GTC CTC ACC TTG GCT CAG GCT AAG ACA GCC GAG GCC TAC Ile Gly Glu Val Leu Thr Leu Ala Gln Ala Lys Thr Ala Glu Ala Tyr 1765	1770	1775	5328
GCA GCT ACT TCC AGG TGG CTC GCT GGC TGC TAC ACG GGG ACG CGG GCC Ala Ala Thr Ser Arg Trp Leu Ala Gly Cys Tyr Thr Gly Thr Arg Ala 1780	1785	1790	5376
GTC CCC ACT GTA TCA ATT GTT GAC AAG CTC TTC GCC GGG GGT TGG GCC Val Pro Thr Val Ser Ile Val Asp Lys Leu Phe Ala Gly Gly Trp Ala 1795	1800	1805	5424
GCC GTG GTG GGT CAC TGT CAC AGC GTC ATT GCT GCG GCG GTG GCT GCC Ala Val Val Gly His Cys His Ser Val Ile Ala Ala Ala Val Ala Ala 1810	1815	1820	5472
TAT GGA GCT TCT CGA AGT CCT CCA CTG GCC GCG GCG GCG TCC TAC CTC Tyr Gly Ala Ser Arg Ser Pro Pro Leu Ala Ala Ala Ala Ser Tyr Leu 1825	1830	1835	5520 1840
ATG GGG TTG GGC GTC GGA GGC AAC GCA CAG GCG CGC TTG GCT TCA GCT Met Gly Leu Gly Val Gly Gly Asn Ala Gln Ala Arg Leu Ala Ser Ala 1845	1850	1855	5568
CTT CTA CTG GGG GCT GCT GGT ACG GCT CTG GGG ACC CCT GTC GTG GGA Leu Leu Leu Gly Ala Ala Gly Thr Ala Leu Gly Thr Pro Val Val Gly 1860	1865	1870	5616
CTC ACC ATG GCG GGG GCC TTC ATG GGC GGT GCC AGC GTG TCC CCC TCC Leu Thr Met Ala Gly Ala Phe Met Gly Gly Ala Ser Val Ser Pro Ser 1875	1880	1885	5664

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CTC GTC ACT GTC CTA CTT GGG GCT GTG GGA GGT TGG GAG GGC GTT GTC Leu Val Thr Val Leu Leu Gly Ala Val Gly Gly Trp Glu Gly Val Val 1890 1895 1900	5712
AAC GCT GCC AGT CTC GTC TTC GAC TTC ATG GCT GGG AAA CTT TCA ACA Asn Ala Ala Ser Leu Val Phe Asp Phe Met Ala Gly Lys Leu Ser Thr 1905 1910 1915 1920	5760
GAA GAC CTT TGG TAT GCC ATC CCG GTA CTC ACT AGT CCT GGR GCG GGC Glu Asp Leu Trp Tyr Ala Ile Pro Val Leu Thr Ser Pro Xaa Ala Gly 1925 1930 1935	5808
CTC GCG GGG ATT GCC CTT GGT CTG GTT TTG TAC TCA GCA AAC AAC TCT Leu Ala Gly Ile Ala Leu Gly Leu Val Leu Tyr Ser Ala Asn Asn Ser 1940 1945 1950	5856
GGC ACT ACC ACA TGG CTG AAC CGT CTG CTG ACG ACG TTG CCA CGG TCA Gly Thr Thr Thr Trp Leu Asn Arg Leu Leu Thr Thr Leu Pro Arg Ser 1955 1960 1965	5904
TCT TGC ATA CCC GAC AGC TAC TTC CAA CAG GCT GAC TAC TGC GAC AAG Ser Cys Ile Pro Asp Ser Tyr Phe Gln Gln Ala Asp Tyr Cys Asp Lys 1970 1975 1980	5952
GTC TCG GCA ATC GTG CGC CGC CTG AGC CTT ACT CGC ACC GTG GTG GCC Val Ser Ala Ile Val Arg Arg Leu Ser Leu Thr Arg Thr Val Val Ala 1985 1990 1995 2000	6000
CTG GTC AAC AGG GAG CCT AAG GTG GAT GAG GTC CAG GTG GGG TAC GTC Leu Val Asn Arg Glu Pro Lys Val Asp Glu Val Gln Val Gly Tyr Val 2005 2010 2015	6048
TGG GAT CTG TGG GAG TGG GTG ATG CGC CAG GTG CGC ATG GTG ATG TCT Trp Asp Leu Trp Glu Trp Val Met Arg Gln Val Arg Met Val Met Ser 2020 2025 2030	6096
AGA CTC CGG GCC CTC TGC CCT GTG GTG TCA CTC CCC TTG TGG CAC TGC Arg Leu Arg Ala Leu Cys Pro Val Val Ser Leu Pro Leu Trp His Cys 2035 2040 2045	6144
GGG GAG GGG TGG TCC GGT GAA TGG CTT CTC GAT GGG CAC GTG GAG AGT Gly Glu Gly Trp Ser Gly Glu Trp Leu Leu Asp Gly His Val Glu Ser 2050 2055 2060	6192
CGT TGT CTG TGC GGG TGT GTA ATC ACC GGC GAC GTC CTC AAT GGG CAA Arg Cys Leu Cys Gly Cys Val Ile Thr Gly Asp Val Leu Asn Gly Gln 2065 2070 2075 2080	6240
CTC AAA GAT CCA GTT TAC TCT ACC AAG CTG TGC AGG CAC TAC TGG ATG Leu Lys Asp Pro Val Tyr Ser Thr Lys Leu Cys Arg His Tyr Trp Met 2085 2090 2095	6288
GGA ACT GTG CCG GTC AAC ATG CTG GGC TAC GGG GAA ACC TCA CCT CTT Gly Thr Val Pro Val Asn Met Leu Gly Tyr Gly Glu Thr Ser Pro Leu 2100 2105 2110	6336
CTC GCC TCT GAC ACC CCG AAG GTG GTA CCC TTC GGG ACG TCG GGG TGG	6384

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Leu Ala Ser Asp Thr Pro Lys Val Val Pro Phe Gly Thr Ser Gly Trp	
2115 2120 2125	
GCT GAG GTG GTG GTG ACC CCT ACC CAC GTG GTG ATC AGG CGC ACG TCC	6432
Ala Glu Val Val Val Thr Pro Thr His Val Val Ile Arg Arg Thr Ser	
2130 2135 2140	
TGT TAC AAA CTG CTT CGC CAG CAA ATT CTT TCA GCA GCT GTA GCT GAG	6480
Cys Tyr Lys Leu Leu Arg Gln Gln Ile Leu Ser Ala Ala Val Ala Glu	
2145 2150 2155 2160	
CCC TAC TAC GTT GAT GGC ATT CCG GTC TCT TGG GAG GCT GAC GCG AGA	6528
Pro Tyr Tyr Val Asp Gly Ile Pro Val Ser Trp Glu Ala Asp Ala Arg	
2165 2170 2175	
GCG CCG GCC ATG GTC TAC GGT CCG GGC CAA AGT GTT ACC ATT GAT GGG	6576
Ala Pro Ala Met Val Tyr Gly Pro Gly Gln Ser Val Thr Ile Asp Gly	
2180 2185 2190	
GAG CGC TAC ACC CTT CCG CAC CAG TTG CGG ATG CGG AAT GTG GCG CCC	6624
Glu Arg Tyr Thr Leu Pro His Gln Leu Arg Met Arg Asn Val Ala Pro	
2195 2200 2205	
TCT GAG GTT TCA TCT GAG GTC AGC ATC GAG ATC GGG ACG GAG ACT GAA	6672
Ser Glu Val Ser Ser Glu Val Ser Ile Glu Ile Gly Thr Glu Thr Glu	
2210 2215 2220	
GAC TCA GAA CTG ACT GAG GCC GAT TTG CCA CCA GCG GCT GCT GCC CTC	6720
Asp Ser Glu Leu Thr Glu Ala Asp Leu Pro Pro Ala Ala Ala Ala Leu	
2225 2230 2235 2240	
CAA GCG ATA GAG AAT GCT GCG AGA ATT CTC GAA CCG CAC ATC GAT GTC	6768
Gln Ala Ile Glu Asn Ala Ala Arg Ile Leu Glu Pro His Ile Asp Val	
2245 2250 2255	
AYC ATG GAG GAT TGC AGT ACA CCC TCT CTC TGT GGT AGT AGC CGA GAG	6816
Xaa Met Glu Asp Cys Ser Thr Pro Ser Leu Cys Gly Ser Ser Arg Glu	
2260 2265 2270	
ATG CCT GTG TGG GGA GAA GAC ATA CCC CGC ACT CCA TCG CCT GCA CTT	6864
Met Pro Val Trp Gly Glu Asp Ile Pro Arg Thr Pro Ser Pro Ala Leu	
2275 2280 2285	
ATC TCG GTT ACG GAG AGC AGC TCA GAT GAG AAG ACC CTG TCG GTG ACC	6912
Ile Ser Val Thr Glu Ser Ser Ser Asp Glu Lys Thr Leu Ser Val Thr	
2290 2295 2300	
TCC TCG CAG GAG GAC ACC CCG TCC TCA GAC TCA TTT GAA GTC ATC CAA	6960
Ser Ser Gln Glu Asp Thr Pro Ser Ser Asp Ser Phe Glu Val Ile Gln	
2305 2310 2315 2320	
GAG TCT GAT ACT GCT GAA TCA GAG GAA AGC GTC TTC AAC GTG GCT CTT	7008
Glu Ser Asp Thr Ala Glu Ser Glu Glu Ser Val Phe Asn Val Ala Leu	
2325 2330 2335	
TCC GTA CTA AAA GCC TTA TTT CCA CAG AGC GAT GCC ACA CGA AAG CTA	7056
Ser Val Leu Lys Ala Leu Phe Pro Gln Ser Asp Ala Thr Arg Lys Leu	

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2340	2345	2350	
ACG GTT AAG ATG TCT TGC TGT GTT GAG AAG AGC GTA ACA CGC TTC TTT Thr Val Lys Met Ser Cys Cys Val Glu Lys Ser Val Thr Arg Phe Phe 2355	2360	2365	7104
TCT TTA GGG TTG ACC GTG GCT GAC GTG GCT AGC CTG TGT GAG ATG GAG Ser Leu Gly Leu Thr Val Ala Asp Val Ala Ser Leu Cys Glu Met Glu 2370	2375	2380	7152
ATC CAG AAC CAT ACA GCC TAT TGT GAC AAG GTG CGC ACT CCG CTC GAA Ile Gln Asn His Thr Ala Tyr Cys Asp Lys Val Arg Thr Pro Leu Glu 2385	2390	2395 2400	7200
TTG CAA GTT GGG TGC TTG GTG GGC AAT GAA CTT ACC TTT GAA TGT GAC Leu Gln Val Gly Cys Leu Val Gly Asn Glu Leu Thr Phe Glu Cys Asp 2405	2410	2415	7248
AAG TGT GAG GCA CGC CAA GAG ACC CTT GCC TCC TTC TCC TAC ATA TGG Lys Cys Glu Ala Arg Gln Glu Thr Leu Ala Ser Phe Ser Tyr Ile Trp 2420	2425	2430	7296
TCC GGG GTC CCA CTT ACT CGG GCC ACT CCG GCC AAA CCA CCA GTG GTG Ser Gly Val Pro Leu Thr Arg Ala Thr Pro Ala Lys Pro Pro Val Val 2435	2440	2445	7344
AGG CCG GTG GGG TCC TTG TTG GTG GCA GAC ACC ACC AAG GTC TAC GTG Arg Pro Val Gly Ser Leu Leu Val Ala Asp Thr Thr Lys Val Tyr Val 2450	2455	2460	7392
ACC AAT CCG GAC AAT GTT GGG AGG AGG GTT GAC AAG GTG ACT TTC TGG Thr Asn Pro Asp Asn Val Gly Arg Arg Val Asp Lys Val Thr Phe Trp 2465	2470	2475 2480	7440
CGC GCT CCT CGG GTA CAC GAC AAG TTC CTC GTG GAC TCG ATC GAG CGC Arg Ala Pro Arg Val His Asp Lys Phe Leu Val Asp Ser Ile Glu Arg 2485	2490	2495	7488
GCT CGG AGA GCT GCT CAA GGC TGC CTA AGC ATG GGT TAC ACT TAT GAG Ala Arg Arg Ala Ala Gln Gly Cys Leu Ser Met Gly Tyr Thr Tyr Glu 2500	2505	2510	7536
GAG GCA ATA AGG ACT GTT AGG CCG CAT GCT GCC ATG GGC TGG GGA TCT Glu Ala Ile Arg Thr Val Arg Pro His Ala Ala Met Gly Trp Gly Ser 2515	2520	2525	7584
AAG GTG TCG GTC AAG GAC TTG GCC ACC CCT GCG GGG AAG ATG GCT GTT Lys Val Ser Val Lys Asp Leu Ala Thr Pro Ala Gly Lys Met Ala Val 2530	2535	2540	7632
CAT GAC CGG CTT CAG GAG ATA CTT GAA GGG ACT CCG GTC CCT TTT ACC His Asp Arg Leu Gln Glu Ile Leu Glu Gly Thr Pro Val Pro Phe Thr 2545	2550	2555 2560	7680
CTG ACT GTC AAA AAG GAG GTG TTC TTC AAA GAT CGT AAG GAG GAG AAG Leu Thr Val Lys Lys Glu Val Phe Phe Lys Asp Arg Lys Glu Glu Lys 2565	2570	2575	7728

470

GCC CCC CGC CTC ATT GTG TTC CCC CCC CTG GAC TTC CGG ATA GCT GAA Ala Pro Arg Leu Ile Val Phe Pro Pro Leu Asp Phe Arg Ile Ala Glu 2580 2585 2590	7776
AAG CTC ATT CTG GGA GAC CCG GGG CGG GTT GCA AAG GCC GGT CTT GGG Lys Leu Ile Leu Gly Asp Pro Gly Arg Val Ala Lys Ala Gly Val Gly 2595 2600 2605	7824
GGG GCT TAC GCC TTC CAG TAC ACC CCC AAC CAG CGG GTT AAG GAG ATG Gly Ala Tyr Ala Phe Gln Tyr Thr Pro Asn Gln Arg Val Lys Glu Met 2610 2615 2620	7872
CTA AAG CTG TGG GAA TCA AAG AAG ACC CCG TGC GCC ATC TGT GTG GAT Leu Lys Leu Trp Glu Ser Lys Lys Thr Pro Cys Ala Ile Cys Val Asp 2625 2630 2635 2640	7920
GCC ACT TGC TTC GAC AGT AGC ATT ACT GAR GAG GAC GTG GCA CTA GAG Ala Thr Cys Phe Asp Ser Ser Ile Thr Xaa Glu Asp Val Ala Leu Glu 2645 2650 2655	7968
ACA GAG CTT TAC GCC CTG GCC TCG GAC CAT CCA GAA TGG GTG CGC GCC Thr Glu Leu Tyr Ala Leu Ala Ser Asp His Pro Glu Trp Val Arg Ala 2660 2665 2670	8016
CTG GGG AAA TAC TRT GCC TCT GGC ACA ATG GTG ACC CCG GAA GGG GTG Leu Gly Lys Tyr Xaa Ala Ser Gly Thr Met Val Thr Pro Glu Gly Val 2675 2680 2685	8064
CCA GTG GGC GAG AGG TAT TGT AGG TCC TCG GGT GTG TTG ACC ACA AGT Pro Val Gly Glu Arg Tyr Cys Arg Ser Ser Gly Val Leu Thr Thr Ser 2690 2695 2700	8112
GCT AGC AAC TGT TTG ACC TGC TAC ATC AAA GTG AGA GCC GCC TGT GAG Ala Ser Asn Cys Leu Thr Cys Tyr Ile Lys Val Arg Ala Ala Cys Glu 2705 2710 2715 2720	8160
AGG ATC GGA CTG AAA AAT GTC TCG CTT CTC ATC GCG GGC GAT GAC TGC Arg Ile Gly Leu Lys Asn Val Ser Leu Leu Ile Ala Gly Asp Asp Cys 2725 2730 2735	8208
TTA ATT GTG TGC GAG AGG CCT GTA TGC GAC CCT TGC GAG GCC CTG GGC Leu Ile Val Cys Glu Arg Pro Val Cys Asp Pro Cys Glu Ala Leu Gly 2740 2745 2750	8256
CGA ACC CTG GCT TCG TAC GGG TAC GCG TGT GAG CCC TCG TAT CAC GCT Arg Thr Leu Ala Ser Tyr Gly Tyr Ala Cys Glu Pro Ser Tyr His Ala 2755 2760 2765	8304
TCA CTG GAC ACA GCC CCC TTC TGC TCC ACT TGG CTC GCT GAG TGC AAT Ser Leu Asp Thr Ala Pro Phe Cys Ser Thr Trp Leu Ala Glu Cys Asn 2770 2775 2780	8352
GCG GAT GGG RAA AGG CAT TTC TTC CTG ACC ACG GAC TTT CGG AGA CCA Ala Asp Gly Xaa Arg His Phe Phe Leu Thr Thr Asp Phe Arg Arg Pro 2785 2790 2795 2800	8400
CTC GCT CGC ATG TCG AGC GAG TAC AGT GAC CCT ATG GCT TCG GCC ATT	8448

471

Leu Ala Arg Met S r Ser Glu Tyr Ser Asp Pro Met Ala Ser Ala Ile	
2805 2810 2815	
GGT TAC ATT CTC CTC TAC CCC TGG CRT CCC ATC ACA CGG TGG GTC ATC	8496
Gly Tyr Ile Leu Leu Tyr Pro Trp Xaa Pro Ile Thr Arg Trp Val Ile	
2820 2825 2830	
ATC CCG CAT GTG CTA ACA TGC GCT TCT TCC CGG GGT GGT GGC ACA CSG	8544
Ile Pro His Val Leu Thr Cys Ala Ser Ser Arg Gly Gly Gly Thr Xaa	
2835 2840 2845	
TCT GAT CCG GTT TGG TGT CAG GTT CAT GGT AAC TAC TAC AAG TTT CCC	8592
Ser Asp Pro Val Trp Cys Gln Val His Gly Asn Tyr Tyr Lys Phe Pro	
2850 2855 2860	
CTG GAC AAA CTG CCT AAC ATC ATC GTG GCC CTC CAC GGA CCA GCA GCG	8640
Leu Asp Lys Leu Pro Asn Ile Ile Val Ala Leu His Gly Pro Ala Ala	
2865 2870 2875 2880	
TTG AGG GTT ACC GCA GAC ACA ACC AAA ACA AAG ATG GAG GCT GGG AAG	8688
Leu Arg Val Thr Ala Asp Thr Thr Lys Thr Lys Met Glu Ala Gly Lys	
2885 2890 2895	
GTT CTG AGC GAC CTC AAG CTC CCT GGT CTA GCC GTC CAC CGC AAG AAG	8736
Val Leu Ser Asp Leu Lys Leu Pro Gly Leu Ala Val His Arg Lys Lys	
2900 2905 2910	
GCC GGG GCA TTG CGA ACA CGC ATG CTC CGG TCG CGC GGT TGG GCG GAG	8784
Ala Gly Ala Leu Arg Thr Arg Met Leu Arg Ser Arg Gly Trp Ala Glu	
2915 2920 2925	
TTG GCT AGG GGC CTG TTG TGG CAT CCA GGA CTC CGG CTT CCT CCC CCT	8832
Leu Ala Arg Gly Leu Leu Trp His Pro Gly Leu Arg Leu Pro Pro Pro	
2930 2935 2940	
GAG ATT GCT GGT ATC CCA GGG GGT TTC CCT CTG TCC CCC CCC TAC ATG	8880
Glu Ile Ala Gly Ile Pro Gly Gly Phe Pro Leu Ser Pro Pro Tyr Met	
2945 2950 2955 2960	
GGG GTG GTT CAT CAA TTG GAT TTC ACA GCS CAG CGG AGT CGC TGG CGG	8928
Gly Val Val His Gln Leu Asp Phe Thr Xaa Gln Arg Ser Arg Trp Arg	
2965 2970 2975	
TGG TTG GGG TTC TTA GCC CTG CTC ATC GTA GCG CTC TTT GGG TGA ACT	8976
Trp Leu Gly Phe Leu Ala Leu Leu Ile Val Ala Leu Phe Gly * Thr	
2980 2985 2990	
AAA TTC ATC TGT TGC GGC CGG AGT CAG ACC TGA GCC CCG TTC AAA AGG	9024
Lys Phe Ile Cys Cys Gly Arg Ser Gln Thr * Ala Pro Phe Lys Arg	
2995 3000 3005	
GGA TTG AGA C	9034
Gly Leu Arg	
3010	

(2) INFORMATION FOR SEQ ID NO:401:

472

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Lys Gly Gly Gly Trp Val Met Thr Gly Leu Val Gly Arg Lys Ser Arg
1 5 10 15

Ser Ser Trp

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Val Gly Leu Lys Gly Arg Leu Arg Ser Leu Leu Arg Ile Trp Arg Lys
1 5 10 15

Ser Ala Arg Ser Thr Gly Val Gly Pro Thr Gly Val Ile Arg Thr Arg
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Thr Glu Pro Val Thr Pro Leu Gly Lys Arg Arg Pro Arg Thr Val His
1 5 10 15

Val Ala Leu Gln Cys Leu Ser
20

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2905 amino acids

(B) TYPE: amino acid

473

(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

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Pro Ile Gly Val Arg Arg Val Asp Lys Asp Gln Trp Gly Pro Gly Gly
 1             5             10             15
Arg Gly Lys Asp Pro His Arg Cys Pro Ser Arg Gly Gly Gly Lys Cys
          20             25             30
Met Gly Pro Pro Ser Ser Ala Ala Ala Tyr Ser Arg Gly Ser Pro Arg
          35             40             45
Thr Ser Gly Glu Gly Gly Trp His Phe Phe Ser Tyr Thr Asp His Gly
          50             55             60
Ser Pro Ser Ala Pro Thr Arg Gly Gly Ala Gly Ala Ile Leu Ala Pro
          65             70             75             80
Ala Thr His Ala Cys Ser Ala Lys Gly Gln Tyr Xaa Leu Thr Asn Cys
          85             90             95
Cys Ala Leu Glu Asp Ile Gly Phe Cys Leu Glu Gly Gly Cys Leu Val
          100            105            110
Ala Leu Gly Cys Thr Ile Cys Thr Asp Arg Cys Trp Pro Leu Tyr Gln
          115            120            125
Ala Gly Leu Ala Val Arg Pro Gly Lys Ser Ala Ala Gln Leu Val Gly
          130            135            140
Glu Leu Gly Ser Leu Tyr Gly Pro Leu Ser Val Ser Ala Tyr Val Ala
          145            150            155            160
Gly Ile Leu Gly Leu Gly Glu Val Tyr Ser Gly Val Leu Thr Val Gly
          165            170            175
Val Ala Leu Thr Arg Arg Val Tyr Pro Val Pro Asn Leu Thr Cys Ala
          180            185            190
Val Glu Cys Glu Leu Lys Trp Glu Ser Glu Phe Trp Arg Trp Thr Glu
          195            200            205
Gln Leu Ala Ser Asn Tyr Trp Ile Leu Glu Tyr Leu Trp Lys Val Pro
          210            215            220
Phe Asp Phe Trp Arg Gly Val Met Ser Leu Thr Pro Leu Leu Val Cys
          225            230            235            240
Val Ala Ala Leu Leu Leu Leu Glu Gln Arg Ile Val Met Val Phe Leu
          245            250            255
Leu Val Thr Met Ala Gly Met Ser Gln Gly Ala Pro Ala Ser Ser Val
          260            265            270

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474

Gly Val Thr Ala Phe Arg Gly Gly Phe Asp Leu Ala Val Leu Phe Leu
 275 280 285

Gln Val Glu Arg Val Pro Arg Ala Asp Arg Glu Arg Val Trp Glu Arg
 290 295 300

Gly Asn Val Thr Leu Leu Cys Asp Cys Pro Asn Gly Pro Trp Val Trp
 305 310 315 320

Val Pro Ala Leu Cys Gln Ala Ile Gly Trp Gly Asp Pro Ile Thr His
 325 330 335

Trp Ser His Gly Gln Asn Gln Trp Pro Leu Ser Cys Pro Gln Phe Val
 340 345 350

Tyr Gly Ala Val Ser Val Thr Cys Val Trp Gly Ser Val Ser Trp Phe
 355 360 365

Ala Ser Thr Gly Gly Arg Asp Ser Lys Val Asp Val Trp Ser Leu Val
 370 375 380

Pro Val Gly Ser Ala Ser Cys Thr Ile Ala Ala Leu Gly Ser Ser Asp
 385 390 395 400

Arg Asp Thr Val Val Glu Leu Ser Glu Trp Gly Ile Pro Cys Ala Thr
 405 410 415

Cys Ile Leu Asp Arg Arg Pro Ala Ser Cys Gly Thr Cys Val Arg Asp
 420 425 430

Cys Trp Pro Glu Thr Gly Ser Val Arg Phe Pro Phe His Arg Cys Gly
 435 440 445

Ala Gly Pro Arg Leu Thr Arg Asp Leu Glu Ala Val Pro Phe Val Asn
 450 455 460

Arg Thr Thr Pro Phe Thr Ile Arg Gly Pro Leu Gly Asn Gln Gly Arg
 465 470 475 480

Gly Asn Pro Val Arg Ser Pro Leu Gly Phe Gly Ser Tyr Thr Met Thr
 485 490 495

Lys Ile Arg Asp Ser Leu His Leu Val Lys Cys Pro Thr Pro Ala Ile
 500 505 510

Glu Pro Pro Thr Gly Thr Phe Gly Phe Phe Pro Gly Val Pro Pro Leu
 515 520 525

Asn Asn Cys Met Leu Leu Gly Thr Glu Val Ser Glu Val Leu Gly Gly
 530 535 540

Ala Gly Leu Thr Gly Gly Phe Tyr Glu Pro Leu Val Arg Arg Cys Ser
 545 550 555 560

Glu Leu Met Gly Arg Arg Asn Pro Val Cys Pro Gly Phe Ala Trp Leu
 565 570 575

475

Ser Ser Gly Arg Pro Asp Gly Phe Ile His Val Gln Gly His Leu Gln
 580 585 590
 Glu Val Asp Ala Gly Asn Phe Ile Pro Pro Pro Arg Trp Leu Leu Leu
 595 600 605
 Asp Phe Val Phe Val Leu Leu Tyr Leu Met Lys Leu Ala Glu Ala Arg
 610 615 620
 Leu Val Pro Leu Ile Leu Leu Leu Leu Trp Trp Trp Val Asn Gln Leu
 625 630 635 640
 Ala Val Leu Xaa Val Xaa Ala Xaa Xaa Ala Ala Val Ala Gly Glu Val
 645 650 655
 Phe Ala Gly Pro Ala Leu Ser Trp Cys Leu Gly Leu Pro Phe Val Ser
 660 665 670
 Met Ile Leu Gly Leu Ala Asn Leu Val Leu Tyr Phe Arg Trp Met Gly
 675 680 685
 Pro Gln Arg Leu Met Phe Leu Val Leu Trp Lys Leu Ala Arg Gly Ala
 690 695 700
 Phe Pro Leu Ala Leu Leu Met Gly Ile Ser Ala Thr Arg Gly Arg Thr
 705 710 715 720
 Ser Val Leu Gly Ala Glu Phe Cys Phe Asp Val Thr Phe Glu Val Asp
 725 730 735
 Thr Ser Val Leu Gly Trp Val Val Ala Ser Val Val Ala Trp Ala Ile
 740 745 750
 Ala Leu Leu Ser Ser Met Ser Ala Gly Gly Trp Lys His Lys Ala Ile
 755 760 765
 Ile Tyr Arg Thr Trp Cys Lys Gly Tyr Gln Xaa Leu Arg Gln Arg Val
 770 775 780
 Val Arg Ser Pro Leu Gly Glu Gly Arg Pro Thr Lys Pro Leu Thr Ile
 785 790 795 800
 Ala Trp Cys Leu Ala Ser Tyr Ile Trp Pro Asp Ala Val Met Leu Val
 805 810 815
 Val Val Ala Met Val Leu Leu Phe Gly Leu Phe Asp Ala Leu Asp Trp
 820 825 830
 Ala Leu Glu Glu Leu Leu Val Ser Arg Pro Ser Leu Arg Arg Leu Ala
 835 840 845
 Arg Val Val Glu Cys Cys Val Met Ala Gly Glu Lys Ala Thr Thr Val
 850 855 860
 Arg Leu Val Ser Lys Met Cys Ala Arg Gly Ala Tyr Leu Phe Asp His
 865 870 875 880

476

Met Gly Ser Phe Ser Arg Ala Val Lys Glu Arg Leu Leu Glu Trp Asp
 885 890 895
 Ala Ala Leu Glu Xaa Leu Ser Phe Thr Arg Thr Asp Cys Arg Ile Ile
 900 905 910
 Arg Asp Ala Ala Arg Thr Leu Ser Cys Gly Gln Cys Val Met Gly Leu
 915 920 925
 Pro Val Val Ala Arg Arg Gly Asp Glu Val Leu Ile Gly Val Phe Gln
 930 935 940
 Asp Val Asn His Leu Pro Pro Gly Phe Xaa Pro Thr Ala Pro Val Val
 945 950 955 960
 Ile Arg Arg Cys Gly Lys Gly Phe Leu Gly Val Thr Lys Ala Ala Leu
 965 970 975
 Thr Gly Arg Asp Pro Asp Leu His Pro Gly Asn Val Met Val Leu Gly
 980 985 990
 Thr Ala Thr Ser Arg Ser Met Gly Thr Cys Leu Asn Gly Leu Leu Phe
 995 1000 1005
 Thr Thr Phe His Gly Ala Ser Ser Arg Thr Ile Ala Thr Pro Val Gly
 1010 1015 1020
 Ala Leu Asn Pro Arg Trp Trp Ser Ala Ser Asp Asp Val Thr Val Tyr
 1025 1030 1035 1040
 Pro Leu Pro Asp Gly Ala Asn Ser Leu Val Pro Cys Ser Cys Gln Ala
 1045 1050 1055
 Glu Ser Cys Trp Val Xaa Arg Ser Asp Gly Ala Leu Cys His Gly Leu
 1060 1065 1070
 Ser Lys Gly Asp Lys Val Glu Leu Asp Val Ala Met Glu Val Ala Asp
 1075 1080 1085
 Phe Arg Gly Ser Ser Gly Ser Pro Val Leu Cys Asp Glu Gly His Ala
 1090 1095 1100
 Val Gly Met Leu Val Ser Val Leu His Ser Gly Gly Arg Val Thr Ala
 1105 1110 1115 1120
 Ala Arg Phe Thr Arg Pro Trp Thr Gln Val Pro Thr Asp Ala Lys Thr
 1125 1130 1135
 Thr Thr Glu Pro Pro Pro Val Pro Ala Lys Gly Val Phe Lys Glu Ala
 1140 1145 1150
 Pro Leu Phe Met Pro Thr Gly Ala Gly Lys Ser Thr Arg Val Pro Leu
 1155 1160 1165
 Glu Tyr Gly Asn Met Gly His Lys Val Leu Ile Leu Asn Pro Ser Val
 1170 1175 1180

477

Ala Thr Val Arg Ala Met Gly Pro Tyr Met Glu Arg Leu Ala Gly Lys
 1185 1190 1195 1200
 His Pro Ser Ile Phe Cys Gly His Asp Thr Thr Ala Phe Thr Arg Ile
 1205 1210 1215
 Thr Asp Ser Pro Leu Thr Tyr Ser Thr Tyr Gly Arg Phe Leu Ala Asn
 1220 1225 1230
 Pro Arg Gln Met Leu Arg Gly Val Ser Val Val Ile Cys Asp Glu Cys
 1235 1240 1245
 His Ser His Asp Ser Thr Val Leu Leu Gly Ile Gly Arg Val Arg Asp
 1250 1255 1260
 Val Ala Arg Gly Cys Gly Val Gln Leu Val Leu Tyr Ala Thr Ala Thr
 1265 1270 1275 1280
 Pro Pro Gly Ser Pro Met Thr Gln His Pro Ser Ile Ile Glu Thr Lys
 1285 1290 1295
 Leu Asp Val Gly Glu Ile Pro Phe Tyr Gly His Gly Ile Pro Leu Glu
 1300 1305 1310
 Arg Met Arg Thr Gly Arg His Leu Val Phe Cys His Ser Lys Ala Glu
 1315 1320 1325
 Cys Glu Arg Leu Ala Gly Gln Phe Ser Ala Arg Gly Val Asn Ala Ile
 1330 1335 1340
 Ala Tyr Tyr Arg Gly Lys Asp Ser Ser Ile Ile Lys Asp Gly Asp Leu
 1345 1350 1355 1360
 Val Val Cys Ala Thr Asp Ala Leu Ser Thr Gly Tyr Thr Gly Asn Phe
 1365 1370 1375
 Asp Ser Val Thr Asp Cys Gly Leu Val Val Glu Glu Val Val Glu Val
 1380 1385 1390
 Thr Leu Asp Pro Thr Ile Thr Ile Ser Leu Arg Thr Val Pro Ala Ser
 1395 1400 1405
 Ala Glu Leu Ser Met Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Ser
 1410 1415 1420
 Gly Arg Tyr Tyr Tyr Ala Gly Val Gly Lys Ala Pro Ala Gly Val Val
 1425 1430 1435 1440
 Arg Ser Gly Pro Val Trp Ser Ala Val Glu Ala Gly Val Thr Trp Tyr
 1445 1450 1455
 Gly Met Glu Pro Asp Leu Thr Ala Asn Leu Leu Arg Leu Tyr Asp Asp
 1460 1465 1470
 Cys Pro Tyr Thr Ala Ala Val Ala Ala Asp Ile Gly Glu Ala Ala Val
 1475 1480 1485

478

Phe Phe Ala Gly Leu Ala Pro Leu Arg Met His Pro Asp Val Ser Trp
 1490 1495 1500

Ala Lys Val Arg Gly Val Asn Trp Pro Leu Leu Val Gly Val Gln Arg
 1505 1510 1515 1520

Thr Met Cys Arg Glu Thr Leu Ser Pro Gly Pro Ser Asp Asp Pro Gln
 1525 1530 1535

Trp Ala Gly Leu Lys Gly Pro Asn Pro Val Pro Leu Leu Leu Arg Trp
 1540 1545 1550

Gly Asn Asp Leu Pro Ser Lys Val Ala Gly His His Ile Val Asp Asp
 1555 1560 1565

Leu Val Arg Arg Leu Gly Val Ala Glu Gly Tyr Val Arg Cys Asp Ala
 1570 1575 1580

Xaa Pro Ile Leu Met Val Gly Leu Ala Ile Ala Gly Gly Met Ile Tyr
 1585 1590 1595 1600

Ala Ser Tyr Thr Gly Ser Leu Val Val Val Thr Asp Trp Asp Val Lys
 1605 1610 1615

Gly Gly Gly Asn Pro Leu Tyr Arg Ser Gly Asp Gln Ala Thr Pro Gln
 1620 1625 1630

Pro Val Val Gln Val Pro Pro Val Asp His Arg Pro Gly Gly Glu Ser
 1635 1640 1645

Ala Pro Arg Asp Ala Lys Thr Val Thr Asp Ala Val Ala Ala Ile Gln
 1650 1655 1660

Val Asn Cys Asp Trp Ser Val Met Thr Leu Ser Ile Gly Glu Val Leu
 1665 1670 1675 1680

Thr Leu Ala Gln Ala Lys Thr Ala Glu Ala Tyr Ala Ala Thr Ser Arg
 1685 1690 1695

Trp Leu Ala Gly Cys Tyr Thr Gly Thr Arg Ala Val Pro Thr Val Ser
 1700 1705 1710

Ile Val Asp Lys Leu Phe Ala Gly Gly Trp Ala Ala Val Val Gly His
 1715 1720 1725

Cys His Ser Val Ile Ala Ala Ala Val Ala Ala Tyr Gly Ala Ser Arg
 1730 1735 1740

Ser Pro Pro Leu Ala Ala Ala Ala Ser Tyr Leu Met Gly Leu Gly Val
 1745 1750 1755 1760

Gly Gly Asn Ala Gln Ala Arg Leu Ala Ser Ala Leu Leu Leu Gly Ala
 1765 1770 1775

Ala Gly Thr Ala Leu Gly Thr Pro Val Val Gly Leu Thr Met Ala Gly
 1780 1785 1790

479

Ala Phe Met Gly Gly Ala Ser Val Ser Pro Ser Leu Val Thr Val Leu
1795 1800 1805

Leu Gly Ala Val Gly Gly Trp Glu Gly Val Val Asn Ala Ala Ser Leu
1810 1815 1820

Val Phe Asp Phe Met Ala Gly Lys Leu Ser Thr Glu Asp Leu Trp Tyr
1825 1830 1835 1840

Ala Ile Pro Val Leu Thr Ser Pro Xaa Ala Gly Leu Ala Gly Ile Ala
1845 1850 1855

Leu Gly Leu Val Leu Tyr Ser Ala Asn Asn Ser Gly Thr Thr Thr Trp
1860 1865 1870

Leu Asn Arg Leu Leu Thr Thr Leu Pro Arg Ser Ser Cys Ile Pro Asp
1875 1880 1885

Ser Tyr Phe Gln Gln Ala Asp Tyr Cys Asp Lys Val Ser Ala Ile Val
1890 1895 1900

Arg Arg Leu Ser Leu Thr Arg Thr Val Val Ala Leu Val Asn Arg Glu
1905 1910 1915 1920

Pro Lys Val Asp Glu Val Gln Val Gly Tyr Val Trp Asp Leu Trp Glu
1925 1930 1935

Trp Val Met Arg Gln Val Arg Met Val Met Ser Arg Leu Arg Ala Leu
1940 1945 1950

Cys Pro Val Val Ser Leu Pro Leu Trp His Cys Gly Glu Gly Trp Ser
1955 1960 1965

Gly Glu Trp Leu Leu Asp Gly His Val Glu Ser Arg Cys Leu Cys Gly
1970 1975 1980

Cys Val Ile Thr Gly Asp Val Leu Asn Gly Gln Leu Lys Asp Pro Val
1985 1990 1995 2000

Tyr Ser Thr Lys Leu Cys Arg His Tyr Trp Met Gly Thr Val Pro Val
2005 2010 2015

Asn Met Leu Gly Tyr Gly Glu Thr Ser Pro Leu Leu Ala Ser Asp Thr
2020 2025 2030

Pro Lys Val Val Pro Phe Gly Thr Ser Gly Trp Ala Glu Val Val Val
2035 2040 2045

Thr Pro Thr His Val Val Ile Arg Arg Thr Ser Cys Tyr Lys Leu Leu
2050 2055 2060

Arg Gln Gln Ile Leu Ser Ala Ala Val Ala Glu Pro Tyr Tyr Val Asp
2065 2070 2075 2080

Gly Ile Pro Val Ser Trp Glu Ala Asp Ala Arg Ala Pro Ala Met Val
2085 2090 2095

480

Tyr Gly Pro Gly Gln Ser Val Thr Ile Asp Gly Glu Arg Tyr Thr Leu
 2100 2105 2110

Pro His Gln Leu Arg Met Arg Asn Val Ala Pro Ser Glu Val Ser Ser
 2115 2120 2125

Glu Val Ser Ile Glu Ile Gly Thr Glu Thr Glu Asp Ser Glu Leu Thr
 2130 2135 2140

Glu Ala Asp Leu Pro Pro Ala Ala Ala Ala Leu Gln Ala Ile Glu Asn
 2145 2150 2155 2160

Ala Ala Arg Ile Leu Glu Pro His Ile Asp Val Xaa Met Glu Asp Cys
 2165 2170 2175

Ser Thr Pro Ser Leu Cys Gly Ser Ser Arg Glu Met Pro Val Trp Gly
 2180 2185 2190

Glu Asp Ile Pro Arg Thr Pro Ser Pro Ala Leu Ile Ser Val Thr Glu
 2195 2200 2205

Ser Ser Ser Asp Glu Lys Thr Leu Ser Val Thr Ser Ser Gln Glu Asp
 2210 2215 2220

Thr Pro Ser Ser Asp Ser Phe Glu Val Ile Gln Glu Ser Asp Thr Ala
 2225 2230 2235 2240

Glu Ser Glu Glu Ser Val Phe Asn Val Ala Leu Ser Val Leu Lys Ala
 2245 2250 2255

Leu Phe Pro Gln Ser Asp Ala Thr Arg Lys Leu Thr Val Lys Met Ser
 2260 2265 2270

Cys Cys Val Glu Lys Ser Val Thr Arg Phe Phe Ser Leu Gly Leu Thr
 2275 2280 2285

Val Ala Asp Val Ala Ser Leu Cys Glu Met Glu Ile Gln Asn His Thr
 2290 2295 2300

Ala Tyr Cys Asp Lys Val Arg Thr Pro Leu Glu Leu Gln Val Gly Cys
 2305 2310 2315 2320

Leu Val Gly Asn Glu Leu Thr Phe Glu Cys Asp Lys Cys Glu Ala Arg
 2325 2330 2335

Gln Glu Thr Leu Ala Ser Phe Ser Tyr Ile Trp Ser Gly Val Pro Leu
 2340 2345 2350

Thr Arg Ala Thr Pro Ala Lys Pro Pro Val Val Arg Pro Val Gly Ser
 2355 2360 2365

Leu Leu Val Ala Asp Thr Thr Lys Val Tyr Val Thr Asn Pro Asp Asn
 2370 2375 2380

Val Gly Arg Arg Val Asp Lys Val Thr Phe Trp Arg Ala Pro Arg Val
 2385 2390 2395 2400

481

His Asp Lys Phe Leu Val Asp Ser Ile Glu Arg Ala Arg Arg Ala Ala
 2405 2410 2415
 Gln Gly Cys Leu Ser Met Gly Tyr Thr Tyr Glu Glu Ala Ile Arg Thr
 2420 2425 2430
 Val Arg Pro His Ala Ala Met Gly Trp Gly Ser Lys Val Ser Val Lys
 2435 2440 2445
 Asp Leu Ala Thr Pro Ala Gly Lys Met Ala Val His Asp Arg Leu Gln
 2450 2455 2460
 Glu Ile Leu Glu Gly Thr Pro Val Pro Phe Thr Leu Thr Val Lys Lys
 2465 2470 2475 2480
 Glu Val Phe Phe Lys Asp Arg Lys Glu Glu Lys Ala Pro Arg Leu Ile
 2485 2490 2495
 Val Phe Pro Pro Leu Asp Phe Arg Ile Ala Glu Lys Leu Ile Leu Gly
 2500 2505 2510
 Asp Pro Gly Arg Val Ala Lys Ala Gly Val Gly Gly Ala Tyr Ala Phe
 2515 2520 2525
 Gln Tyr Thr Pro Asn Gln Arg Val Lys Glu Met Leu Lys Leu Trp Glu
 2530 2535 2540
 Ser Lys Lys Thr Pro Cys Ala Ile Cys Val Asp Ala Thr Cys Phe Asp
 2545 2550 2555 2560
 Ser Ser Ile Thr Xaa Glu Asp Val Ala Leu Glu Thr Glu Leu Tyr Ala
 2565 2570 2575
 Leu Ala Ser Asp His Pro Glu Trp Val Arg Ala Leu Gly Lys Tyr Xaa
 2580 2585 2590
 Ala Ser Gly Thr Met Val Thr Pro Glu Gly Val Pro Val Gly Glu Arg
 2595 2600 2605
 Tyr Cys Arg Ser Ser Gly Val Leu Thr Thr Ser Ala Ser Asn Cys Leu
 2610 2615 2620
 Thr Cys Tyr Ile Lys Val Arg Ala Ala Cys Glu Arg Ile Gly Leu Lys
 2625 2630 2635 2640
 Asn Val Ser Leu Leu Ile Ala Gly Asp Asp Cys Leu Ile Val Cys Glu
 2645 2650 2655
 Arg Pro Val Cys Asp Pro Cys Glu Ala Leu Gly Arg Thr Leu Ala Ser
 2660 2665 2670
 Tyr Gly Tyr Ala Cys Glu Pro Ser Tyr His Ala Ser Leu Asp Thr Ala
 2675 2680 2685
 Pro Phe Cys Ser Thr Trp Leu Ala Glu Cys Asn Ala Asp Gly Xaa Arg
 2690 2695 2700

482

His Phe Phe Leu Thr Thr Asp Phe Arg Arg Pro Leu Ala Arg Met Ser
 2705 2710 2715 2720
 Ser Glu Tyr Ser Asp Pro Met Ala Ser Ala Ile Gly Tyr Ile Leu Leu
 2725 2730 2735
 Tyr Pro Trp Xaa Pro Ile Thr Arg Trp Val Ile Ile Pro His Val Leu
 2740 2745 2750
 Thr Cys Ala Ser Ser Arg Gly Gly Gly Thr Xaa Ser Asp Pro Val Trp
 2755 2760 2765
 Cys Gln Val His Gly Asn Tyr Tyr Lys Phe Pro Leu Asp Lys Leu Pro
 2770 2775 2780
 Asn Ile Ile Val Ala Leu His Gly Pro Ala Ala Leu Arg Val Thr Ala
 2785 2790 2795 2800
 Asp Thr Thr Lys Thr Lys Met Glu Ala Gly Lys Val Leu Ser Asp Leu
 2805 2810 2815
 Lys Leu Pro Gly Leu Ala Val His Arg Lys Lys Ala Gly Ala Leu Arg
 2820 2825 2830
 Thr Arg Met Leu Arg Ser Arg Gly Trp Ala Glu Leu Ala Arg Gly Leu
 2835 2840 2845
 Leu Trp His Pro Gly Leu Arg Leu Pro Pro Pro Glu Ile Ala Gly Ile
 2850 2855 2860
 Pro Gly Gly Phe Pro Leu Ser Pro Pro Tyr Met Gly Val Val His Gln
 2865 2870 2875 2880
 Leu Asp Phe Thr Xaa Gln Arg Ser Arg Trp Arg Trp Leu Gly Phe Leu
 2885 2890 2895
 Ala Leu Leu Ile Val Ala Leu Phe Gly
 2900 2905

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Thr Lys Phe Ile Cys Cys Gly Arg Ser Gln Thr
 1 5 10

483

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Ala Pro Phe Lys Arg Gly Leu Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..9034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

AAG GTG GTG GAT GGG TGA TGA CAG GGT TGG TAG GTC GTA AAT CCC GGT	48
Lys Val Val Asp Gly * * Gln Gly Trp * Val Val Asn Pro Gly	
1 5 10 15	
CAT CCT GGT AGC CAC TAT AGG TGG GTC TTA AGG GGA GGC TAC GGT CCC	96
His Pro Gly Ser His Tyr Arg Trp Val Leu Arg Gly Gly Tyr Gly Pro	
20 25 30	
TCT TGC GCA TAT GGA GGA AAA GCG CAC GGT CCA CAG GTG TTG GTC CTA	144
Ser Cys Ala Tyr Gly Gly Lys Ala His Gly Pro Gln Val Leu Val Leu	
35 40 45	
CCG GTG TAA TAA GGA CCC GGC GCT AGG CAC GCC GTT AAA CCG AGC CCG	192
Pro Val * * Gly Pro Gly Ala Arg His Ala Val Lys Pro Ser Pro	
50 55 60	
TTA CTC CCC TGG GCA AAC GAC GCC CAC GTA CGG TCC ACG TCG CCC TTC	240
Leu Leu Pro Trp Ala Asn Asp Ala His Val Arg Ser Thr Ser Pro Phe	
65 70 75 80	

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AAT GTC TCT CTT GAC CAA TAG GCG TAC GGC GAG TTG ACA AGG ACC AGT	288
Asn Val Ser Leu Asp Gln * Ala Tyr Gly Glu Leu Thr Arg Thr Ser	
85 90 95	
GGG GGC CGG GCG GGA GGG GGA AGG ACC CCC ACC GCT GCC CTT CCC GGG	336
Gly Gly Arg Ala Gly Gly Gly Arg Thr Pro Thr Ala Ala Leu Pro Gly	
100 105 110	
GAG GCG GGA AAT GCA TGG GGC CAC CCA GCT CCG CGG CGG CCT ACA GCC	384
Glu Ala Gly Asn Ala Trp Gly His Pro Ala Pro Arg Arg Pro Thr Ala	
115 120 125	
GGG GTA GCC CAA GAA CTT CGG GTG AGG GCG GGT GGC ATT TCT TTT CCT	432
Gly Val Ala Gln Glu Leu Arg Val Arg Ala Gly Gly Ile Ser Phe Pro	
130 135 140	
ATA CCG ATC ATG GCA GTC CTT CTG CTC CTA CTC GTG GTG GAG CCG GGG	480
Ile Pro Ile Met Ala Val Leu Leu Leu Leu Val Val Glu Pro Gly	
145 150 155 160	
CTA TTT TAG CCC CGG CCA CCC ATG CTT GTA GCG CGA AAG GGC AAT ATT	528
Leu Phe * Pro Arg Pro Pro Met Leu Val Ala Arg Lys Gly Asn Ile	
165 170 175	
TSC TCA CAA ACT GTT GCG CCC TGG AGG ACA TAG GCT TCT GCC TGG AGG	576
Xaa Ser Gln Thr Val Ala Pro Trp Arg Thr * Ala Ser Ala Trp Arg	
180 185 190	
GCG GAT GCC TGG TGG CTC TGG GGT GCA CCA TTT GCA CCG ACC GCT GCT	624
Ala Asp Ala Trp Trp Leu Trp Gly Ala Pro Phe Ala Pro Thr Ala Ala	
195 200 205	
GGC CAC TGT ATC AGG CGG GTT TGG CCG TGC GGC CCG GCA AGT CCG CCG	672
Gly His Cys Ile Arg Arg Val Trp Pro Cys Gly Pro Ala Ser Pro Pro	
210 215 220	
CCC AGT TGG TGG GGG AAC TCG GTA GTC TCT ACG GGC CCT TGT CGG TCT	720
Pro Ser Trp Trp Gly Asn Ser Val Val Ser Thr Gly Pro Cys Arg Ser	
225 230 235 240	
CGG CTT ATG TGG CCG GGA TCC TGG GGC TTG GGG AGG TCT ACT CGG GGG	768
Arg Leu Met Trp Pro Gly Ser Trp Gly Leu Gly Arg Ser Thr Arg Gly	
245 250 255	
TCC TCA CCG TCG GGG TGG CGT TGA CGC GCA GGG TCT ACC CGG TCC CGA	816
Ser Ser Pro Ser Gly Trp Arg * Arg Ala Gly Ser Thr Arg Ser Arg	
260 265 270	
ACC TGA CGT GTG CAG TAG AGT GTG AGT TGA AGT GGG AAA GTG AGT TTT	864
Thr * Arg Val Gln * Ser Val Ser * Ser Gly Lys Val Ser Phe	
275 280 285	
GGA GAT GGA CTG AAC AGC TGG CCT CAA ACT ACT GGA TTC TGG AAT ACC	912
Gly Asp Gly Leu Asn Ser Trp Pro Gln Thr Thr Gly Phe Trp Asn Thr	
290 295 300	
TCT GGA AGG TGC CTT TCG ACT TTT GGC GGG GAG TGA TGA GCC TTA CTC	960

485

Ser Gly Arg Cys Leu Ser Thr Phe Gly Gly Glu * * Ala Leu Leu	
305 310 315 320	
CTC TCT TGG TGT GCG TGG CGG CCC TCC TCC TGC TGG AGC AGC GTA TTG	1008
Leu Ser Trp Cys Ala Trp Arg Pro Ser Ser Cys Trp Ser Ser Val Leu	
325 330 335	
TCA TGG TCT TCC TCC TGG TCA CTA TGG CGG GCA TGT CGC AAG GCG CGC	1056
Ser Trp Ser Ser Ser Trp Ser Leu Trp Arg Ala Cys Arg Lys Ala Arg	
340 345 350	
CCG CCT CAA GTG TTG GGG TCA CGG CCT TTC GAG GCG GGT TTG ACT TGG	1104
Pro Pro Gln Val Leu Gly Ser Arg Pro Phe Glu Ala Gly Leu Thr Trp	
355 360 365	
CAG TCT TGT TCT TGC AGG TCG AAC GGG TCC CGC GTG CCG ACA GGG AGA	1152
Gln Ser Cys Ser Cys Arg Ser Asn Gly Ser Arg Val Pro Thr Gly Arg	
370 375 380	
GGG TTT GGG AAC GTG GGA ACG TCA CAC TTT TGT GTG ACT GCC CCA ACG	1200
Gly Phe Gly Asn Val Gly Thr Ser His Phe Cys Val Thr Ala Pro Thr	
385 390 395 400	
GTC CTT GGG TGT GGG TCC CGG CCC TTT GCC AGG CAA TCG GAT GGG GCG	1248
Val Leu Gly Cys Gly Ser Arg Pro Phe Ala Arg Gln Ser Asp Gly Ala	
405 410 415	
ACC CTA TCA CTC ATT GGA GCC ACG GAC AAA ATC AGT GGC CCC TTT CTT	1296
Thr Leu Ser Leu Ile Gly Ala Thr Asp Lys Ile Ser Gly Pro Phe Leu	
420 425 430	
GTC CCC AAT TTG TCT ACG GCG CCG TTT CAG TGA CCT GCG TGT GGG GTT	1344
Val Pro Asn Leu Ser Thr Ala Pro Phe Gln * Pro Ala Cys Gly Val	
435 440 445	
CTG TGT CTT GGT TTG CTT CCA CTG GGG GTC GCG ACT CCA AGG TTG ATG	1392
Leu Cys Leu Gly Leu Leu Pro Leu Gly Val Ala Thr Pro Arg Leu Met	
450 455 460	
TGT GGA GTT TGG TTC CAG TTG GCT CTG CCA GCT GCA CCA TAG CCG CAC	1440
Cys Gly Val Trp Phe Gln Leu Ala Leu Pro Ala Ala Pro * Pro His	
465 470 475 480	
TGG GAT CTT CGG ATC GCG ACA CAG TGG TTG AGC TCT CCG AGT GGG GAA	1488
Trp Asp Leu Arg Ile Ala Thr Gln Trp Leu Ser Ser Pro Ser Gly Glu	
485 490 495	
TTC CCT GCG CCA CTT GTA TCC TGG ACA GGC GGC CTG CCT CGT GTG GCA	1536
Phe Pro Ala Pro Leu Val Ser Trp Thr Gly Gly Leu Pro Arg Val Ala	
500 505 510	
CCT GTG TGA GGG ACT GCT GGC CCG AGA CCG GGT CCG TAC GTT TCC CAT	1584
Pro Val * Gly Thr Ala Gly Pro Arg Pro Gly Arg Tyr Val Ser His	
515 520 525	
TCC ACA GGT GTG GCG CGG GAC CGA GGC TGA CCA GAG ACC TTG AGG CTG	1632
Ser Thr Gly Val Ala Arg Asp Arg Gly * Pro Glu Thr Leu Arg Leu	

486

530	535	540	
TGC CCT TCG TCA ATA GGA CAA CTC CCT TCA CCA TAA GGG GGC CCC TGG Cys Pro Ser Ser Ile Gly Gln Leu Pro Ser Pro * Gly Gly Pro Trp 545 550 555 560			1680
GCA ACC AGG GGC GAG GCA ACC CGG TGC GGT CGC CCT TGG GTT TTG GGT Ala Thr Arg Gly Glu Ala Thr Arg Cys Gly Arg Pro Trp Val Leu Gly 565 570 575			1728
CCT ACA CCA TGA CCA AGA TCC GAG ACT CCT TAC ACT TGG TGA AAT GTC Pro Thr Pro * Pro Arg Ser Glu Thr Pro Tyr Thr Trp * Asn Val 580 585 590			1776
CCA CCC CAG CCA TTG AGC CTC CCA CCG GAA CGT TTG GGT TCT TCC CAG Pro Pro Gln Pro Leu Ser Leu Pro Pro Glu Arg Leu Gly Ser Ser Gln 595 600 605			1824
GAG TCC CCC CCC TTA ACA ACT GCA TGC TTC TCG GCA CTG AGG TGT CAG Glu Ser Pro Pro Leu Thr Thr Ala Cys Phe Ser Ala Leu Arg Cys Gln 610 615 620			1872
AGG TAT TGG GTG GGG CGG GCC TCA CTG GGG GGT TTT ACG AAC CTC TGG Arg Tyr Trp Val Gly Arg Ala Ser Leu Gly Gly Phe Thr Asn Leu Trp 625 630 635 640			1920
TGC GGC GGT GTT CAG AGC TGA TGG GTC GGC GGA ATC CGG TCT GCC CGG Cys Gly Gly Val Gln Ser * Trp Val Gly Gly Ile Arg Ser Ala Arg 645 650 655			1968
GGT TTG CAT GGC TCT CTT CGG GAC GGC CTG ATG GGT TCA TAC ATG TTC Gly Leu His Gly Ser Leu Arg Asp Gly Leu Met Gly Ser Tyr Met Phe 660 665 670			2016
AGG GCC ACT TGC AGG AGG TGG ATG CGG GCA ACT TCA TTC CGC CCC CAC Arg Ala Thr Cys Arg Arg Trp Met Arg Ala Thr Ser Phe Arg Pro His 675 680 685			2064
GCT GGT TGC TCT TGG ACT TTG TAT TTG TCC TGT TAT ACC TGA TGA AGC Ala Gly Cys Ser Trp Thr Leu Tyr Leu Ser Cys Tyr Thr * * Ser 690 695 700			2112
TGG CAG AGG CAC GGT TGG TCC CGC TGA TCC TCC TCC TGC TAT GGT GGT Trp Gln Arg His Gly Trp Ser Arg * Ser Ser Ser Cys Tyr Gly Gly 705 710 715 720			2160
GGG TGA ACC AGT TGG CGG TCC TTG KTG TGS CGG CTG CKC RCG CCG CCG Gly * Thr Ser Trp Arg Ser Leu Xaa Xaa Arg Leu Xaa Xaa Pro Pro 725 730 735			2208
TGG CTG GAG AGG TGT TTG CGG GCC CTG CCT TGT CCT GGT GTC TGG GCC Trp Leu Glu Arg Cys Leu Arg Ala Leu Pro Cys Pro Gly Val Trp Ala 740 745 750			2256
TAC CCT TCG TGA GTA TGA TCC TGG GGC TAG CAA ACC TGG TGT TGT ACT Tyr Pro Ser * Val * Ser Trp Gly * Gln Thr Trp Cys Cys Thr 755 760 765			2304

487

TCC GCT GGA TGG GTC CTC AAC GCC TGA TGT TCC TCG TGT TGT GGA AGC Ser Ala Gly Trp Val Leu Asn Ala * Cys Ser Ser Cys Cys Gly Ser 770 775 780	2352
TCG CTC GGG GGG CTT TCC CGC TGG CAT TAC TGA TGG GGA TTT CCG CCA Ser Leu Gly Gly Leu Ser Arg Trp His Tyr * Trp Gly Phe Pro Pro 785 790 795 800	2400
CTC GCG GCC GCA CCT CTG TGC TTG GCG CCG AAT TCT GCT TTG ATG TCA Leu Ala Ala Ala Pro Leu Cys Leu Ala Pro Asn Ser Ala Leu Met Ser 805 810 815	2448
CCT TTG AAG TGG ACA CGT CAG TCT TGG GTT GGG TGG TTG CTA GTG TGG Pro Leu Lys Trp Thr Arg Gln Ser Trp Val Gly Trp Leu Leu Val Trp 820 825 830	2496
TGG CTT GGG CCA TAG CGC TCC TGA GCT CTA TGA GCG CGG GGG GGT GGA Trp Leu Gly Pro * Arg Ser * Ala Leu * Ala Arg Gly Gly Gly 835 840 845	2544
AGC ACA AAG CCA TAA TCT ATA GGA CGT GGT GTA AAG GGT ACC AGG CYC Ser Thr Lys Pro * Ser Ile Gly Arg Gly Val Lys Gly Thr Arg Xaa 850 855 860	2592
TTC GCC AGC GCG TGG TGC GTA GCC CCC TCG GGG AGG GGC GGC CCA CCA Phe Ala Ser Ala Trp Cys Val Ala Pro Ser Gly Arg Gly Gly Pro Pro 865 870 875 880	2640
AGC CGC TGA CGA TAG CCT GGT GTC TGG CCT CTT ACA TCT GGC CGG ACG Ser Arg * Arg * Pro Gly Val Trp Pro Leu Thr Ser Gly Arg Thr 885 890 895	2688
CTG TGA TGT TGG TGG TTG TGG CCA TGG TCC TCC TCT TCG GCC TTT TCG Leu * Cys Trp Trp Leu Trp Pro Trp Ser Ser Ser Ser Ala Phe Ser 900 905 910	2736
ACG CGC TCG ATT GGG CCT TGG AGG AGC TCC TTG TGT CGC GGC CTT CGT Thr Arg Ser Ile Gly Pro Trp Arg Ser Ser Leu Cys Arg Gly Leu Arg 915 920 925	2784
TGC GTC GTT TGG CAA GGG TGG TGG AGT GTT GTG TGA TGG CGG GCG AGA Cys Val Val Trp Gln Gly Trp Trp Ser Val Val * Trp Arg Ala Arg 930 935 940	2832
AGG CCA CTA CCG TCC GGC TTG TGT CCA AGA TGT GCG CGA GAG GGG CCT Arg Pro Leu Pro Ser Gly Leu Cys Pro Arg Cys Ala Arg Glu Gly Pro 945 950 955 960	2880
ACC TGT TTG ACC ACA TGG GGT CGT TCT CGC GCG CGG TCA AGG AGC GCT Thr Cys Leu Thr Thr Trp Gly Arg Ser Arg Ala Arg Ser Arg Ser Ala 965 970 975	2928
TGC TGG AGT GGG ACG CGG CTT TGG AGM CCC TGT CAT TCA CTA GGA CGG Cys Trp Ser Gly Thr Arg Leu Trp Xaa Pro Cys His Ser Leu Gly Arg 980 985 990	2976
ACT GTC GCA TCA TAC GAG ACG CCG CCA GGA CCC TGA GCT GCG GCC AAT	3024

488

Thr Val Ala Ser Tyr Glu Thr Pro Pro Gly Pro * Ala Ala Ala Asn	
995 1000 1005	
GCG TCA TGG GCT TGC CCG TGG TGG CTA GGC GCG GCG ATG AGG TCC TGA	3072
Ala Ser Trp Ala Cys Pro Trp Trp Leu Gly Ala Ala Met Arg Ser *	
1010 1015 1020	
TTG GGG TCT TTC AGG ATG TGA ACC ACT TGC CTC CCG GGT TTG YTC CTA	3120
Leu Gly Ser Phe Arg Met * Thr Thr Cys Leu Arg Gly Leu Xaa Leu	
1025 1030 1035 1040	
CAG CGC CTG TTG TCA TCC GTC GGT GCG GAA AGG GCT TCC TCG GGG TCA	3168
Gln Arg Leu Leu Ser Ser Val Gly Ala Glu Arg Ala Ser Ser Gly Ser	
1045 1050 1055	
CTA AGG CTG CCT TGA CTG GTC GGG ATC CTG ACT TAC ACC CAG GAA ACG	3216
Leu Arg Leu Pro * Leu Val Gly Ile Leu Thr Tyr Thr Gln Glu Thr	
1060 1065 1070	
TCA TGG TTT TGG GGA CGG CTA CCT CGC GCA GCA TGG GAA CGT GCT TAA	3264
Ser Trp Phe Trp Gly Arg Leu Pro Arg Ala Ala Trp Glu Arg Ala *	
1075 1080 1085	
ACG GGT TGC TGT TCA CGA CAT TCC ATG GGG CTT CTT CCC GAA CCA TTG	3312
Thr Gly Cys Cys Ser Arg His Ser Met Gly Leu Leu Pro Glu Pro Leu	
1090 1095 1100	
CGA CAC CTG TGG GGG CCC TTA ACC CAA GGT GGT GGT CGG CCA GTG ATG	3360
Arg His Leu Trp Gly Pro Leu Thr Gln Gly Gly Gly Arg Pro Val Met	
1105 1110 1115 1120	
ACG TCA CGG TCT ATC CCC TCC CCG ATG GAG CTA ACT CGT TGG TTC CCT	3408
Thr Ser Arg Ser Ile Pro Ser Pro Met Glu Leu Thr Arg Trp Phe Pro	
1125 1130 1135	
GCT CGT GTC AGG CTG AGT CCT GTT GGG TCA TYC GAT CCG ATG GGG CTC	3456
Ala Arg Val Arg Leu Ser Pro Val Gly Ser Xaa Asp Pro Met Gly Leu	
1140 1145 1150	
TTT GCC ATG GCT TGA GCA AGG GGG ACA AGG TAG AAC TGG ACG TGG CCA	3504
Phe Ala Met Ala * Ala Arg Gly Thr Arg * Asn Trp Thr Trp Pro	
1155 1160 1165	
TGG AGG TTG CTG ACT TTC GTG GGT CGT CTG GGT CTC CTG TCC TAT GCG	3552
Trp Arg Leu Leu Thr Phe Val Gly Arg Leu Gly Leu Leu Ser Tyr Ala	
1170 1175 1180	
ACG AGG GGC ACG CTG TAG GAA TGC TCG TGT CCG TCC TTC ATT CGG GGG	3600
Thr Arg Gly Thr Leu * Glu Cys Ser Cys Pro Ser Phe Ile Arg Gly	
1185 1190 1195 1200	
GGA GGG TGA CCG CGG CTC GAT TCA CTC GGC CGT GGA CCC AAG TCC CAA	3648
Gly Gly * Pro Arg Leu Asp Ser Leu Gly Arg Gly Pro Lys Ser Gln	
1205 1210 1215	
CAG ACG CCA AGA CTA CCA CTG AGC CAC CCC CGG TGC CAG CTA AAG GGG	3696
Gln Thr Pro Arg Leu Pro Leu Ser His Pro Arg Cys Gln Leu Lys Gly	

489

1220	1225	1230	
TTT TCA AAG AGG CTC CTC TTT TCA TGC CAA CAG GGG CGG GGA AAA GCA Phe Ser Lys Arg Leu Leu Phe Ser Cys Gln Gln Gly Arg Gly Lys Ala 1235 1240 1245			3744
CAC GCG TCC CTT TGG AGT ATG GAA ACA TGG GGC ACA AGG TCC TGA TTC His Ala Ser Leu Trp Ser Met Glu Thr Trp Gly Thr Arg Ser * Phe 1250 1255 1260			3792
TCA ACC CGT CGG TTG CCA CTG TGA GGG CCA TGG GCC CTT ACA TGG AGA Ser Thr Arg Arg Leu Pro Leu * Gly Pro Trp Ala Leu Thr Trp Arg 1265 1270 1275 1280			3840
GGC TGG CGG GGA AAC ATC CTA GCA TTT TCT GTG GAC ACG ACA CAA CAG Gly Trp Arg Gly Asn Ile Leu Ala Phe Ser Val Asp Thr Thr Gln Gln 1285 1290 1295			3888
CTT TCA CAC GGA TCA CGG ACT CTC CAT TGA CGT ACT CTA CCT ATG GGA Leu Ser His Gly Ser Arg Thr Leu His * Arg Thr Leu Pro Met Gly 1300 1305 1310			3936
GGT TTC TGG CCA ACC CGA GGC AGA TGC TGA GGG GAG TTT CCG TGG TCA Gly Phe Trp Pro Thr Arg Gly Arg Cys * Gly Glu Phe Pro Trp Ser 1315 1320 1325			3984
TCT GTG ATG AGT GCC ACA GTC ATG ACT CAA CTG TGT TGC TGG GTA TAG Ser Val Met Ser Ala Thr Val Met Thr Gln Leu Cys Cys Trp Val * 1330 1335 1340			4032
GCA GGG TCA GGG ACG TGG CGC GGG GGT GTG GAG TGC AAT TAG TGC TCT Ala Gly Ser Gly Thr Trp Arg Gly Gly Val Glu Cys Asn * Cys Ser 1345 1350 1355 1360			4080
ACG CTA CTG CGA CTC CCC CGG GCT CGC CTA TGA CTC AGC ATC CAT CCA Thr Leu Leu Arg Leu Pro Arg Ala Arg Leu * Leu Ser Ile His Pro 1365 1370 1375			4128
TAA TTG AGA CAA AGC TGG ACG TTG GTG AGA TCC CCT TTT ATG GGC ATG * Leu Arg Gln Ser Trp Thr Leu Val Arg Ser Pro Phe Met Gly Met 1380 1385 1390			4176
GTA TCC CCC TCG AGC GTA TGA GGA CTG GTC GCC ACC TTG TAT TCT GCC Val Ser Pro Ser Ser Val * Gly Leu Val Ala Thr Leu Tyr Ser Ala 1395 1400 1405			4224
ATT CCA AGG CGG AGT GCG AGA GAT TGG CCG GCC AGT TCT CCG CGC GGG Ile Pro Arg Arg Ser Ala Arg Asp Trp Pro Ala Ser Ser Pro Arg Gly 1410 1415 1420			4272
GGG TTA ATG CCA TCG CCT ATT ATA GGG GTA AGG ACA GTT CCA TCA TCA Gly Leu Met Pro Ser Pro Ile Ile Gly Val Arg Thr Val Pro Ser Ser 1425 1430 1435 1440			4320
AAG ACG GAG ACC TGG TGG TTT GTG CGA CAG ACG CGC TCT CTA CCG GGT Lys Thr Glu Thr Trp Trp Phe Val Arg Gln Thr Arg Ser Leu Pro Gly 1445 1450 1455			4368

490

ACA CAG GAA ACT TCG ATT CTG TCA CCG ACT GTG GGT TGG TGG TGG AGG Thr Gln Glu Thr Ser Ile Leu Ser Pro Thr Val Gly Trp Trp Trp Arg 1460 1465 1470	4416
AGG TCG TTG AGG TGA CCC TTG ATC CCA CCA TTA CCA TTT CCT TGC GGA Arg Ser Leu Arg * Pro Leu Ile Pro Pro Leu Pro Phe Pro Cys Gly 1475 1480 1485	4464
CTG TCC CTG CTT CGG CTG AAT TGT CGA TGC AGC GGC GCG GAC GCA CGG Leu Ser Leu Leu Arg Leu Asn Cys Arg Cys Ser Gly Ala Asp Ala Arg 1490 1495 1500	4512
GGA GAG GTC GGT CGG GCC GCT ACT ACT ACG CTG GGG TCG GTA AGG CTC Gly Glu Val Gly Arg Ala Ala Thr Thr Thr Leu Gly Ser Val Arg Leu 1505 1510 1515 1520	4560
CCG CGG GGG TGG TGC GGT CTG GTC CGG TCT GGT CGG CAG TGG AAG CTG Pro Arg Gly Trp Cys Gly Leu Val Arg Ser Gly Arg Gln Trp Lys Leu 1525 1530 1535	4608
GAG TGA CCT GGT ATG GAA TGG AAC CTG ACT TGA CAG CAA ACC TTC TGA Glu * Pro Gly Met Glu Trp Asn Leu Thr * Gln Gln Thr Phe * 1540 1545 1550	4656
GAC TTT ACG ACG ACT GCC CTT ACA CCG CAG CCG TCG CAG CTG ACA TTG Asp Phe Thr Thr Thr Ala Leu Thr Pro Gln Pro Ser Gln Leu Thr Leu 1555 1560 1565	4704
GTG AAG CCG CGG TGT TCT TTG CGG GCC TCG CGC CCC TCA GGA TGC ATC Val Lys Pro Arg Cys Ser Leu Arg Ala Ser Arg Pro Ser Gly Cys Ile 1570 1575 1580	4752
CCG ATG TTA GCT GGG CAA AAG TTC GCG GCG TCA ATT GGC CCC TCC TGG Pro Met Leu Ala Gly Gln Lys Phe Ala Ala Ser Ile Gly Pro Ser Trp 1585 1590 1595 1600	4800
TGG GTG TTC AGC GGA CGA TGT GTC GGG AAA CAC TGT CTC CCG GCC CGT Trp Val Phe Ser Gly Arg Cys Val Gly Lys His Cys Leu Pro Ala Arg 1605 1610 1615	4848
CGG ACG ACC CTC AGT GGG CAG GTC TGA AAG GCC CGA ATC CTG TCC CAC Arg Thr Thr Leu Ser Gly Gln Val * Lys Ala Arg Ile Leu Ser His 1620 1625 1630	4896
TAC TGC TGA GGT GGG GCA ATG ATT TGC CAT CAA AAG TGG CCG GCC ACC Tyr Cys * Gly Gly Ala Met Ile Cys His Gln Lys Trp Pro Ala Thr 1635 1640 1645	4944
ACA TAG TTG ACG ATC TGG TCC GTC GGC TCG GTG TGG CGG AGG GAT ACG Thr * Leu Thr Ile Trp Ser Val Gly Ser Val Trp Arg Arg Asp Thr 1650 1655 1660	4992
TGC GCT GTG ATG CTG GRC CCA TCC TCA TGG TGG GCT TGG CCA TAG CGG Cys Ala Val Met Leu Xaa Pro Ser Ser Trp Trp Ala Trp Pro * Arg 1665 1670 1675 1680	5040
GCG GCA TGA TCT ACG CCT CTT ACA CTG GGT CGC TAG TGG TGG TAA CAG	5088

491

Ala Ala * Ser Thr Pro Leu Thr Leu Gly Arg * Trp Trp * Gln	
1685 1690 1695	
ACT GGG ATG TGA AGG GAG GTG GCA ATC CCC TTT ATA GGA GTG GTG ACC	5136
Thr Gly Met * Arg Glu Val Ala Ile Pro Phe Ile Gly Val Val Thr	
1700 1705 1710	
AGG CCA CCC CTC AAC CCG TGG TGC AGG TCC CCC CGG TAG ACC ATC GGC	5184
Arg Pro Pro Leu Asn Pro Trp Cys Arg Ser Pro Arg * Thr Ile Gly	
1715 1720 1725	
CGG GGG GGG AGT CTG CGC CAC GGG ATG CCA AGA CAG TGA CAG ATG CGG	5232
Arg Gly Gly Ser Leu Arg His Gly Met Pro Arg Gln * Gln Met Arg	
1730 1735 1740	
TGG CAG CCA TCC AGG TGA ACT GCG ATT GGT CTG TGA TGA CCC TGT CGA	5280
Trp Gln Pro Ser Arg * Thr Ala Ile Gly Leu * * Pro Cys Arg	
1745 1750 1755 1760	
TCG GGG AAG TCC TCA CCT TGG CTC AGG CTA AGA CAG CCG AGG CCT ACG	5328
Ser Gly Lys Ser Ser Pro Trp Leu Arg Leu Arg Gln Pro Arg Pro Thr	
1765 1770 1775	
CAG CTA CTT CCA GGT GGC TCG CTG GCT GCT ACA CGG GGA CGC GGG CCG	5376
Gln Leu Leu Pro Gly Gly Ser Leu Ala Ala Thr Arg Gly Arg Gly Pro	
1780 1785 1790	
TCC CCA CTG TAT CAA TTG TTG ACA AGC TCT TCG CCG GGG GTT GGG CCG	5424
Ser Pro Leu Tyr Gln Leu Leu Thr Ser Ser Ser Pro Gly Val Gly Pro	
1795 1800 1805	
CCG TGG TGG GTC ACT GTC ACA GCG TCA TTG CTG CGG CGG TGG CTG CCT	5472
Pro Trp Trp Val Thr Val Thr Ala Ser Leu Leu Arg Arg Trp Leu Pro	
1810 1815 1820	
ATG GAG CTT CTC GAA GTC CTC CAC TGG CCG CGG CGG CGT CCT ACC TCA	5520
Met Glu Leu Leu Glu Val Leu His Trp Pro Arg Arg Arg Pro Thr Ser	
1825 1830 1835 1840	
TGG GGT TGG GCG TCG GAG GCA ACG CAC AGG CGC GCT TGG CTT CAG CTC	5568
Trp Gly Trp Ala Ser Glu Ala Thr His Arg Arg Ala Trp Leu Gln Leu	
1845 1850 1855	
TTC TAC TGG GGG CTG CTG GTA CGG CTC TGG GGA CCC CTG TCG TGG GAC	5616
Phe Tyr Trp Gly Leu Leu Val Arg Leu Trp Gly Pro Leu Ser Trp Asp	
1860 1865 1870	
TCA CCA TGG CGG GGG CCT TCA TGG GCG GTG CCA GCG TGT CCC CCT CCC	5664
Ser Pro Trp Arg Gly Pro Ser Trp Ala Val Pro Ala Cys Pro Pro Pro	
1875 1880 1885	
TCG TCA CTG TCC TAC TTG GGG CTG TGG GAG GTT GGG AGG GCG TTG TCA	5712
Ser Ser Leu Ser Tyr Leu Gly Leu Trp Glu Val Gly Arg Ala Leu Ser	
1890 1895 1900	
ACG CTG CCA GTC TCG TCT TCG ACT TCA TGG CTG GGA AAC TTT CAA CAG	5760
Thr Leu Pro Val Ser Ser Ser Thr Ser Trp Leu Gly Asn Phe Gln Gln	

492

1905	1910	1915	1920	
AAG ACC TTT GGT ATG CCA TCC CGG TAC TCA CTA GTC CTG GRG CGG GCC				5808
Lys Thr Phe Gly Met Pro Ser Arg Tyr Ser Leu Val Leu Xaa Arg Ala				
	1925	1930	1935	
TCG CGG GGA TTG CCC TTG GTC TGG TTT TGT ACT CAG CAA ACA ACT CTG				5856
Ser Arg Gly Leu Pro Leu Val Trp Phe Cys Thr Gln Gln Thr Thr Leu				
	1940	1945	1950	
GCA CTA CCA CAT GGC TGA ACC GTC TGC TGA CGA CGT TGC CAC GGT CAT				5904
Ala Leu Pro His Gly * Thr Val Cys * Arg Arg Cys His Gly His				
	1955	1960	1965	
CTT GCA TAC CCG ACA GCT ACT TCC AAC AGG CTG ACT ACT GCG ACA AGG				5952
Leu Ala Tyr Pro Thr Ala Thr Ser Asn Arg Leu Thr Thr Ala Thr Arg				
	1970	1975	1980	
TCT CGG CAA TCG TGC GCC GCC TGA GCC TTA CTC GCA CCG TGG TGG CCC				6000
Ser Arg Gln Ser Cys Ala Ala * Ala Leu Leu Ala Pro Trp Trp Pro				
	1985	1990	1995	2000
TGG TCA ACA GGG AGC CTA AGG TGG ATG AGG TCC AGG TGG GGT ACG TCT				6048
Trp Ser Thr Gly Ser Leu Arg Trp Met Arg Ser Arg Trp Gly Thr Ser				
	2005	2010	2015	
GGG ATC TGT GGG AGT GGG TGA TGC GCC AGG TGC GCA TGG TGA TGT CTA				6096
Gly Ile Cys Gly Ser Gly * Cys Ala Arg Cys Ala Trp * Cys Leu				
	2020	2025	2030	
GAC TCC GGG CCC TCT GCC CTG TGG TGT CAC TCC CCT TGT GGC ACT GCG				6144
Asp Ser Gly Pro Ser Ala Leu Trp Cys His Ser Pro Cys Gly Thr Ala				
	2035	2040	2045	
GGG AGG GGT GGT CCG GTG AAT GGC TTC TCG ATG GGC ACG TGG AGA GTC				6192
Gly Arg Gly Gly Pro Val Asn Gly Phe Ser Met Gly Thr Trp Arg Val				
	2050	2055	2060	
GTT GTC TGT GCG GGT GTG TAA TCA CCG GCG ACG TCC TCA ATG GGC AAC				6240
Val Val Cys Ala Gly Val * Ser Pro Ala Thr Ser Ser Met Gly Asn				
	2065	2070	2075	2080
TCA AAG ATC CAG TTT ACT CTA CCA AGC TGT GCA GGC ACT ACT GGA TGG				6288
Ser Lys Ile Gln Phe Thr Leu Pro Ser Cys Ala Gly Thr Thr Gly Trp				
	2085	2090	2095	
GAA CTG TGC CGG TCA ACA TGC TGG GCT ACG GGG AAA CCT CAC CTC TTC				6336
Glu Leu Cys Arg Ser Thr Cys Trp Ala Thr Gly Lys Pro His Leu Phe				
	2100	2105	2110	
TCG CCT CTG ACA CCC CGA AGG TGG TAC CCT TCG GGA CGT CGG GGT GGG				6384
Ser Pro Leu Thr Pro Arg Arg Trp Tyr Pro Ser Gly Arg Arg Gly Gly				
	2115	2120	2125	
CTG AGG TGG TGG TGA CCC CTA CCC ACG TGG TGA TCA GGC GCA CGT CCT				6432
Leu Arg Trp Trp * Pro Leu Pro Thr Trp * Ser Gly Ala Arg Pro				
	2130	2135	2140	

GTT ACA AAC TGC TTT GCC AGC AAA TTC TTT CAG CAG CTG TAG CTG AGC	6480
Val Thr Asn Cys Phe Ala Ser Lys Phe Phe Gln Gln Leu * Leu Ser	
2145 2150 2155 2160	
CCT ACT ACG TTG ATG GCA TTC CGG TCT CTT GGG AGG CTG ACG CGA GAG	6528
Pro Thr Thr Leu Met Ala Phe Arg Ser Leu Gly Arg Leu Thr Arg Glu	
2165 2170 2175	
CGC CGG CCA TGG TCT ACG GTC CGG GCC AAA GTG TTA CCA TTG ATG GGG	6576
Arg Arg Pro Trp Ser Thr Val Arg Ala Lys Val Leu Pro Leu Met Gly	
2180 2185 2190	
AGC GCT ACA CCC TTC CGC ACC AGT TGC GGA TGC GGA ATG TGG CGC CCT	6624
Ser Ala Thr Pro Phe Arg Thr Ser Cys Gly Cys Gly Met Trp Arg Pro	
2195 2200 2205	
CTG AGG TTT CAT CTG AGG TCA GCA TCG AGA TCG GGA CGG AGA CTG AAG	6672
Leu Arg Phe His Leu Arg Ser Ala Ser Arg Ser Gly Arg Arg Leu Lys	
2210 2215 2220	
ACT CAG AAC TGA CTG AGG CCG ATT TGC CAC CAG CGG CTG CTG CCC TCC	6720
Thr Gln Asn * Leu Arg Pro Ile Cys His Gln Arg Leu Leu Pro Ser	
2225 2230 2235 2240	
AAG CGA TAG AGA ATG CTG CGA GAA TTC TCG AAC CGC ACA TCG ATG TCA	6768
Lys Arg * Arg Met Leu Arg Glu Phe Ser Asn Arg Thr Ser Met Ser	
2245 2250 2255	
YCA TGG AGG ATT GCA GTA CAC CCT CTC TCT GTG GTA GTA GCC GAG AGA	6816
Xaa Trp Arg Ile Ala Val His Pro Leu Ser Val Val Val Ala Glu Arg	
2260 2265 2270	
TGC CTG TGT GGG GAG AAG ACA TAC CCC GCA CTC CAT CGC CTG CAC TTA	6864
Cys Leu Cys Gly Glu Lys Thr Tyr Pro Ala Leu His Arg Leu His Leu	
2275 2280 2285	
TCT CGG TTA CGG AGA GCA GCT CAG ATG AGA AGA CCC TGT CGG TGA CCT	6912
Ser Arg Leu Arg Arg Ala Ala Gln Met Arg Arg Pro Cys Arg * Pro	
2290 2295 2300	
CCT CGC AGG AGG ACA CCC CGT CCT CAG ACT CAT TTG AAG TCA TCC AAG	6960
Pro Arg Arg Arg Thr Pro Arg Pro Gln Thr His Leu Lys Ser Ser Lys	
2305 2310 2315 2320	
AGT CTG ATA CTG CTG AAT CAG AGG AAA GCG TCT TCA ACG TGG CTC TTT	7008
Ser Leu Ile Leu Leu Asn Gln Arg Lys Ala Ser Ser Thr Trp Leu Phe	
2325 2330 2335	
CCG TAC TAA AAG CCT TAT TTC CAC AGA GCG ATG CCA CAC GAA AGC TAA	7056
Pro Tyr * Lys Pro Tyr Phe His Arg Ala Met Pro His Glu Ser *	
2340 2345 2350	
CGG TTA AGA TGT CTT GCT GTG TTG AGA AGA GCG TAA CAC GCT TCT TTT	7104
Arg Leu Arg Cys Leu Ala Val Leu Arg Arg Ala * His Ala Ser Phe	
2355 2360 2365	
CTT TAG GGT TGA CCG TGG CTG ACG TGG CTA GCC TGT GTG AGA TGG AGA	7152

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Leu * Gly * Pro Trp Leu Thr Trp Leu Ala Cys Val Arg Trp Arg	
2370 2375 2380	
TCC AGA ACC ATA CAG CCT ATT GTG ACA AGG TGC GCA CTC CGC TCG AAT	7200
Ser Arg Thr Ile Gln Pro Ile Val Thr Arg Cys Ala Leu Arg Ser Asn	
2385 2390 2395 2400	
TGC AAG TTG GGT GCT TGG TGG GCA ATG AAC TTA CCT TTG AAT GTG ACA	7248
Cys Lys Leu Gly Ala Trp Trp Ala Met Asn Leu Pro Leu Asn Val Thr	
2405 2410 2415	
AGT GTG AGG CAC GCC AAG AGA CCC TTG CCT CCT TCT CCT ACA TAT GGT	7296
Ser Val Arg His Ala Lys Arg Pro Leu Pro Pro Ser Pro Thr Tyr Gly	
2420 2425 2430	
CCG GGG TCC CAC TTA CTC GGG CCA CTC CGG CCA AAC CAC CAG TGG TGA	7344
Pro Gly Ser His Leu Leu Gly Pro Leu Arg Pro Asn His Gln Trp *	
2435 2440 2445	
GGC CGG TGG GGT CCT TGT TGG TGG CAG ACA CCA CCA AGG TCT ACG TGA	7392
Gly Arg Trp Gly Pro Cys Trp Trp Gln Thr Pro Pro Arg Ser Thr *	
2450 2455 2460	
CCA ATC CGG ACA ATG TTG GGA GGA GGG TTG ACA AGG TGA CTT TCT GGC	7440
Pro Ile Arg Thr Met Leu Gly Gly Gly Leu Thr Arg * Leu Ser Gly	
2465 2470 2475 2480	
GCG CTC CTC GGG TAC ACG ACA AGT TCC TCG TGG ACT CGA TCG AGC GCG	7488
Ala Leu Leu Gly Tyr Thr Thr Ser Ser Ser Trp Thr Arg Ser Ser Ala	
2485 2490 2495	
CTC GGA GAG CTG CTC AAG GCT GCC TAA GCA TGG GTT ACA CTT ATG AGG	7536
Leu Gly Glu Leu Leu Lys Ala Ala * Ala Trp Val Thr Leu Met Arg	
2500 2505 2510	
AGG CAA TAA GGA CTG TTA GGC CGC ATG CTG CCA TGG GCT GGG GAT CTA	7584
Arg Gln * Gly Leu Leu Gly Arg Met Leu Pro Trp Ala Gly Asp Leu	
2515 2520 2525	
AGG TGT CGG TCA AGG ACT TGG CCA CCC CTG CGG GGA AGA TGG CTG TTC	7632
Arg Cys Arg Ser Arg Thr Trp Pro Pro Leu Arg Gly Arg Trp Leu Phe	
2530 2535 2540	
ATG ACC GGC TTC AGG AGA TAC TTG AAG GGA CTC CGG TCC CTT TTA CCC	7680
Met Thr Gly Phe Arg Arg Tyr Leu Lys Gly Leu Arg Ser Leu Leu Pro	
2545 2550 2555 2560	
TGA CTG TCA AAA AGG AGG TGT TCT TCA AAG ATC GTA AGG AGG AGA AGG	7728
* Leu Ser Lys Arg Arg Cys Ser Ser Lys Ile Val Arg Arg Arg Arg	
2565 2570 2575	
CCC CCC GCC TCA TTG TGT TCC CCC CCC TGG ACT TCC GGA TAG CTG AAA	7776
Pro Pro Ala Ser Leu Cys Ser Pro Pro Trp Thr Ser Gly * Leu Lys	
2580 2585 2590	
AGC TCA TTC TGG GAG ACC CGG GGC GGG TTG CAA AGG CCG GTG TTG GGG	7824
Ser Ser Phe Trp Glu Thr Arg Gly Gly Leu Gln Arg Pro Val Leu Gly	

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2595	2600	2605	
GGG CTT ACG CCT TCC AGT ACA CCC CCA ACC AGC	GGG TTA AGG AGA TGC	7872	
Gly Leu Thr Pro Ser Ser Thr Pro Pro Thr Ser	Gly Leu Arg Arg Cys		
2610	2615	2620	
TAA AGC TGT GGG AAT CAA AGA AGA CCC CGT GCG CCA TCT GTG TGG ATG	7920		
* Ser Cys Gly Asn Gln Arg Arg Pro Arg Ala Pro Ser Val Trp Met			
2625	2630	2635	2640
CCA CTT GCT TCG ACA GTA GCA TTA CTG ARG AGG ACG TGG CAC TAG AGA	7968		
Pro Leu Ala Ser Thr Val Ala Leu Leu Xaa Arg Thr Trp His * Arg			
2645	2650	2655	
CAG AGC TTT ACG CCC TGG CCT CGG ACC ATC CAG AAT GGG TGC GCG CCC	8016		
Gln Ser Phe Thr Pro Trp Pro Arg Thr Ile Gln Asn Gly Cys Ala Pro			
2660	2665	2670	
TGG GGA AAT ACT RTG CCT CTG GCA CAA TGG TGA CCC CGG AAG GGG TGC	8064		
Trp Gly Asn Thr Xaa Pro Leu Ala Gln Trp * Pro Arg Lys Gly Cys			
2675	2680	2685	
CAG TGG GCG AGA GGT ATT GTA GGT CCT CGG GTG TGT TGA CCA CAA GTG	8112		
Gln Trp Ala Arg Gly Ile Val Gly Pro Arg Val Cys * Pro Gln Val			
2690	2695	2700	
CTA GCA ACT GTT TGA CCT GCT ACA TCA AAG TGA GAG CCG CCT GTG AGA	8160		
Leu Ala Thr Val * Pro Ala Thr Ser Lys * Glu Pro Pro Val Arg			
2705	2710	2715	2720
GGA TCG GAC TGA AAA ATG TCT CGC TTC TCA TCG CGG GCG ATG ACT GCT	8208		
Gly Ser Asp * Lys Met Ser Arg Phe Ser Ser Arg Ala Met Thr Ala			
2725	2730	2735	
TAA TTG TGT GCG AGA GGC CTG TAT GCG ACC CTT GCG AGG CCC TGG GCC	8256		
* Leu Cys Ala Arg Gly Leu Tyr Ala Thr Leu Ala Arg Pro Trp Ala			
2740	2745	2750	
GAA CCC TGG CTT CGT ACG GGT ACG CGT GTG AGC CCT CGT ATC ACG CTT	8304		
Glu Pro Trp Leu Arg Thr Gly Thr Arg Val Ser Pro Arg Ile Thr Leu			
2755	2760	2765	
CAC TGG ACA CAG CCC CCT TCT GCT CCA CTT GGC TCG CTG AGT GCA ATG	8352		
His Trp Thr Gln Pro Pro Ser Ala Pro Leu Gly Ser Leu Ser Ala Met			
2770	2775	2780	
CGG ATG GGR AAA GGC ATT TCT TCC TGA CCA CGG ACT TTC GGA GAC CAC	8400		
Arg Met Xaa Lys Gly Ile Ser Ser * Pro Arg Thr Phe Gly Asp His			
2785	2790	2795	2800
TCG CTC GCA TGT CGA GCG AGT ACA GTG ACC CTA TGG CTT CGG CCA TTG	8448		
Ser Leu Ala Cys Arg Ala Ser Thr Val Thr Leu Trp Leu Arg Pro Leu			
2805	2810	2815	
GTT ACA TTC TCC TCT ACC CCT GGC RTC CCA TCA CAC GGT GGG TCA TCA	8496		
Val Thr Phe Ser Ser Thr Pro Gly Xaa Pro Ser His Gly Gly Ser Ser			
2820	2825	2830	

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TCC CGC ATG TGC TAA CAT GCG CTT CTT CCC GGG GTG GTG GCA CAC SGT	8544
Ser Arg Met Cys * His Ala Leu Leu Pro Gly Val Val Ala His Xaa	
2835 2840 2845	
CTG ATC CGG TTT GGT GTC AGG TTC ATG GTA ACT ACT ACA AGT TTC CCC	8592
Leu Ile Arg Phe Gly Val Arg Phe Met Val Thr Thr Ser Phe Pro	
2850 2855 2860	
TGG ACA AAC TGC CTA ACA TCA TCG TGG CCC TCC ACG GAC CAG CAG CGT	8640
Trp Thr Asn Cys Leu Thr Ser Ser Trp Pro Ser Thr Asp Gln Gln Arg	
2865 2870 2875 2880	
TGA GGG TTA CCG CAG ACA CAA CCA AAA CAA AGA TGG AGG CTG GGA AGG	8688
* Gly Leu Pro Gln Thr Gln Pro Lys Gln Arg Trp Arg Leu Gly Arg	
2885 2890 2895	
TTC TGA GCG ACC TCA AGC TCC CTG GTC TAG CCG TCC ACC GCA AGA AGG	8736
Phe * Ala Thr Ser Ser Leu Val * Pro Ser Thr Ala Arg Arg	
2900 2905 2910	
CCG GGG CAT TGC GAA CAC GCA TGC TCC GGT CGC GCG GTT GGG CGG AGT	8784
Pro Gly His Cys Glu His Ala Cys Ser Gly Arg Ala Val Gly Arg Ser	
2915 2920 2925	
TGG CTA GGG GCC TGT TGT GGC ATC CAG GAC TCC GGC TTC CTC CCC CTG	8832
Trp Leu Gly Ala Cys Cys Gly Ile Gln Asp Ser Gly Phe Leu Pro Leu	
2930 2935 2940	
AGA TTG CTG GTA TCC CAG GGG GTT TCC CTC TGT CCC CCC CCT ACA TGG	8880
Arg Leu Leu Val Ser Gln Gly Val Ser Leu Cys Pro Pro Pro Thr Trp	
2945 2950 2955 2960	
GGG TGG TTC ATC AAT TGG ATT TCA CAG CSC AGC GGA GTC GCT GGC GGT	8928
Gly Trp Phe Ile Asn Trp Ile Ser Gln Xaa Ser Gly Val Ala Gly Gly	
2965 2970 2975	
GGT TGG GGT TCT TAG CCC TGC TCA TCG TAG CGC TCT TTG GGT GAA CTA	8976
Gly Trp Gly Ser * Pro Cys Ser Ser * Arg Ser Leu Gly Glu Leu	
2980 2985 2990	
AAT TCA TCT GTT GCG GCC GGA GTC AGA CCT GAG CCC CGT TCA AAA GGG	9024
Asn Ser Ser Val Ala Ala Gly Val Arg Pro Glu Pro Arg Ser Lys Gly	
2995 3000 3005	
GAT TGA GAC	9033
Asp * Asp	
3010	

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

497

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Lys Val Val Asp Gly
1 5

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Val Val Asn Pro Gly His Pro Gly Ser His Tyr Arg Trp Val Leu Arg
1 5 10 15
Gly Gly Tyr Gly Pro Ser Cys Ala Tyr Gly Lys Ala His Gly Pro
20 25 30
Gln Val Leu Val Leu Pro Val
35

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Gly Pro Gly Ala Arg His Ala Val Lys Pro Ser Pro Leu Leu Pro Trp
1 5 10 15
Ala Asn Asp Ala His Val Arg Ser Thr Ser Pro Phe Asn Val Ser Leu
20 25 30
Asp Gln

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

498

```

Ala Tyr Gly Glu Leu Thr Arg Thr Ser Gly Gly Arg Ala Gly Gly Gly
 1           5           10           15
Arg Thr Pro Thr Ala Ala Leu Pro Gly Glu Ala Gly Asn Ala Trp Gly
          20           25           30
His Pro Ala Pro Arg Arg Pro Thr Ala Gly Val Ala Gln Glu Leu Arg
          35           40           45
Val Arg Ala Gly Gly Ile Ser Phe Pro Ile Pro Ile Met Ala Val Leu
          50           55           60
Leu Leu Leu Leu Val Val Glu Pro Gly Leu Phe
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

Pro Arg Pro Pro Met Leu Val Ala Arg Lys Gly Asn Ile Xaa Ser Gln
 1           5           10           15
Thr Val Ala Pro Trp Arg Thr
          20

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

Ala Ser Ala Trp Arg Ala Asp Ala Trp Trp Leu Trp Gly Ala Pro Phe
 1           5           10           15
Ala Pro Thr Ala Ala Gly His Cys Ile Arg Arg Val Trp Pro Cys Gly
          20           25           30
Pro Ala Ser Pro Pro Pro Ser Trp Trp Gly Asn Ser Val Val Ser Thr
          35           40           45
Gly Pro Cys Arg Ser Arg Leu Met Trp Pro Gly Ser Trp Gly Leu Gly
          50           55           60
Arg Ser Thr Arg Gly Ser Ser Pro Ser Gly Trp Arg
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids

499

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Arg Ala Gly Ser Thr Arg Ser Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Ser Gly Lys Val Ser Phe Gly Asp Gly Leu Asn Ser Trp Pro Gln Thr
1 5 10 15
Thr Gly Phe Trp Asn Thr Ser Gly Arg Cys Leu Ser Thr Phe Gly Gly
20 25 30
Glu

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Ala Leu Leu Leu Ser Trp Cys Ala Trp Arg Pro Ser Ser Cys Trp Ser
1 5 10 15
Ser Val Leu Ser Trp Ser Ser Ser Trp Ser Leu Trp Arg Ala Cys Arg
20 25 30
Lys Ala Arg Pro Pro Gln Val Leu Gly Ser Arg Pro Phe Glu Ala Gly
35 40 45
Leu Thr Trp Gln Ser Cys Ser Cys Arg Ser Asn Gly Ser Arg Val Pro
50 55 60
Thr Gly Arg Gly Phe Gly Asn Val Gly Thr Ser His Phe Cys Val Thr
65 70 75 80
Ala Pro Thr Val Leu Gly Cys Gly Ser Arg Pro Phe Ala Arg Gln Ser
85 90 95
Asp Gly Ala Thr Leu Ser Leu Ile Gly Ala Thr Asp Lys Ile Ser Gly
100 105 110
Pro Phe Leu Val Pro Asn Leu Ser Thr Ala Pro Phe Gln

500

115

120

125

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Pro	Ala	Cys	Gly	Val	Leu	Cys	Leu	Gly	Leu	Leu	Pro	Leu	Gly	Val	Ala
1				5					10					15	
Thr	Pro	Arg	Leu	Met	Cys	Gly	Val	Trp	Phe	Gln	Leu	Ala	Leu	Pro	Ala
			20					25					30		
Ala	Pro														

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Pro	His	Trp	Asp	Leu	Arg	Ile	Ala	Thr	Gln	Trp	Leu	Ser	Ser	Pro	Ser
1				5					10					15	
Gly	Glu	Phe	Pro	Ala	Pro	Leu	Val	Ser	Trp	Thr	Gly	Gly	Leu	Pro	Arg
			20					25					30		
Val	Ala	Pro	Val												
			35												

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

501

Gly Thr Ala Gly Pro Arg Pro Gly Arg Tyr Val Ser His Ser Thr Gly
 1 5 10 15
 Val Ala Arg Asp Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Pro Glu Thr Leu Arg Leu Cys Pro Ser Ser Ile Gly Gln Leu Pro Ser
 1 5 10 15
 Pro

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Gly Gly Pro Trp Ala Thr Arg Gly Glu Ala Thr Arg Cys Gly Arg Pro
 1 5 10 15
 Trp Val Leu Gly Pro Thr Pro
 20

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

a

Pro Arg Ser Glu Thr Pro Tyr Thr Trp
 1 5

(2) INFORMATION FOR SEQ ID NO:423:

502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Asn Val Pro Pro Gln Pro Leu Ser Leu Pro Pro Glu Arg Leu Gly Ser
 1           5           10           15
Ser Gln Glu Ser Pro Pro Leu Thr Thr Ala Cys Phe Ser Ala Leu Arg
          20           25           30
Cys Gln Arg Tyr Trp Val Gly Arg Ala Ser Leu Gly Gly Phe Thr Asn
          35           40           45
Leu Trp Cys Gly Gly Val Gln Ser
 50           55

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Trp Val Gly Gly Ile Arg Ser Ala Arg Gly Leu His Gly Ser Leu Arg
 1           5           10           15
Asp Gly Leu Met Gly Ser Tyr Met Phe Arg Ala Thr Cys Arg Arg Trp
          20           25           30
Met Arg Ala Thr Ser Phe Arg Pro His Ala Gly Cys Ser Trp Thr Leu
          35           40           45
Tyr Leu Ser Cys Tyr Thr
 50

```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```

Ser Trp Gln Arg His Gly Trp Ser Arg
 1           5

```

503

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Ser Ser Ser Cys Tyr Gly Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Thr Ser Trp Arg Ser Leu Xaa Xaa Arg Leu Xaa Xaa Pro Pro Trp Leu
1 5 10 15
Glu Arg Cys Leu Arg Ala Leu Pro Cys Pro Gly Val Trp Ala Tyr Pro
20 25 30
Ser

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Gln Thr Trp Cys Cys Thr Ser Ala Gly Trp Val Leu Asn Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Cys Ser Ser Cys Cys Gly Ser Ser Leu Gly Gly Leu Ser Arg Trp His
 1 5 10 15
 Tyr

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Trp Gly Phe Pro Pro Leu Ala Ala Ala Pro Leu Cys Leu Ala Pro Asn
 1 5 10 15
 Ser Ala Leu Met Ser Pro Leu Lys Trp Thr Arg Gln Ser Trp Val Gly
 20 25 30
 Trp Leu Leu Val Trp Trp Leu Gly Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Ala Arg Gly Gly Gly Ser Thr Lys Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Ser Ile Gly Arg Gly Val Lys Gly Thr Arg Xaa Phe Ala Ser Ala Trp
 1 5 10 15
 Cys Val Ala Pro Ser Gly Arg Gly Gly Pro Pro Ser Arg
 20 25

505

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Pro Gly Val Trp Pro Leu Thr Ser Gly Arg Thr Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Cys Trp Trp Leu Trp Pro Trp Ser Ser Ser Ser Ala Phe Ser Thr Arg
 1 5 10 15
 Ser Ile Gly Pro Trp Arg Ser Ser Leu Cys Arg Gly Leu Arg Cys Val
 20 25 30
 Val Trp Gln Gly Trp Trp Ser Val Val
 35 40

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Trp Arg Ala Arg Arg Pro Leu Pro Ser Gly Leu Cys Pro Arg Cys Ala
 1 5 10 15
 Arg Glu Gly Pro Thr Cys Leu Thr Thr Trp Gly Arg Ser Arg Ala Arg
 20 25 30
 Ser Arg Ser Ala Cys Trp Ser Gly Thr Arg Leu Trp Xaa Pro Cys His
 35 40 45
 Ser Leu Gly Arg Thr Val Ala Ser Tyr Glu Thr Pro Pro Gly Pro
 50 55 60

506

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Ala Ala Ala Asn Ala Ser Trp Ala Cys Pro Trp Trp Leu Gly Ala Ala
 1 5 10 15
Met Arg Ser

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Leu Gly Ser Phe Arg Met
 1 5

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Thr Thr Cys Leu Arg Gly Leu Xaa Leu Gln Arg Leu Leu Ser Ser Val
 1 5 10 15
Gly Ala Glu Arg Ala Ser Ser Gly Ser Leu Arg Leu Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

Leu Val Gly Ile Leu Thr Tyr Thr Gln Glu Thr Ser Trp Phe Trp Gly
 1           5           10           15
Arg Leu Pro Arg Ala Ala Trp Glu Arg Ala
      20           25

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Thr Gly Cys Cys Ser Arg His Ser Met Gly Leu Leu Pro Glu Pro Leu
 1           5           10           15
Arg His Leu Trp Gly Pro Leu Thr Gln Gly Gly Gly Arg Pro Val Met
      20           25           30
Thr Ser Arg Ser Ile Pro Ser Pro Met Glu Leu Thr Arg Trp Phe Pro
      35           40           45
Ala Arg Val Arg Leu Ser Pro Val Gly Ser Xaa Asp Pro Met Gly Leu
      50           55           60
Phe Ala Met Ala
      65

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Ala Arg Gly Thr Arg
 1           5

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Asn Trp Thr Trp Pro Trp Arg Leu Leu Thr Phe Val Gly Arg Leu Gly
 1           5           10           15
Leu Leu Ser Tyr Ala Thr Arg Gly Thr Leu

```

508

20

25

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Glu Cys Ser Cys Pro Ser Phe Ile Arg Gly Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Pro	Arg	Leu	Asp	Ser	Leu	Gly	Arg	Gly	Pro	Lys	Ser	Gln	Gln	Thr	Pro
1				5					10					15	
Arg	Leu	Pro	Leu	Ser	His	Pro	Arg	Cys	Gln	Leu	Lys	Gly	Phe	Ser	Lys
			20					25					30		
Arg	Leu	Leu	Phe	Ser	Cys	Gln	Gln	Gly	Arg	Gly	Lys	Ala	His	Ala	Ser
		35				40						45			
Leu	Trp	Ser	Met	Glu	Thr	Trp	Gly	Thr	Arg	Ser					
	50					55									

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Phe Ser Thr Arg Arg Leu Pro Leu
1 5

(2) INFORMATION FOR SEQ ID NO:446:

509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Gly Pro Trp Ala Leu Thr Trp Arg Gly Trp Arg Gly Asn Ile Leu Ala
 1              5              10              15
Phe Ser Val Asp Thr Thr Gln Gln Leu Ser His Gly Ser Arg Thr Leu
      20              25              30
His

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

Arg Thr Leu Pro Met Gly Gly Phe Trp Pro Thr Arg Gly Arg Cys
 1              5              10              15

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

Gly Glu Phe Pro Trp Ser Ser Val Met Ser Ala Thr Val Met Thr Gln
 1              5              10              15
Leu Cys Cys Trp Val
      20

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Ala Gly Ser Gly Thr Trp Arg Gly Gly Val Glu Cys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Cys Ser Thr Leu Leu Arg Leu Pro Arg Ala Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Leu Ser Ile His Pro
1 5

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Leu Arg Gln Ser Trp Thr Leu Val Arg Ser Pro Phe Met Gly Met Val
1 5 10 15
Ser Pro Ser Ser Val
20

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

511

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```

Gly Leu Val Ala Thr Leu Tyr Ser Ala Ile Pro Arg Arg Ser Ala Arg
 1             5             10             15
Asp Trp Pro Ala Ser Ser Pro Arg Gly Gly Leu Met Pro Ser Pro Ile
      20             25             30
Ile Gly Val Arg Thr Val Pro Ser Ser Lys Thr Glu Thr Trp Trp Phe
      35             40             45
Val Arg Gln Thr Arg Ser Leu Pro Gly Thr Gln Glu Thr Ser Ile Leu
      50             55             60
Ser Pro Thr Val Gly Trp Trp Trp Arg Arg Ser Leu Arg
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```

Pro Leu Ile Pro Pro Leu Pro Phe Pro Cys Gly Leu Ser Leu Leu Arg
 1             5             10             15
Leu Asn Cys Arg Cys Ser Gly Ala Asp Ala Arg Gly Glu Val Gly Arg
      20             25             30
Ala Ala Thr Thr Thr Leu Gly Ser Val Arg Leu Pro Arg Gly Trp Cys
      35             40             45
Gly Leu Val Arg Ser Gly Arg Gln Trp Lys Leu Glu
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

```

Pro Gly Met Glu Trp Asn Leu Thr
 1             5

```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid

512

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Gln Gln Thr Phe

1

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Asp	Phe	Thr	Thr	Thr	Ala	Leu	Thr	Pro	Gln	Pro	Ser	Gln	Leu	Thr	Leu
1				5				10				15			
Val	Lys	Pro	Arg	Cys	Ser	Leu	Arg	Ala	Ser	Arg	Pro	Ser	Gly	Cys	Ile
			20					25					30		
Pro	Met	Leu	Ala	Gly	Gln	Lys	Phe	Ala	Ala	Ser	Ile	Gly	Pro	Ser	Trp
		35				40						45			
Trp	Val	Phe	Ser	Gly	Arg	Cys	Val	Gly	Lys	His	Cys	Leu	Pro	Ala	Arg
	50					55					60				
Arg	Thr	Thr	Leu	Ser	Gly	Gln	Val								
65						70									

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Lys	Ala	Arg	Ile	Leu	Ser	His	Tyr	Cys
1				5				

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Gly Gly Ala Met Ile Cys His Gln Lys Trp Pro Ala Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Leu Thr Ile Trp Ser Val Gly Ser Val Trp Arg Arg Asp Thr Cys Ala
1 5 10 15
Val Met Leu Xaa Pro Ser Ser Trp Trp Ala Trp Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Ser Thr Pro Leu Thr Leu Gly Arg
1 5

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Gln Thr Gly Met
1

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid

514

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Arg	Glu	Val	Ala	Ile	Pro	Phe	Ile	Gly	Val	Val	Thr	Arg	Pro	Pro	Leu
1				5				10						15	
Asn	Pro	Trp	Cys	Arg	Ser	Pro	Arg								
			20												

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Thr	Ile	Gly	Arg	Gly	Gly	Ser	Leu	Arg	His	Gly	Met	Pro	Arg	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Gln	Met	Arg	Trp	Gln	Pro	Ser	Arg
1				5			

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Thr Ala Ile Gly Leu

515

1

5

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

Pro Cys Arg Ser Gly Lys Ser Ser Pro Trp Leu Arg Leu Arg Gln Pro
 1           5           10           15
Arg Pro Thr Gln Leu Leu Pro Gly Gly Ser Leu Ala Ala Thr Arg Gly
          20           25           30
Arg Gly Pro Ser Pro Leu Tyr Gln Leu Leu Thr Ser Ser Ser Pro Gly
          35           40           45
Val Gly Pro Pro Trp Trp Val Thr Val Thr Ala Ser Leu Leu Arg Arg
          50           55           60
Trp Leu Pro Met Glu Leu Leu Glu Val Leu His Trp Pro Arg Arg Arg
          65           70           75           80
Pro Thr Ser Trp Gly Trp Ala Ser Glu Ala Thr His Arg Arg Ala Trp
          85           90           95
Leu Gln Leu Phe Tyr Trp Gly Leu Leu Val Arg Leu Trp Gly Pro Leu
          100          105          110
Ser Trp Asp Ser Pro Trp Arg Gly Pro Ser Trp Ala Val Pro Ala Cys
          115          120          125
Pro Pro Pro Ser Ser Leu Ser Tyr Leu Gly Leu Trp Glu Val Gly Arg
          130          135          140
Ala Leu Ser Thr Leu Pro Val Ser Ser Ser Thr Ser Trp Leu Gly Asn
          145          150          155          160
Phe Gln Gln Lys Thr Phe Gly Met Pro Ser Arg Tyr Ser Leu Val Leu
          165          170          175
Xaa Arg Ala Ser Arg Gly Leu Pro Leu Val Trp Phe Cys Thr Gln Gln
          180          185          190
Thr Thr Leu Ala Leu Pro His Gly
          195          200

```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```

Arg Arg Cys His Gly His Leu Ala Tyr Pro Thr Ala Thr Ser Asn Arg
 1           5           10           15
Leu Thr Thr Ala Thr Arg Ser Arg Gln Ser Cys Ala Ala
          20           25

```

516

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Ala	Leu	Leu	Ala	Pro	Trp	Trp	Pro	Trp	Ser	Thr	Gly	Ser	Leu	Arg	Trp
1				5					10					15	
Met	Arg	Ser	Arg	Trp	Gly	Thr	Ser	Gly	Ile	Cys	Gly	Ser	Gly		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Cys	Ala	Arg	Cys	Ala	Trp
1				5	

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Cys	Leu	Asp	Ser	Gly	Pro	Ser	Ala	Leu	Trp	Cys	His	Ser	Pro	Cys	Gly
1				5					10					15	
Thr	Ala	Gly	Arg	Gly	Gly	Pro	Val	Asn	Gly	Phe	Ser	Met	Gly	Thr	Trp
			20					25					30		
Arg	Val	Val	Val	Cys	Ala	Gly	Val								
			35				40								

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid

517

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

Ser Pro Ala Thr Ser Ser Met Gly Asn Ser Lys Ile Gln Phe Thr Leu
 1           5           10           15
Pro Ser Cys Ala Gly Thr Thr Gly Trp Glu Leu Cys Arg Ser Thr Cys
          20           25           30
Trp Ala Thr Gly Lys Pro His Leu Phe Ser Pro Leu Thr Pro Arg Arg
      35           40           45
Trp Tyr Pro Ser Gly Arg Arg Gly Gly Leu Arg Trp Trp
    50           55           60

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Pro Leu Pro Thr Trp
 1           5

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Ser Gly Ala Arg Pro Val Thr Asn Cys Phe Ala Ser Lys Phe Phe Gln
 1           5           10           15
Gln Leu

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

518

```

Leu Ser Pro Thr Thr Leu Met Ala Phe Arg Ser Leu Gly Arg Leu Thr
 1           5           10           15
Arg Glu Arg Arg Pro Trp Ser Thr Val Arg Ala Lys Val Leu Pro Leu
           20           25           30
Met Gly Ser Ala Thr Pro Phe Arg Thr Ser Cys Gly Cys Gly Met Trp
           35           40           45
Arg Pro Leu Arg Phe His Leu Arg Ser Ala Ser Arg Ser Gly Arg Arg
           50           55           60
Leu Lys Thr Gln Asn
65

```

(2) INFORMATION FOR SEQ ID NO:476:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Leu Arg Pro Ile Cys His Gln Arg Leu Leu Pro Ser Lys Arg
 1           5           10

```

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```

Arg Met Leu Arg Glu Phe Ser Asn Arg Thr Ser Met Ser Xaa Trp Arg
 1           5           10           15
Ile Ala Val His Pro Leu Ser Val Val Val Ala Glu Arg Cys Leu Cys
           20           25           30
Gly Glu Lys Thr Tyr Pro Ala Leu His Arg Leu His Leu Ser Arg Leu
           35           40           45
Arg Arg Ala Ala Gln Met Arg Arg Pro Cys Arg
           50           55

```

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```

Pro Pro Arg Arg Arg Thr Pro Arg Pro Gln Thr His Leu Lys Ser Ser
 1           5           10           15
Lys Ser Leu Ile Leu Leu Asn Gln Arg Lys Ala Ser Ser Thr Trp Leu
          20           25           30
Phe Pro Tyr
          35

```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```

Lys Pro Tyr Phe His Arg Ala Met Pro His Glu Ser
 1           5           10

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```

Arg Leu Arg Cys Leu Ala Val Leu Arg Arg Ala
 1           5           10

```

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

His Ala Ser Phe Leu
 1           5

```

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

520

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

Pro Trp Leu Thr Trp Leu Ala Cys Val Arg Trp Arg Ser Arg Thr Ile
 1           5           10           15
Gln Pro Ile Val Thr Arg Cys Ala Leu Arg Ser Asn Cys Lys Leu Gly
          20           25           30
Ala Trp Trp Ala Met Asn Leu Pro Leu Asn Val Thr Ser Val Arg His
          35           40           45
Ala Lys Arg Pro Leu Pro Pro Ser Pro Thr Tyr Gly Pro Gly Ser His
          50           55           60
Leu Leu Gly Pro Leu Arg Pro Asn His Gln Trp
 65           70           75

```

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

Gly Arg Trp Gly Pro Cys Trp Trp Gln Thr Pro Pro Arg Ser Thr
 1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

Pro Ile Arg Thr Met Leu Gly Gly Gly Leu Thr Arg
 1           5           10

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

521

Leu Ser Gly Ala Leu Leu Gly Tyr Thr Thr Ser Ser Ser Trp Thr Arg
 1 5 10 15
 Ser Ser Ala Leu Gly Glu Leu Leu Lys Ala Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Ala Trp Val Thr Leu Met Arg Arg Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Gly Leu Leu Gly Arg Met Leu Pro Trp Ala Gly Asp Leu Arg Cys Arg
 1 5 10 15
 Ser Arg Thr Trp Pro Pro Leu Arg Gly Arg Trp Leu Phe Met Thr Gly
 20 25 30
 Phe Arg Arg Tyr Leu Lys Gly Leu Arg Ser Leu Leu Pro
 35 40 45

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Leu Ser Lys Arg Arg Cys Ser Ser Lys Ile Val Arg Arg Arg Arg Pro
 1 5 10 15
 Pro Ala Ser Leu Cys Ser Pro Pro Trp Thr Ser Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:489:

522

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

Leu Lys Ser Ser Phe Trp Glu Thr Arg Gly Gly Leu Gln Arg Pro Val
 1             5             10             15
Leu Gly Gly Leu Thr Pro Ser Ser Thr Pro Pro Thr Ser Gly Leu Arg
                20             25             30
Arg Cys

```

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```

Ser Cys Gly Asn Gln Arg Arg Pro Arg Ala Pro Ser Val Trp Met Pro
 1             5             10             15
Leu Ala Ser Thr Val Ala Leu Leu Xaa Arg Thr Trp His
                20             25

```

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```

Arg Gln Ser Phe Thr Pro Trp Pro Arg Thr Ile Gln Asn Gly Cys Ala
 1             5             10             15
Pro Trp Gly Asn Thr Xaa Pro Leu Ala Gln Trp
                20             25

```

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Pro Arg Lys Gly Cys Gln Trp Ala Arg Gly Ile Val Gly Pro Arg Val
1 5 10 15
Cys

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Pro Gln Val Leu Ala Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Pro Ala Thr Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Glu Pro Pro Val Arg Gly Ser Asp
1 5

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

524

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Lys Met Ser Arg Phe Ser Ser Arg Ala Met Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Leu Cys Ala Arg Gly Leu Tyr Ala Thr Leu Ala Arg Pro Trp Ala Glu
1 5 10 15
Pro Trp Leu Arg Thr Gly Thr Arg Val Ser Pro Arg Ile Thr Leu His
20 25 30
Trp Thr Gln Pro Pro Ser Ala Pro Leu Gly Ser Leu Ser Ala Met Arg
35 40 45
Met Xaa Lys Gly Ile Ser Ser
50 55

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Pro Arg Thr Phe Gly Asp His Ser Leu Ala Cys Arg Ala Ser Thr Val
1 5 10 15
Thr Leu Trp Leu Arg Pro Leu Val Thr Phe Ser Ser Thr Pro Gly Xaa
20 25 30
Pro Ser His Gly Gly Ser Ser Ser Arg Met Cys
35 40

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

His Ala Leu Leu Pro Gly Val Val Ala His Xaa Leu Ile Arg Phe Gly

525

```

      1           5           10           15
Val Arg Phe Met Val Thr Thr Thr Ser Phe Pro Trp Thr Asn Cys Leu
      20           25           30
Thr Ser Ser Trp Pro Ser Thr Asp Gln Gln Arg
      35           40

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

Gly Leu Pro Gln Thr Gln Pro Lys Gln Arg Trp Arg Leu Gly Arg Phe
 1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

Ala Thr Ser Ser Ser Leu Val
 1           5

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Pro Ser Thr Ala Arg Arg Pro Gly His Cys Glu His Ala Cys Ser Gly
 1           5           10           15
Arg Ala Val Gly Arg Ser Trp Leu Gly Ala Cys Cys Gly Ile Gln Asp
      20           25           30
Ser Gly Phe Leu Pro Leu Arg Leu Leu Val Ser Gln Gly Val Ser Leu
      35           40           45
Cys Pro Pro Pro Thr Trp Gly Trp Phe Ile Asn Trp Ile Ser Gln Xaa
      50           55           60
Ser Gly Val Ala Gly Gly Gly Trp Gly Ser
      65           70

```

526

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Pro Cys Ser Ser

1

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Arg Ser Leu Gly Glu Leu Asn Ser Ser Val Ala Ala Gly Val Arg Pro
1 5 10 15
Glu Pro Arg Ser Lys Gly Asp
20

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..9034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

AGG TGG TGG ATG GGT GAT GAC AGG GTT GGT AGG TCG TAA ATC CCG GTC 48
Arg Trp Trp Met Gly Asp Asp Arg Val Gly Arg Ser * Ile Pro Val
1 5 10 15
ATC CTG GTA GCC ACT ATA GGT GGG TCT TAA GGG GAG GCT ACG GTC CCT 96
Ile Leu Val Ala Thr Ile Gly Gly Ser * Gly Glu Ala Thr Val Pro

527

20							25					30					
CTT	GCG	CAT	ATG	GAG	GAA	AAG	CGC	ACG	GTC	CAC	AGG	TGT	TGG	TCC	TAC	144	
Leu	Ala	His	Met	Glu	Glu	Lys	Arg	Thr	Val	His	Arg	Cys	Trp	Ser	Tyr		
35			40				45										
CGG	TGT	AAT	AAG	GAC	CCG	GCG	CTA	GGC	ACG	CCG	TTA	AAC	CGA	GCC	CGT	192	
Arg	Cys	Asn	Lys	Asp	Pro	Ala	Leu	Gly	Thr	Pro	Leu	Asn	Arg	Ala	Arg		
50			55				60										
TAC	TCC	CCT	GGG	CAA	ACG	ACG	CCC	ACG	TAC	GGT	CCA	CGT	CGC	CCT	TCA	240	
Tyr	Ser	Pro	Gly	Gln	Thr	Thr	Pro	Thr	Tyr	Gly	Pro	Arg	Arg	Pro	Ser		
65			70				75					80					
ATG	TCT	CTC	TTG	ACC	AAT	AGG	CGT	ACG	GCG	AGT	TGA	CAA	GGA	CCA	GTG	288	
Met	Ser	Leu	Leu	Thr	Asn	Arg	Arg	Thr	Ala	Ser	*	Gln	Gly	Pro	Val		
85				90					95								
GGG	GCC	GGG	CGG	GAG	GGG	GAA	GGA	CCC	CCA	CCG	CTG	CCC	TTC	CCG	GGG	336	
Gly	Ala	Gly	Arg	Glu	Gly	Glu	Gly	Pro	Pro	Pro	Leu	Pro	Phe	Pro	Gly		
100			105					110									
AGG	CGG	GAA	ATG	CAT	GGG	GCC	ACC	CAG	CTC	CGC	GGC	GGC	CTA	CAG	CCG	384	
Arg	Arg	Glu	Met	His	Gly	Ala	Thr	Gln	Leu	Arg	Gly	Gly	Leu	Gln	Pro		
115			120					125									
GGG	TAG	CCC	AAG	AAC	TTC	GGG	TGA	GGG	CGG	GTG	GCA	TTT	CTT	TTC	CTA	432	
Gly	*	Pro	Lys	Asn	Phe	Gly	*	Gly	Arg	Val	Ala	Phe	Leu	Phe	Leu		
130			135				140										
TAC	CGA	TCA	TGG	CAG	TCC	TTC	TGC	TCC	TAC	TCG	TGG	TGG	AGC	CGG	GGC	480	
Tyr	Arg	Ser	Trp	Gln	Ser	Phe	Cys	Ser	Tyr	Ser	Trp	Trp	Ser	Arg	Gly		
145			150				155					160					
TAT	TTT	AGC	CCC	GGC	CAC	CCA	TGC	TTG	TAG	CGC	GAA	AGG	GCA	ATA	TTT	528	
Tyr	Phe	Ser	Pro	Gly	His	Pro	Cys	Leu	*	Arg	Glu	Arg	Ala	Ile	Phe		
165				170					175								
SCT	CAC	AAA	CTG	TTG	CGC	CCT	GGA	GGA	CAT	AGG	CTT	CTG	CCT	GGA	GGG	576	
Xaa	His	Lys	Leu	Leu	Arg	Pro	Gly	Gly	His	Arg	Leu	Leu	Pro	Gly	Gly		
180			185					190									
CGG	ATG	CCT	GGT	GGC	TCT	GGG	GTG	CAC	CAT	TTG	CAC	CGA	CCG	CTG	CTG	624	
Arg	Met	Pro	Gly	Gly	Ser	Gly	Val	His	His	Leu	His	Arg	Pro	Leu	Leu		
195			200					205									
GCC	ACT	GTA	TCA	GGC	GGG	TTT	GGC	CGT	GCG	GCC	CGG	CAA	GTC	CGC	CGC	672	
Ala	Thr	Val	Ser	Gly	Gly	Phe	Gly	Arg	Ala	Ala	Arg	Gln	Val	Arg	Arg		
210			215				220										
CCA	GTT	GGT	GGG	GGA	ACT	CGG	TAG	TCT	CTA	CGG	GCC	CTT	GTC	GGT	CTC	720	
Pro	Val	Gly	Gly	Gly	Thr	Arg	*	Ser	Leu	Arg	Ala	Leu	Val	Gly	Leu		
225			230				235					240					
GGC	TTA	TGT	GGC	CGG	GAT	CCT	GGG	GCT	TGG	GGA	GGT	CTA	CTC	GGG	GGT	768	
Gly	Leu	Cys	Gly	Arg	Asp	Pro	Gly	Ala	Trp	Gly	Gly	Leu	Leu	Gly	Gly		
245				250					255								

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CCT CAC CGT CGG GGT GGC GTT GAC GCG CAG GGT CTA CCC GGT CCC GAA	816
Pro His Arg Arg Gly Gly Val Asp Ala Gln Gly Leu Pro Gly Pro Glu	
260 265 270	
CCT GAC GTG TGC AGT AGA GTG TGA GTT GAA GTG GGA AAG TGA GTT TTG	864
Pro Asp Val Cys Ser Arg Val * Val Glu Val Gly Lys * Val Leu	
275 280 285	
GAG ATG GAC TGA ACA GCT GGC CTC AAA CTA CTG GAT TCT GGA ATA CCT	912
Glu Met Asp * Thr Ala Gly Leu Lys Leu Leu Asp Ser Gly Ile Pro	
290 295 300	
CTG GAA GGT GCC TTT CGA CTT TTG GCG GGG AGT GAT GAG CCT TAC TCC	960
Leu Glu Gly Ala Phe Arg Leu Leu Ala Gly Ser Asp Glu Pro Tyr Ser	
305 310 315 320	
TCT CTT GGT GTG CGT GGC GGC CCT CCT CCT GCT GGA GCA GCG TAT TGT	1008
Ser Leu Gly Val Arg Gly Gly Pro Pro Pro Ala Gly Ala Ala Tyr Cys	
325 330 335	
CAT GGT CTT CCT CCT GGT CAC TAT GGC GGG CAT GTC GCA AGG CGC GCC	1056
His Gly Leu Pro Pro Gly His Tyr Gly Gly His Val Ala Arg Arg Ala	
340 345 350	
CGC CTC AAG TGT TGG GGT CAC GGC CTT TCG AGG CGG GTT TGA CTT GGC	1104
Arg Leu Lys Cys Trp Gly His Gly Leu Ser Arg Arg Val * Leu Gly	
355 360 365	
AGT CTT GTT CTT GCA GGT CGA ACG GGT CCC GCG TGC CGA CAG GGA GAG	1152
Ser Leu Val Leu Ala Gly Arg Thr Gly Pro Ala Cys Arg Gln Gly Glu	
370 375 380	
GGT TTG GGA ACG TGG GAA CGT CAC ACT TTT GTG TGA CTG CCC CAA CGG	1200
Gly Leu Gly Thr Trp Glu Arg His Thr Phe Val * Leu Pro Gln Arg	
385 390 395 400	
TCC TTG GGT GTG GGT CCC GGC CCT TTG CCA GGC AAT CGG ATG GGG CGA	1248
Ser Leu Gly Val Gly Pro Gly Pro Leu Pro Gly Asn Arg Met Gly Arg	
405 410 415	
CCC TAT CAC TCA TTG GAG CCA CGG ACA AAA TCA GTG GCC CCT TTC TTG	1296
Pro Tyr His Ser Leu Glu Pro Arg Thr Lys Ser Val Ala Pro Phe Leu	
420 425 430	
TCC CCA ATT TGT CTA CGG CGC CGT TTC AGT GAC CTG CGT GTG GGG TTC	1344
Ser Pro Ile Cys Leu Arg Arg Arg Phe Ser Asp Leu Arg Val Gly Phe	
435 440 445	
TGT GTC TTG GTT TGC TTC CAC TGG GGG TCG CGA CTC CAA GGT TGA TGT	1392
Cys Val Leu Val Cys Phe His Trp Gly Ser Arg Leu Gln Gly * Cys	
450 455 460	
GTG GAG TTT GGT TCC AGT TGG CTC TGC CAG CTG CAC CAT AGC CGC ACT	1440
Val Glu Phe Gly Ser Ser Trp Leu Cys Gln Leu His His Ser Arg Thr	
465 470 475 480	
GGG ATC TTC GGA TCG CGA CAC AGT GGT TGA GCT CTC CGA GTG GGG AAT	1488

529

Gly	Ile	Phe	Gly	Ser	Arg	His	Ser	Gly	*	Ala	Leu	Arg	Val	Gly	Asn	
				485					490					495		
TCC	CTG	CGC	CAC	TTG	TAT	CCT	GGA	CAG	GCG	GCC	TGC	CTC	GTG	TGG	CAC	1536
Ser	Leu	Arg	His	Leu	Tyr	Pro	Gly	Gln	Ala	Ala	Cys	Leu	Val	Trp	His	
			500					505					510			
CTG	TGT	GAG	GGA	CTG	CTG	GCC	CGA	GAC	CGG	GTC	GGT	ACG	TTT	CCC	ATT	1584
Leu	Cys	Glu	Gly	Leu	Leu	Ala	Arg	Asp	Arg	Val	Gly	Thr	Phe	Pro	Ile	
		515					520					525				
CCA	CAG	GTG	TGG	CGC	GGG	ACC	GAG	GCT	GAC	CAG	AGA	CCT	TGA	GGC	TGT	1632
Pro	Gln	Val	Trp	Arg	Gly	Thr	Glu	Ala	Asp	Gln	Arg	Pro	*	Gly	Cys	
		530				535					540					
GCC	CTT	CGT	CAA	TAG	GAC	AAC	TCC	CTT	CAC	CAT	AAG	GGG	GCC	CCT	GGG	1680
Ala	Leu	Arg	Gln	*	Asp	Asn	Ser	Leu	His	His	Lys	Gly	Ala	Pro	Gly	
545					550					555					560	
CAA	CCA	GGG	GCG	AGG	CAA	CCC	GGT	GCG	GTC	GCC	CTT	GGG	TTT	TGG	GTC	1728
Gln	Pro	Gly	Ala	Arg	Gln	Pro	Gly	Ala	Val	Ala	Leu	Gly	Phe	Trp	Val	
				565					570					575		
CTA	CAC	CAT	GAC	CAA	GAT	CCG	AGA	CTC	CTT	ACA	CTT	GGT	GAA	ATG	TCC	1776
Leu	His	His	Asp	Gln	Asp	Pro	Arg	Leu	Leu	Thr	Leu	Gly	Glu	Met	Ser	
			580					585					590			
CAC	CCC	AGC	CAT	TGA	GCC	TCC	CAC	CGG	AAC	GTT	TGG	GTT	CTT	CCC	AGG	1824
His	Pro	Ser	His	*	Ala	Ser	His	Arg	Asn	Val	Trp	Val	Leu	Pro	Arg	
		595					600					605				
AGT	CCC	CCC	CCT	TAA	CAA	CTG	CAT	GCT	TCT	CGG	CAC	TGA	GGT	GTC	AGA	1872
Ser	Pro	Pro	Pro	*	Gln	Leu	His	Ala	Ser	Arg	His	*	Gly	Val	Arg	
	610					615						620				
GGT	ATT	GGG	TGG	GGC	GGG	CCT	CAC	TGG	GGG	GTT	TTA	CGA	ACC	TCT	GGT	1920
Gly	Ile	Gly	Trp	Gly	Gly	Pro	His	Trp	Gly	Val	Leu	Arg	Thr	Ser	Gly	
625					630					635					640	
GCG	GCG	GTG	TTC	AGA	GCT	GAT	GGG	TCG	GCG	GAA	TCC	GGT	CTG	CCC	GGG	1968
Ala	Ala	Val	Phe	Arg	Ala	Asp	Gly	Ser	Ala	Glu	Ser	Gly	Leu	Pro	Gly	
				645					650					655		
GTT	TGC	ATG	GCT	CTC	TTC	GGG	ACG	GCC	TGA	TGG	GTT	CAT	ACA	TGT	TCA	2016
Val	Cys	Met	Ala	Leu	Phe	Gly	Thr	Ala	*	Trp	Val	His	Thr	Cys	Ser	
			660					665					670			
GGG	CCA	CTT	GCA	GGA	GGT	GGA	TGC	GGG	CAA	CTT	CAT	TCC	GCC	CCC	ACG	2064
Gly	Pro	Leu	Ala	Gly	Gly	Gly	Cys	Gly	Gln	Leu	His	Ser	Ala	Pro	Thr	
		675					680					685				
CTG	GTT	GCT	CTT	GGA	CTT	TGT	ATT	TGT	CCT	GTT	ATA	CCT	GAT	GAA	GCT	2112
Leu	Val	Ala	Leu	Gly	Leu	Cys	Ile	Cys	Pro	Val	Ile	Pro	Asp	Glu	Ala	
		690				695					700					
GGC	AGA	GGC	ACG	GTT	GGT	CCC	GCT	GAT	CCT	CCT	CCT	GCT	ATG	GTG	GTG	2160
Gly	Arg	Gly	Thr	Val	Gly	Pro	Ala	Asp	Pro	Pro	Pro	Ala	Met	Val	Val	

530

705	710	715	720	
GGT GAA CCA GTT GGC GGT CCT TGC TGT GSC GGC TGC KCR CGC CGC CGT				2208
Gly Glu Pro Val Gly Gly Pro Xaa Cys Xaa Gly Cys Xaa Arg Arg Arg				
725		730	735	
GGC TGG AGA GGT GTT TGC GGG CCC TGC CTT GTC CTG GTG TCT GGG CCT				2256
Gly Trp Arg Gly Val Cys Gly Pro Cys Leu Val Leu Val Ser Gly Pro				
740		745	750	
ACC CTT CGT GAG TAT GAT CCT GGG GCT AGC AAA CCT GGT GTT GTA CTT				2304
Thr Leu Arg Glu Tyr Asp Pro Gly Ala Ser Lys Pro Gly Val Val Leu				
755		760	765	
CCG CTG GAT GGG TCC TCA ACG CCT GAT GTT CCT CGT GTT GTG GAA GCT				2352
Pro Leu Asp Gly Ser Ser Thr Pro Asp Val Pro Arg Val Val Glu Ala				
770		775	780	
CGC TCG GGG GGC TTT CCC GCT GGC ATT ACT GAT GGG GAT TTC CGC CAC				2400
Arg Ser Gly Gly Phe Pro Ala Gly Ile Thr Asp Gly Asp Phe Arg His				
785		790	795	800
TCG CGG CCG CAC CTC TGT GCT TGG CGC CGA ATT CTG CTT TGA TGT CAC				2448
Ser Arg Pro His Leu Cys Ala Trp Arg Arg Ile Leu Leu * Cys His				
805		810		815
CTT TGA AGT GGA CAC GTC AGT CTT GGG TTG GGT GGT TGC TAG TGT GGT				2496
Leu * Ser Gly His Val Ser Leu Gly Leu Gly Gly Cys * Cys Gly				
820		825		830
GGC TTG GGC CAT AGC GCT CCT GAG CTC TAT GAG CGC GGG GGG GTG GAA				2544
Gly Leu Gly His Ser Ala Pro Glu Leu Tyr Glu Arg Gly Gly Val Glu				
835		840		845
GCA CAA AGC CAT AAT CTA TAG GAC GTG GTG TAA AGG GTA CCA GGC YCT				2592
Ala Gln Ser His Asn Leu * Asp Val Val * Arg Val Pro Gly Xaa				
850		855		860
TCG CCA GCG CGT GGT GCG TAG CCC CCT CGG GGA GGG GCG GCC CAC CAA				2640
Ser Pro Ala Arg Gly Ala * Pro Pro Arg Gly Gly Ala Ala His Gln				
865		870		880
GCC GCT GAC GAT AGC CTG GTG TCT GGC CTC TTA CAT CTG GCC GGA CGC				2688
Ala Ala Asp Asp Ser Leu Val Ser Gly Leu Leu His Leu Ala Gly Arg				
885		890		895
TGT GAT GTT GGT GGT TGT GGC CAT GGT CCT CCT CTT CGG CCT TTT CGA				2736
Cys Asp Val Gly Gly Cys Gly His Gly Pro Pro Leu Arg Pro Phe Arg				
900		905		910
CGC GCT CGA TTG GGC CTT GGA GGA GCT CCT TGT GTC GCG GCC TTC GTT				2784
Arg Ala Arg Leu Gly Leu Gly Gly Ala Pro Cys Val Ala Ala Phe Val				
915		920		925
GCG TCG TTT GGC AAG GGT GGT GGA GTG TTG TGT GAT GGC GGG CGA GAA				2832
Ala Ser Phe Gly Lys Gly Gly Gly Val Leu Cys Asp Gly Gly Arg Glu				
930		935		940

531

GGC CAC TAC CGT CCG GCT TGT GTC CAA GAT GTG CGC GAG AGG GGC CTA	2880
Gly His Tyr Arg Pro Ala Cys Val Gln Asp Val Arg Glu Arg Gly Leu	
945 950 955 960	
CCT GTT TGA CCA CAT GGG GTC GTT CTC GCG CGC GGT CAA GGA GCG CTT	2928
Pro Val * Pro His Gly Val Val Leu Ala Arg Gly Gln Gly Ala Leu	
965 970 975	
GCT GGA GTG GGA CGC GGC TTT GGA GMC CCT GTC ATT CAC TAG GAC GGA	2976
Ala Gly Val Gly Arg Gly Phe Gly Xaa Pro Val Ile His * Asp Gly	
980 985 990	
CTG TCG CAT CAT ACG AGA CGC CGC CAG GAC CCT GAG CTG CGG CCA ATG	3024
Leu Ser His His Thr Arg Arg Gln Asp Pro Glu Leu Arg Pro Met	
995 1000 1005	
CGT CAT GGG CTT GCC CGT GGT GGC TAG GCG CGG CGA TGA GGT CCT GAT	3072
Arg His Gly Leu Ala Arg Gly Gly * Ala Arg Arg * Gly Pro Asp	
1010 1015 1020	
TGG GGT CTT TCA GGA TGT GAA CCA CTT GCC TCC GGG GTT TGY TCC TAC	3120
Trp Gly Leu Ser Gly Cys Glu Pro Leu Ala Ser Gly Val Xaa Ser Tyr	
1025 1030 1035 1040	
AGC GCC TGT TGT CAT CCG TCG GTG CGG AAA GGG CTT CCT CGG GGT CAC	3168
Ser Ala Cys Cys His Pro Ser Val Arg Lys Gly Leu Pro Arg Gly His	
1045 1050 1055	
TAA GGC TGC CTT GAC TGG TCG GGA TCC TGA CTT ACA CCC AGG AAA CGT	3216
* Gly Cys Leu Asp Trp Ser Gly Ser * Leu Thr Pro Arg Lys Arg	
1060 1065 1070	
CAT GGT TTT GGG GAC GGC TAC CTC GCG CAG CAT GGG AAC GTG CTT AAA	3264
His Gly Phe Gly Asp Gly Tyr Leu Ala Gln His Gly Asn Val Leu Lys	
1075 1080 1085	
CGG GTT GCT GTT CAC GAC ATT CCA TGG GGC TTC TTC CCG AAC CAT TGC	3312
Arg Val Ala Val His Asp Ile Pro Trp Gly Phe Phe Pro Asn His Cys	
1090 1095 1100	
GAC ACC TGT GGG GGC CCT TAA CCC AAG GTG GTG GTC GGC CAG TGA TGA	3360
Asp Thr Cys Gly Gly Pro * Pro Lys Val Val Val Gly Gln * *	
1105 1110 1115 1120	
CGT CAC GGT CTA TCC CCT CCC CGA TGG AGC TAA CTC GTT GGT TCC CTG	3408
Arg His Gly Leu Ser Pro Pro Arg Trp Ser * Leu Val Gly Ser Leu	
1125 1130 1135	
CTC GTG TCA GGC TGA GTC CTG TTG GGT CAT YCG ATC CGA TGG GGC TCT	3456
Leu Val Ser Gly * Val Leu Leu Gly His Xaa Ile Arg Trp Gly Ser	
1140 1145 1150	
TTG CCA TGG CTT GAG CAA GGG GGA CAA GGT AGA ACT GGA CGT GGC CAT	3504
Leu Pro Trp Leu Glu Gln Gly Gly Gln Gly Arg Thr Gly Arg Gly His	
1155 1160 1165	
GGA GGT TGC TGA CTT TCG TGG GTC GTC TGG GTC TCC TGT CCT ATG CGA	3552

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Gly Gly Cys * Leu Ser Trp Val Val Trp Val Ser Cys Pro Met Arg	
1170 1175 1180	
CGA GGG GCA CGC TGT AGG AAT GCT CGT GTC CGT CCT TCA TTC GGG GGG	3600
Arg Gly Ala Arg Cys Arg Asn Ala Arg Val Arg Pro Ser Phe Gly Gly	
1185 1190 1195 1200	
GAG GGT GAC CGC GGC TCG ATT CAC TCG GCC GTG GAC CCA AGT CCC AAC	3648
Glu Gly Asp Arg Gly Ser Ile His Ser Ala Val Asp Pro Ser Pro Asn	
1205 1210 1215	
AGA CGC CAA GAC TAC CAC TGA GCC ACC CCC GGT GCC AGC TAA AGG GGT	3696
Arg Arg Gln Asp Tyr His * Ala Thr Pro Gly Ala Ser * Arg Gly	
1220 1225 1230	
TTT CAA AGA GGC TCC TCT TTT CAT GCC AAC AGG GGC GGG GAA AAG CAC	3744
Phe Gln Arg Gly Ser Ser Phe His Ala Asn Arg Gly Gly Glu Lys His	
1235 1240 1245	
ACG CGT CCC TTT GGA GTA TGG AAA CAT GGG GCA CAA GGT CCT GAT TCT	3792
Thr Arg Pro Phe Gly Val Trp Lys His Gly Ala Gln Gly Pro Asp Ser	
1250 1255 1260	
CAA CCC GTC GGT TGC CAC TGT GAG GGC CAT GGG CCC TTA CAT GGA GAG	3840
Gln Pro Val Gly Cys His Cys Glu Gly His Gly Pro Leu His Gly Glu	
1265 1270 1275 1280	
GCT GGC GGG GAA ACA TCC TAG CAT TTT CTG TGG ACA CGA CAC AAC AGC	3888
Ala Gly Gly Glu Thr Ser * His Phe Leu Trp Thr Arg His Asn Ser	
1285 1290 1295	
TTT CAC ACG GAT CAC GGA CTC TCC ATT GAC GTA CTC TAC CTA TGG GAG	3936
Phe His Thr Asp His Gly Leu Ser Ile Asp Val Leu Tyr Leu Trp Glu	
1300 1305 1310	
GTT TCT GGC CAA CCC GAG GCA GAT GCT GAG GGG AGT TTC CGT GGT CAT	3984
Val Ser Gly Gln Pro Glu Ala Asp Ala Glu Gly Ser Phe Arg Gly His	
1315 1320 1325	
CTG TGA TGA GTG CCA CAG TCA TGA CTC AAC TGT GTT GCT GGG TAT AGG	4032
Leu * * Val Pro Gln Ser * Leu Asn Cys Val Ala Gly Tyr Arg	
1330 1335 1340	
CAG GGT CAG GGA CGT GGC GCG GGG GTG TGG AGT GCA ATT AGT GCT CTA	4080
Gln Gly Gln Gly Arg Gly Ala Gly Val Trp Ser Ala Ile Ser Ala Leu	
1345 1350 1355 1360	
CGC TAC TGC GAC TCC CCC GGG CTC GCC TAT GAC TCA GCA TCC ATC CAT	4128
Arg Tyr Cys Asp Ser Pro Gly Leu Ala Tyr Asp Ser Ala Ser Ile His	
1365 1370 1375	
AAT TGA GAC AAA GCT GGA CGT TGG TGA GAT CCC CTT TTA TGG GCA TGG	4176
Asn * Asp Lys Ala Gly Arg Trp * Asp Pro Leu Leu Trp Ala Trp	
1380 1385 1390	
TAT CCC CCT CGA GCG TAT GAG GAC TGG TCG CCA CCT TGT ATT CTG CCA	4224
Tyr Pro Pro Arg Ala Tyr Glu Asp Trp Ser Pro Pro Cys Ile Leu Pro	

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1395	1400	1405	
TTC CAA GGC GGA GTG CGA GAG ATT GGC CGG CCA GTT CTC CGC GCG GGG Phe Gln Gly Gly Val Arg Glu Ile Gly Arg Pro Val Leu Arg Ala Gly 1410 1415 1420			4272
GGT TAA TGC CAT CGC CTA TTA TAG GGG TAA GGA CAG TTC CAT CAT CAA Gly * Cys His Arg Leu Leu * Gly * Gly Gln Phe His His Gln 1425 1430 1435 1440			4320
AGA CGG AGA CCT GGT GGT TTG TGC GAC AGA CGC GCT CTC TAC CGG GTA Arg Arg Arg Pro Gly Gly Leu Cys Asp Arg Arg Ala Leu Tyr Arg Val 1445 1450 1455			4368
CAC AGG AAA CTT CGA TTC TGT CAC CGA CTG TGG GTT GGT GGT GGA GGA His Arg Lys Leu Arg Phe Cys His Arg Leu Trp Val Gly Gly Gly Gly 1460 1465 1470			4416
GGT CGT TGA GGT GAC CCT TGA TCC CAC CAT TAC CAT TTC CTT GCG GAC Gly Arg * Gly Asp Pro * Ser His His Tyr His Phe Leu Ala Asp 1475 1480 1485			4464
TGT CCC TGC TTC GGC TGA ATT GTC GAT GCA GCG GCG CGG ACG CAC GGG Cys Pro Cys Phe Gly * Ile Val Asp Ala Ala Ala Arg Thr His Gly 1490 1495 1500			4512
GAG AGG TCG GTC GGG CCG CTA CTA CTA CGC TGG GGT CGG TAA GGC TCC Glu Arg Ser Val Gly Pro Leu Leu Leu Arg Trp Gly Arg * Gly Ser 1505 1510 1515 1520			4560
CGC GGG GGT GGT GCG GTC TGG TCC GGT CTG GTC GGC AGT GGA AGC TGG Arg Gly Gly Gly Ala Val Trp Ser Gly Leu Val Gly Ser Gly Ser Trp 1525 1530 1535			4608
AGT GAC CTG GTA TGG AAT GGA ACC TGA CTT GAC AGC AAA CCT TCT GAG Ser Asp Leu Val Trp Asn Gly Thr * Leu Asp Ser Lys Pro Ser Glu 1540 1545 1550			4656
ACT TTA CGA CGA CTG CCC TTA CAC CGC AGC CGT CGC AGC TGA CAT TGG Thr Leu Arg Arg Leu Pro Leu His Arg Ser Arg Arg * His Trp 1555 1560 1565			4704
TGA AGC CGC GGT GTT CTT TGC GGG CCT CGC GCC CCT CAG GAT GCA TCC * Ser Arg Gly Val Leu Cys Gly Pro Arg Ala Pro Gln Asp Ala Ser 1570 1575 1580			4752
CGA TGT TAG CTG GGC AAA AGT TCG CGG CGT CAA TTG GCC CCT CCT GGT Arg Cys * Leu Gly Lys Ser Ser Arg Arg Gln Leu Ala Pro Pro Gly 1585 1590 1595 1600			4800
GGG TGT TCA GCG GAC GAT GTG TCG GGA AAC ACT GTC TCC CGG CCC GTC Gly Cys Ser Ala Asp Asp Val Ser Gly Asn Thr Val Ser Arg Pro Val 1605 1610 1615			4848
GGA CGA CCC TCA GTG GGC AGG TCT GAA AGG CCC GAA TCC TGT CCC ACT Gly Arg Pro Ser Val Gly Arg Ser Glu Arg Pro Glu Ser Cys Pro Thr 1620 1625 1630			4896

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ACT GCT GAG GTG GGG CAA TGA TTT GCC ATC AAA AGT GGC CGG CCA CCA	4944
Thr Ala Glu Val Gly Gln * Phe Ala Ile Lys Ser Gly Arg Pro Pro	
1635 1640 1645	
CAT AGT TGA CGA TCT GGT CCG TCG GCT CGG TGT GGC GGA GGG ATA CGT	4992
His Ser * Arg Ser Gly Pro Ser Ala Arg Cys Gly Gly Gly Ile Arg	
1650 1655 1660	
GCG CTG TGA TGC TGG RCC CAT CCT CAT GGT GGG CTT GGC CAT AGC GGG	5040
Ala Leu * Cys Trp Xaa His Pro His Gly Gly Leu Gly His Ser Gly	
1665 1670 1675 1680	
CGG CAT GAT CTA CGC CTC TTA CAC TGG GTC GCT AGT GGT GGT AAC AGA	5088
Arg His Asp Leu Arg Leu Leu His Trp Val Ala Ser Gly Gly Asn Arg	
1685 1690 1695	
CTG GGA TGT GAA GGG AGG TGG CAA TCC CCT TTA TAG GAG TGG TGA CCA	5136
Leu Gly Cys Glu Gly Arg Trp Gln Ser Pro Leu * Glu Trp * Pro	
1700 1705 1710	
GGC CAC CCC TCA ACC CGT GGT GCA GGT CCC CCC GGT AGA CCA TCG GCC	5184
Gly His Pro Ser Thr Arg Gly Ala Gly Pro Pro Gly Arg Pro Ser Ala	
1715 1720 1725	
GGG GGG GGA GTC TGC GCC ACG GGA TGC CAA GAC AGT GAC AGA TGC GGT	5232
Gly Gly Gly Val Cys Ala Thr Gly Cys Gln Asp Ser Asp Arg Cys Gly	
1730 1735 1740	
GGC AGC CAT CCA GGT GAA CTG CGA TTG GTC TGT GAT GAC CCT GTC GAT	5280
Gly Ser His Pro Gly Glu Leu Arg Leu Val Cys Asp Asp Pro Val Asp	
1745 1750 1755 1760	
CGG GGA AGT CCT CAC CTT GGC TCA GGC TAA GAC AGC CGA GGC CTA CGC	5328
Arg Gly Ser Pro His Leu Gly Ser Gly * Asp Ser Arg Gly Leu Arg	
1765 1770 1775	
AGC TAC TTC CAG GTG GCT CGC TGG CTG CTA CAC GGG GAC GCG GGC CGT	5376
Ser Tyr Phe Gln Val Ala Arg Trp Leu Leu His Gly Asp Ala Gly Arg	
1780 1785 1790	
CCC CAC TGT ATC AAT TGT TGA CAA GCT CTT CGC CGG GGG TTG GGC CGC	5424
Pro His Cys Ile Asn Cys * Gln Ala Leu Arg Arg Gly Leu Gly Arg	
1795 1800 1805	
CGT GGT GGG TCA CTG TCA CAG CGT CAT TGC TGC GGC GGT GGC TGC CTA	5472
Arg Gly Gly Ser Leu Ser Gln Arg His Cys Cys Gly Gly Gly Cys Leu	
1810 1815 1820	
TGG AGC TTC TCG AAG TCC TCC ACT GGC CGC GGC GGC GTC CTA CCT CAT	5520
Trp Ser Phe Ser Lys Ser Ser Thr Gly Arg Gly Gly Val Leu Pro His	
1825 1830 1835 1840	
GGG GTT GGG CGT CGG AGG CAA CGC ACA GGC GCG CTT GGC TTC AGC TCT	5568
Gly Val Gly Arg Arg Arg Gln Arg Thr Gly Ala Leu Gly Phe Ser Ser	
1845 1850 1855	
TCT ACT GGG GGC TGC TGG TAC GGC TCT GGG GAC CCC TGT CGT GGG ACT	5616

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Ser Thr Gly Gly Cys Trp Tyr Gly Ser Gly Asp Pro Cys Arg Gly Thr	
1860 1865 1870	
CAC CAT GGC GGG GGC CTT CAT GGG CGG TGC CAG CGT GTC CCC CTC CCT	5664
His His Gly Gly Gly Leu His Gly Arg Cys Gln Arg Val Pro Leu Pro	
1875 1880 1885	
CGT CAC TGT CCT ACT TGG GGC TGT GGG AGG TTG GGA GGG CGT TGT CAA	5712
Arg His Cys Pro Thr Trp Gly Cys Gly Arg Leu Gly Gly Arg Cys Gln	
1890 1895 1900	
CGC TGC CAG TCT CGT CTT CGA CTT CAT GGC TGG GAA ACT TTC AAC AGA	5760
Arg Cys Gln Ser Arg Leu Arg Leu His Gly Trp Glu Thr Phe Asn Arg	
1905 1910 1915 1920	
AGA CCT TTG GTA TGC CAT CCC GGT ACT CAC TAG TCC TGG RGC GGG CCT	5808
Arg Pro Leu Val Cys His Pro Gly Thr His * Ser Trp Xaa Gly Pro	
1925 1930 1935	
CGC GGG GAT TGC CCT TGG TCT GGT TTT GTA CTC AGC AAA CAA CTC TGG	5856
Arg Gly Asp Cys Pro Trp Ser Gly Phe Val Leu Ser Lys Gln Leu Trp	
1940 1945 1950	
CAC TAC CAC ATG GCT GAA CCG TCT GCT GAC GAC GTT GCC ACG GTC ATC	5904
His Tyr His Met Ala Glu Pro Ser Ala Asp Asp Val Ala Thr Val Ile	
1955 1960 1965	
TTG CAT ACC CGA CAG CTA CTT CCA ACA GGC TGA CTA CTG CGA CAA GGT	5952
Leu His Thr Arg Gln Leu Leu Pro Thr Gly * Leu Leu Arg Gln Gly	
1970 1975 1980	
CTC GGC AAT CGT GCG CCG CCT GAG CCT TAC TCG CAC CGT GGT GGC CCT	6000
Leu Gly Asn Arg Ala Pro Pro Glu Pro Tyr Ser His Arg Gly Gly Pro	
1985 1990 1995 2000	
GGT CAA CAG GGA GCC TAA GGT GGA TGA GGT CCA GGT GGG GTA CGT CTG	6048
Gly Gln Gln Gly Ala * Gly Gly * Gly Pro Gly Gly Val Arg Leu	
2005 2010 2015	
GGA TCT GTG GGA GTG GGT GAT GCG CCA GGT GCG CAT GGT GAT GTC TAG	6096
Gly Ser Val Gly Val Gly Asp Ala Pro Gly Ala His Gly Asp Val *	
2020 2025 2030	
ACT CCG GGC CCT CTG CCC TGT GGT GTC ACT CCC CTT GTG GCA CTG CGG	6144
Thr Pro Gly Pro Leu Pro Cys Gly Val Thr Pro Leu Val Ala Leu Arg	
2035 2040 2045	
GGA GGG GTG GTC CGG TGA ATG GCT TCT CGA TGG GCA CGT GGA GAG TCG	6192
Gly Gly Val Val Arg * Met Ala Ser Arg Trp Ala Arg Gly Glu Ser	
2050 2055 2060	
TTG TCT GTG CGG GTG TGT AAT CAC CGG CGA CGT CCT CAA TGG GCA ACT	6240
Leu Ser Val Arg Val Cys Asn His Arg Arg Arg Pro Gln Trp Ala Thr	
2065 2070 2075 2080	
CAA AGA TCC AGT TTA CTC TAC CAA GCT GTG CAG GCA CTA CTG GAT GGG	6288
Gln Arg Ser Ser Leu Leu Tyr Gln Ala Val Gln Ala Leu Leu Asp Gly	

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2085										2090										2095										
AAC	TGT	GCC	GGT	CAA	CAT	GCT	GGG	CTA	CGG	GGA	AAC	CTC	ACC	TCT	TCT															6336
Asn	Cys	Ala	Gly	Gln	His	Ala	Gly	Leu	Arg	Gly	Asn	Leu	Thr	Ser	Ser															
			2100						2105						2110															
CGC	CTC	TGA	CAC	CCC	GAA	GGT	GGT	ACC	CTT	CGG	GAC	GTC	GGG	GTG	GGC															6384
Arg	Leu	*	His	Pro	Glu	Gly	Gly	Thr	Leu	Arg	Asp	Val	Gly	Val	Gly															
			2115						2120						2125															
TGA	GGT	GGT	GGT	GAC	CCC	TAC	CCA	CGT	GGT	GAT	CAG	GCG	CAC	GTC	CTG															6432
*	Gly	Gly	Gly	Asp	Pro	Tyr	Pro	Arg	Gly	Asp	Gln	Ala	His	Val	Leu															
			2130						2135						2140															
TTA	CAA	ACT	GCT	TCG	CCA	GCA	AAT	TCT	TTC	AGC	AGC	TGT	AGC	TGA	GCC															6480
Leu	Gln	Thr	Ala	Ser	Pro	Ala	Asn	Ser	Phe	Ser	Ser	Cys	Ser	*	Ala															
			2145						2150						2155															
CTA	CTA	CGT	TGA	TGG	CAT	TCC	GGT	CTC	TTG	GGA	GGC	TGA	CGC	GAG	AGC															6528
Leu	Leu	Arg	*	Trp	His	Ser	Gly	Leu	Leu	Gly	Gly	*	Arg	Glu	Ser															
									2165						2170															
GCC	GGC	CAT	GGT	CTA	CGG	TCC	GGG	CCA	AAG	TGT	TAC	CAT	TGA	TGG	GGA															6576
Ala	Gly	His	Gly	Leu	Arg	Ser	Gly	Pro	Lys	Cys	Tyr	His	*	Trp	Gly															
									2180						2185															
GCG	CTA	CAC	CCT	TCC	GCA	CCA	GTT	GCG	GAT	GCG	GAA	TGT	GGC	GCC	CTC															6624
Ala	Leu	His	Pro	Ser	Ala	Pro	Val	Ala	Asp	Ala	Glu	Cys	Gly	Ala	Leu															
									2195						2200															
TGA	GGT	TTC	ATC	TGA	GGT	CAG	CAT	CGA	GAT	CGG	GAC	GGA	GAC	TGA	AGA															6672
*	Gly	Phe	Ile	*	Gly	Gln	His	Arg	Asp	Arg	Asp	Gly	Asp	*	Arg															
									2210						2215															
CTC	AGA	ACT	GAC	TGA	GGC	CGA	TTT	GCC	ACC	AGC	GGC	TGC	TGC	CCT	CCA															6720
Leu	Arg	Thr	Asp	*	Gly	Arg	Phe	Ala	Thr	Ser	Gly	Cys	Cys	Pro	Pro															
									2225						2230															
AGC	GAT	AGA	GAA	TGC	TGC	GAG	AAT	TCT	CGA	ACC	GCA	CAT	CGA	TGT	CAY															6768
Ser	Asp	Arg	Glu	Cys	Cys	Glu	Asn	Ser	Arg	Thr	Ala	His	Arg	Cys	Xaa															
									2245						2250															
CAT	GGA	GGA	TTG	CAG	TAC	ACC	CTC	TCT	CTG	TGG	TAG	TAG	CCG	AGA	GAT															6816
His	Gly	Gly	Leu	Gln	Tyr	Thr	Leu	Ser	Leu	Trp	*	*	Pro	Arg	Asp															
									2260						2265															
GCC	TGT	GTG	GGG	AGA	AGA	CAT	ACC	CCG	CAC	TCC	ATC	GCC	TGC	ACT	TAT															6864
Ala	Cys	Val	Gly	Arg	Arg	His	Thr	Pro	His	Ser	Ile	Ala	Cys	Thr	Tyr															
									2275						2280															
CTC	GGT	TAC	GGA	GAG	CAG	CTC	AGA	TGA	GAA	GAC	CCT	GTC	GGT	GAC	CTC															6912
Leu	Gly	Tyr	Gly	Glu	Gln	Leu	Arg	*	Glu	Asp	Pro	Val	Gly	Asp	Leu															
									2290						2295															
CTC	GCA	GGA	GGA	CAC	CCC	GTC	CTC	AGA	CTC	ATT	TGA	AGT	CAT	CCA	AGA															6960
Leu	Ala	Gly	Gly	His	Pro	Val	Leu	Arg	Leu	Ile	*	Ser	His	Pro	Arg															
									2305						2310															

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GTC TGA TAC TGC TGA ATC AGA GGA AAG CGT CTT CAA CGT GGC TCT TTC	7008
Val * Tyr Cys * Ile Arg Gly Lys Arg Leu Gln Arg Gly Ser Phe	
2325 2330 2335	
CGT ACT AAA AGC CTT ATT TCC ACA GAG CGA TGC CAC ACG AAA GCT AAC	7056
Arg Thr Lys Ser Leu Ile Ser Thr Glu Arg Cys His Thr Lys Ala Asn	
2340 2345 2350	
GGT TAA GAT GTC TTG CTG TGT TGA GAA GAG CGT AAC ACG CTT CTT TTC	7104
Gly * Asp Val Leu Leu Cys * Glu Glu Arg Asn Thr Leu Leu Phe	
2355 2360 2365	
TTT AGG GTT GAC CGT GGC TGA CGT GGC TAG CCT GTG TGA GAT GGA GAT	7152
Phe Arg Val Asp Arg Gly * Arg Gly * Pro Val * Asp Gly Asp	
2370 2375 2380	
CCA GAA CCA TAC AGC CTA TTG TGA CAA GGT GCG CAC TCC GCT CGA ATT	7200
Pro Glu Pro Tyr Ser Leu Leu * Gln Gly Ala His Ser Ala Arg Ile	
2385 2390 2395 2400	
GCA AGT TGG GTG CTT GGT GGG CAA TGA ACT TAC CTT TGA ATG TGA CAA	7248
Ala Ser Trp Val Leu Gly Gly Gln * Thr Tyr Leu * Met * Gln	
2405 2410 2415	
GTG TGA GGC ACG CCA AGA GAC CCT TGC CTC CTT CTC CTA CAT ATG GTC	7296
Val * Gly Thr Pro Arg Asp Pro Cys Leu Leu Leu Leu His Met Val	
2420 2425 2430	
CGG GGT CCC ACT TAC TCG GGC CAC TCC GGC CAA ACC ACC AGT GGT GAG	7344
Arg Gly Pro Thr Tyr Ser Gly His Ser Gly Gln Thr Thr Ser Gly Glu	
2435 2440 2445	
GCC GGT GGG GTC CTT GTT GGT GGC AGA CAC CAC CAA GGT CTA CGT GAC	7392
Ala Gly Gly Val Leu Val Gly Gly Arg His His Gln Gly Leu Arg Asp	
2450 2455 2460	
CAA TCC GGA CAA TGT TGG GAG GAG GGT TGA CAA GGT GAC TTT CTG GCG	7440
Gln Ser Gly Gln Cys Trp Glu Glu Gly * Gln Gly Asp Phe Leu Ala	
2465 2470 2475 2480	
CGC TCC TCG GGT ACA CGA CAA GTT CCT CGT GGA CTC GAT CGA GCG CGC	7488
Arg Ser Ser Gly Thr Arg Gln Val Pro Arg Gly Leu Asp Arg Ala Arg	
2485 2490 2495	
TCG GAG AGC TGC TCA AGG CTG CCT AAG CAT GGG TTA CAC TTA TGA GGA	7536
Ser Glu Ser Cys Ser Arg Leu Pro Lys His Gly Leu His Leu * Gly	
2500 2505 2510	
GGC AAT AAG GAC TGT TAG GCC GCA TGC TGC CAT GGG CTG GGG ATC TAA	7584
Gly Asn Lys Asp Cys * Ala Ala Cys Cys His Gly Leu Gly Ile *	
2515 2520 2525	
GGT GTC GGT CAA GGA CTT GGC CAC CCC TGC GGG GAA GAT GGC TGT TCA	7632
Gly Val Gly Gln Gly Leu Gly His Pro Cys Gly Glu Asp Gly Cys Ser	
2530 2535 2540	
TGA CCG GCT TCA GGA GAT ACT TGA AGG GAC TCC GGT CCC TTT TAC CCT	7680

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* Pro Ala Ser Gly Asp Thr	* Arg Asp Ser Gly Pro Phe Tyr Pro	
2545	2550 2555 2560	
GAC TGT CAA AAA GGA GGT GTT CTT CAA AGA TCG TAA GGA GGA GAA GGC		7728
Asp Cys Gln Lys Gly Gly Val Leu Gln Arg Ser * Gly Gly Glu Gly		
2565	2570 2575	
CCC CCG CCT CAT TGT GTT CCC CCC CCT GGA CTT CCG GAT AGC TGA AAA		7776
Pro Pro Pro His Cys Val Pro Pro Pro Gly Leu Pro Asp Ser * Lys		
2580	2585 2590	
GCT CAT TCT GGG AGA CCC GGG GCG GGT TGC AAA GGC CGG TGT TGG GGG		7824
Ala His Ser Gly Arg Pro Gly Ala Gly Cys Lys Gly Arg Cys Trp Gly		
2595	2600 2605	
GGC TTA CGC CTT CCA GTA CAC CCC CAA CCA GCG GGT TAA GGA GAT GCT		7872
Gly Leu Arg Leu Pro Val His Pro Gln Pro Ala Gly * Gly Asp Ala		
2610	2615 2620	
AAA GCT GTG GGA ATC AAA GAA GAC CCC GTG CGC CAT CTG TGT GGA TGC		7920
Lys Ala Val Gly Ile Lys Glu Asp Pro Val Arg His Leu Cys Gly Cys		
2625	2630 2635 2640	
CAC TTG CTT CGA CAG TAG CAT TAC TGA RGA GGA CGT GGC ACT AGA GAC		7968
His Leu Leu Arg Gln * His Tyr * Xaa Gly Arg Gly Thr Arg Asp		
2645	2650 2655	
AGA GCT TTA CGC CCT GGC CTC GGA CCA TCC AGA ATG GGT GCG CGC CCT		8016
Arg Ala Leu Arg Pro Gly Leu Gly Pro Ser Arg Met Gly Ala Arg Pro		
2660	2665 2670	
GGG GAA ATA CTR TGC CTC TGG CAC AAT GGT GAC CCC GGA AGG GGT GCC		8064
Gly Glu Ile Xaa Cys Leu Trp His Asn Gly Asp Pro Gly Arg Gly Ala		
2675	2680 2685	
AGT GGG CGA GAG GTA TTG TAG GTC CTC GGG TGT GTT GAC CAC AAG TGC		8112
Ser Gly Arg Glu Val Leu * Val Leu Gly Cys Val Asp His Lys Cys		
2690	2695 2700	
TAG CAA CTG TTT GAC CTG CTA CAT CAA AGT GAG AGC CGC CTG TGA GAG		8160
* Gln Leu Phe Asp Leu Leu His Gln Ser Glu Ser Arg Leu * Glu		
2705	2710 2715 2720	
GAT CGG ACT GAA AAA TGT CTC GCT TCT CAT CGC GGG CGA TGA CTG CTT		8208
Asp Arg Thr Glu Lys Cys Leu Ala Ser His Arg Gly Arg * Leu Leu		
2725	2730 2735	
AAT TGT GTG CGA GAG GCC TGT ATG CGA CCC TTG CGA GGC CCT GGG CCG		8256
Asn Cys Val Arg Glu Ala Cys Met Arg Pro Leu Arg Gly Pro Gly Pro		
2740	2745 2750	
AAC CCT GGC TTC GTA CGG GTA CGC GTG TGA GCC CTC GTA TCA CGC TTC		8304
Asn Pro Gly Phe Val Arg Val Arg Val * Ala Leu Val Ser Arg Phe		
2755	2760 2765	
ACT GGA CAC AGC CCC CTT CTG CTC CAC TTG GCT CGC TGA GTG CAA TGC		8352
Thr Gly His Ser Pro Leu Leu Leu His Leu Ala Arg * Val Gln Cys		

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2770	2775	2780	
GGA TGG GRA AAG GCA TTT CTT CCT GAC CAC GGA CTT TCG GAG ACC ACT			8400
Gly Trp Xaa Lys Ala Phe Leu Pro Asp His Gly Leu Ser Glu Thr Thr			
2785	2790	2795	2800
CGC TCG CAT GTC GAG CGA GTA CAG TGA CCC TAT GGC TTC GGC CAT TGG			8448
Arg Ser His Val Glu Arg Val Gln * Pro Tyr Gly Phe Gly His Trp			
2805	2810	2815	
TTA CAT TCT CCT CTA CCC CTG GCR TCC CAT CAC ACG GTG GGT CAT CAT			8496
Leu His Ser Pro Leu Pro Leu Xaa Ser His His Thr Val Gly His His			
2820	2825	2830	
CCC GCA TGT GCT AAC ATG CGC TTC TTC CCG GGG TGG TGG CAC ACS GTC			8544
Pro Ala Cys Ala Asn Met Arg Phe Phe Pro Gly Trp Trp His Xaa Val			
2835	2840	2845	
TGA TCC GGT TTG GTG TCA GGT TCA TGG TAA CTA CTA CAA GTT TCC CCT			8592
* Ser Gly Leu Val Ser Gly Ser Trp * Leu Leu Gln Val Ser Pro			
2850	2855	2860	
GGA CAA ACT GCC TAA CAT CAT CGT GGC CCT CCA CGG ACC AGC AGC GTT			8640
Gly Gln Thr Ala * His His Arg Gly Pro Pro Arg Thr Ser Ser Val			
2865	2870	2875	2880
GAG GGT TAC CGC AGA CAC AAC CAA AAC AAA GAT GGA GGC TGG GAA GGT			8688
Glu Gly Tyr Arg Arg His Asn Gln Asn Lys Asp Gly Gly Trp Glu Gly			
2885	2890	2895	
TCT GAG CGA CCT CAA GCT CCC TGG TCT AGC CGT CCA CCG CAA GAA GGC			8736
Ser Glu Arg Pro Gln Ala Pro Trp Ser Ser Arg Pro Pro Gln Glu Gly			
2900	2905	2910	
CGG GGC ATT GCG AAC ACG CAT GCT CCG GTC GCG CGG TTG GGC GGA GTT			8784
Arg Gly Ile Ala Asn Thr His Ala Pro Val Ala Arg Leu Gly Gly Val			
2915	2920	2925	
GGC TAG GGG CCT GTT GTG GCA TCC AGG ACT CCG GCT TCC TCC CCC TGA			8832
Gly * Gly Pro Val Val Ala Ser Arg Thr Pro Ala Ser Ser Pro *			
2930	2935	2940	
GAT TGC TGG TAT CCC AGG GGG TTT CCC TCT GTC CCC CCC CTA CAT GGG			8880
Asp Cys Trp Tyr Pro Arg Gly Phe Pro Ser Val Pro Pro Leu His Gly			
2945	2950	2955	2960
GGT GGT TCA TCA ATT GGA TTT CAC AGC SCA GCG GAG TCG CTG GCG GTG			8928
Gly Gly Ser Ser Ile Gly Phe His Ser Xaa Ala Glu Ser Leu Ala Val			
2965	2970	2975	
GTT GGG GTT CTT AGC CCT GCT CAT CGT AGC GCT CTT TGG GTG AAC TAA			8976
Val Gly Val Leu Ser Pro Ala His Arg Ser Ala Leu Trp Val Asn *			
2980	2985	2990	
ATT CAT CTG TTG CGG CCG GAG TCA GAC CTG AGC CCC GTT CAA AAG GGG			9024
Ile His Leu Leu Arg Pro Glu Ser Asp Leu Ser Pro Val Gln Lys Gly			
2995	3000	3005	

540

ATT GAG AC
Ile Glu
3010

9032

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Arg Trp Trp Met Gly Asp Asp Arg Val Gly Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Ile Pro Val Ile Leu Val Ala Thr Ile Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Gly Glu Ala Thr Val Pro Leu Ala His Met Glu Glu Lys Arg Thr Val
1 5 10 15
His Arg Cys Trp Ser Tyr Arg Cys Asn Lys Asp Pro Ala Leu Gly Thr
20 25 30
Pro Leu Asn Arg Ala Arg Tyr Ser Pro Gly Gln Thr Thr Pro Thr Tyr
35 40 45
Gly Pro Arg Arg Pro Ser Met Ser Leu Leu Thr Asn Arg Arg Thr Ala
50 55 60
Ser
65

(2) INFORMATION FOR SEQ ID NO:509:

541

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Gln Gly Pro Val Gly Ala Gly Arg Glu Gly Glu Gly Pro Pro Pro Leu
1 5 10 15
Pro Phe Pro Gly Arg Arg Glu Met His Gly Ala Thr Gln Leu Arg Gly
20 25 30
Gly Leu Gln Pro Gly
35

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

Pro Lys Asn Phe Gly
1 5

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

Gly Arg Val Ala Phe Leu Phe Leu Tyr Arg Ser Trp Gln Ser Phe Cys
1 5 10 15
Ser Tyr Ser Trp Trp Ser Arg Gly Tyr Phe Ser Pro Gly His Pro Cys
20 25 30
Leu

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

Arg Glu Arg Ala Ile Phe Xaa His Lys Leu Leu Arg Pro Gly Gly His
 1           5           10           15
Arg Leu Leu Pro Gly Gly Arg Met Pro Gly Gly Ser Gly Val His His
          20           25           30
Leu His Arg Pro Leu Leu Ala Thr Val Ser Gly Gly Phe Gly Arg Ala
          35           40           45
Ala Arg Gln Val Arg Arg Pro Val Gly Gly Gly Thr Arg
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```

Ser Leu Arg Ala Leu Val Gly Leu Gly Leu Cys Gly Arg Asp Pro Gly
 1           5           10           15
Ala Trp Gly Gly Leu Leu Gly Gly Pro His Arg Arg Gly Gly Val Asp
          20           25           30
Ala Gln Gly Leu Pro Gly Pro Glu Pro Asp Val Cys Ser Arg Val
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

Val Glu Val Gly Lys
 1           5

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

543

Val Leu Glu Met Asp
1 5

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

```

Thr Ala Gly Leu Lys Leu Leu Asp Ser Gly Ile Pro Leu Glu Gly Ala
 1           5           10           15
Phe Arg Leu Leu Ala Gly Ser Asp Glu Pro Tyr Ser Ser Leu Gly Val
          20           25           30
Arg Gly Gly Pro Pro Pro Ala Gly Ala Ala Tyr Cys His Gly Leu Pro
      35           40           45
Pro Gly His Tyr Gly Gly His Val Ala Arg Arg Ala Arg Leu Lys Cys
 50           55           60
Trp Gly His Gly Leu Ser Arg Arg Val
65           70

```

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

```

Leu Gly Ser Leu Val Leu Ala Gly Arg Thr Gly Pro Ala Cys Arg Gln
 1           5           10           15
Gly Glu Gly Leu Gly Thr Trp Glu Arg His Thr Phe Val
      20           25

```

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

```

Leu Pro Gln Arg Ser Leu Gly Val Gly Pro Gly Pro Leu Pro Gly Asn
 1           5           10           15
Arg Met Gly Arg Pro Tyr His Ser Leu Glu Pro Arg Thr Lys Ser Val

```

544

```

                20                25                30
Ala Pro Phe Leu Ser Pro Ile Cys Leu Arg Arg Arg Phe Ser Asr Leu
           35                40                45
Arg Val Gly Phe Cys Val Leu Val Cys Phe His Trp Gly Ser Arg Leu
           50                55                60
Gln Gly
           65

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

Cys Val Glu Phe Gly Ser Ser Trp Leu Cys Gln Leu His His Ser Arg
 1           5           10           15
Thr Gly Ile Phe Gly Ser Arg His Ser Gly
           20           25

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

Ala Leu Arg Val Gly Asn Ser Leu Arg His Leu Tyr Pro Gly Gln Ala
 1           5           10           15
Ala Cys Leu Val Trp His Leu Cys Glu Gly Leu Leu Ala Arg Asp Arg
           20           25           30
Val Gly Thr Phe Pro Ile Pro Gln Val Trp Arg Gly Thr Glu Ala Asp
           35           40           45
Gln Arg Pro
           50

```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

545

Gly Cys Ala Leu Arg Gln
1 5

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Asp Asn Ser Leu His His Lys Gly Ala Pro Gly Gln Pro Gly Ala Arg
1 5 10 15
Gln Pro Gly Ala Val Ala Leu Gly Phe Trp Val Leu His His Asp Gln
20 25 30
Asp Pro Arg Leu Leu Thr Leu Gly Glu Met Ser His Pro Ser His
35 40 45

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

Ala Ser His Arg Asn Val Trp Val Leu Pro Arg Ser Pro Pro Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Gln Leu His Ala Ser Arg His
1 5

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids

546

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

```

Gly Val Arg Gly Ile Gly Trp Gly Gly Pro His Trp Gly Val Leu Arg
 1           5           10           15
Thr Ser Gly Ala Ala Val Phe Arg Ala Asp Gly Ser Ala Glu Ser Gly
      20           25           30
Leu Pro Gly Val Cys Met Ala Leu Phe Gly Thr Ala
      35           40

```

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

```

Trp Val His Thr Cys Ser Gly Pro Leu Ala Gly Gly Gly Cys Gly Gln
 1           5           10           15
Leu His Ser Ala Pro Thr Leu Val Ala Leu Gly Leu Cys Ile Cys Pro
      20           25           30
Val Ile Pro Asp Glu Ala Gly Arg Gly Thr Val Gly Pro Ala Asp Pro
      35           40           45
Pro Pro Ala Met Val Val Gly Glu Pro Val Gly Gly Pro Xaa Cys Xaa
      50           55           60
Gly Cys Xaa Arg Arg Arg Gly Trp Arg Gly Val Cys Gly Pro Cys Leu
      65           70           75           80
Val Leu Val Ser Gly Pro Thr Leu Arg Glu Tyr Asp Pro Gly Ala Ser
      85           90           95
Lys Pro Gly Val Val Leu Pro Leu Asp Gly Ser Ser Thr Pro Asp Val
      100          105          110
Pro Arg Val Val Glu Ala Arg Ser Gly Gly Phe Pro Ala Gly Ile Thr
      115          120          125
Asp Gly Asp Phe Arg His Ser Arg Pro His Leu Cys Ala Trp Arg Arg
      130          135          140
Ile Leu Leu
145

```

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

547

Ser Gly His Val Ser Leu Gly Leu Gly Gly Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Cys Gly Gly Leu Gly His Ser Ala Pro Glu Leu Tyr Glu Arg Gly Gly
 1 5 10 15
 Val Glu Ala Gln Ser His Asn Leu
 20

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Arg Val Pro Gly Xaa Ser Pro Ala Arg Gly Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Pro Pro Arg Gly Gly Ala Ala His Gln Ala Ala Asp Asp Ser Leu Val
 1 5 10 15
 Ser Gly Leu Leu His Leu Ala Gly Arg Cys Asp Val Gly Gly Cys Gly
 20 25 30
 His Gly Pro Pro Leu Arg Pro Phe Arg Arg Ala Arg Leu Gly Leu Gly
 35 40 45
 Gly Ala Pro Cys Val Ala Ala Phe Val Ala Ser Phe Gly Lys Gly Gly
 50 55 60
 Gly Val Leu Cys Asp Gly Gly Arg Glu Gly His Tyr Arg Pro Ala Cys
 65 70 75 80

548

Val Gln Asp Val Arg Glu Arg Gly Leu Pro Val
 85 90

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Pro His Gly Val Val Leu Ala Arg Gly Gln Gly Ala Leu Ala Gly Val
 1 5 10 15
 Gly Arg Gly Phe Gly Xaa Pro Val Ile His
 20 25

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Asp Gly Leu Ser His His Thr Arg Arg Arg Gln Asp Pro Glu Leu Arg
 1 5 10 15
 Pro Met Arg His Gly Leu Ala Arg Gly Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Gly Pro Asp Trp Gly Leu Ser Gly Cys Glu Pro Leu Ala Ser Gly Val
 1 5 10 15
 Xaa Ser Tyr Ser Ala Cys Cys His Pro Ser Val Arg Lys Gly Leu Pro
 20 25 30
 Arg Gly His
 35

(2) INFORMATION FOR SEQ ID NO:533:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Gly Cys Leu Asp Trp Ser Gly Ser
1 5

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Leu Thr Pro Arg Lys Arg His Gly Phe Gly Asp Gly Tyr Leu Ala Gln
 1 5 10 15
 His Gly Asn Val Leu Lys Arg Val Ala Val His Asp Ile Pro Trp Gly
 20 25 30
 Phe Phe Pro Asn His Cys Asp Thr Cys Gly Gly Pro
 35 40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Pro Lys Val Val Val Gly Gln
1 5

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Arg His Gly Leu Ser Pro Pro Arg Trp Ser

550

1 5 10

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

Leu Val Gly Ser Leu Leu Val Ser Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Val Leu Leu Gly His Xaa Ile Arg Trp Gly Ser Leu Pro Trp Leu Glu
 1 5 10 15
 Gln Gly Gly Gln Gly Arg Thr Gly Arg Gly His Gly Gly Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Leu Ser Trp Val Val Trp Val Ser Cys Pro Met Arg Arg Gly Ala Arg
 1 5 10 15
 Cys Arg Asn Ala Arg Val Arg Pro Ser Phe Gly Gly Glu Gly Asp Arg
 20 25 30
 Gly Ser Ile His Ser Ala Val Asp Pro Ser Pro Asn Arg Arg Gln Asp
 35 40 45
 Tyr His
 50

(2) INFORMATION FOR SEQ ID NO:540:

551

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Ala Thr Pro Gly Ala Ser
1 5

(2) INFORMATION FOR SEQ ID NO:541:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Arg Gly Phe Gln Arg Gly Ser Ser Phe His Ala Asn Arg Gly Gly Glu
1 5 10 15
Lys His Thr Arg Pro Phe Gly Val Trp Lys His Gly Ala Gln Gly Pro
 20 25 30
Asp Ser Gln Pro Val Gly Cys His Cys Glu Gly His Gly Pro Leu His
 35 40 45
Gly Glu Ala Gly Gly Glu Thr Ser
50 55

(2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

His Phe Leu Trp Thr Arg His Asn Ser Phe His Thr Asp His Gly Leu
1 5 10 15
Ser Ile Asp Val Leu Tyr Leu Trp Glu Val Ser Gly Gln Pro Glu Ala
 20 25 30
Asp Ala Glu Gly Ser Phe Arg Gly His Leu
 35 40

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids

552

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

Val Pro Gln Ser
1

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Leu Asn Cys Val Ala Gly Tyr Arg Gln Gly Gln Gly Arg Gly Ala Gly
1 5 10 15
Val Trp Ser Ala Ile Ser Ala Leu Arg Tyr Cys Asp Ser Pro Gly Leu
20 25 30
Ala Tyr Asp Ser Ala Ser Ile His Asn
35 40

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Asp Lys Ala Gly Arg Trp
1 5

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Asp Pro Leu Leu Trp Ala Trp Tyr Pro Pro Arg Ala Tyr Glu Asp Trp
1 5 10 15
Ser Pro Pro Cys Ile Leu Pro Phe Gln Gly Gly Val Arg Glu Ile Gly

553

20 25 30
 Arg Pro Val Leu Arg Ala Gly Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

Cys His Arg Leu Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Gly Gln Phe His His Gln Arg Arg Arg Pro Gly Gly Leu Cys Asp Arg
 1 5 10 15
 Arg Ala Leu Tyr Arg Val His Arg Lys Leu Arg Phe Cys His Arg Leu
 20 25 30
 Trp Val Gly Gly Gly Gly Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Ser His His Tyr His Phe Leu Ala Asp Cys Pro Cys Phe Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids

554

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

Ile Val Asp Ala Ala Ala Arg Thr His Gly Glu Arg Ser Val Gly Pro
1 5 10 15
Leu Leu Leu Arg Trp Gly Arg
20

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

Gly Ser Arg Gly Gly Gly Ala Val Trp Ser Gly Leu Val Gly Ser Gly
1 5 10 15
Ser Trp Ser Asp Leu Val Trp Asn Gly Thr
20 25

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Leu Asp Ser Lys Pro Ser Glu Thr Leu Arg Arg Leu Pro Leu His Arg
1 5 10 15
Ser Arg Arg Ser
20

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

S r Arg Gly Val Leu Cys Gly Pro Arg Ala Pro Gln Asp Ala Ser Arg
1 5 10 15

555

Cys

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Leu	Gly	Lys	Ser	Ser	Arg	Arg	Gln	Leu	Ala	Pro	Pro	Gly	Gly	Cys	Ser	
1				5					10					15		
Ala	Asp	Asp	Val	Ser	Gly	Asn	Thr	Val	Ser	Arg	Pro	Val	Gly	Arg	Pro	
			20				25						30			
Ser	Val	Gly	Arg	Ser	Glu	Arg	Pro	Glu	Ser	Cys	Pro	Thr	Thr	Ala	Glu	
			35				40						45			
Val	Gly	Gln														
		50														

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Phe	Ala	Ile	Lys	Ser	Gly	Arg	Pro	Pro	His	Ser	
1				5					10		

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Arg	Ser	Gly	Pro	Ser	Ala	Arg	Cys	Gly	Gly	Gly	Ile	Arg	Ala	Leu	
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

556

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```

Cys Trp Xaa His Pro His Gly Gly Leu Gly His Ser Gly Arg His Asp
 1           5           10           15
Leu Arg Leu Leu His Trp Val Ala Ser Gly Gly Asn Arg Leu Gly Cys
          20           25           30
Glu Gly Arg Trp Gln Ser Pro Leu
          35           40

```

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

Pro Gly His Pro Ser Thr Arg Gly Ala Gly Pro Pro Gly Arg Pro Ser
 1           5           10           15
Ala Gly Gly Gly Val Cys Ala Thr Gly Cys Gln Asp Ser Asp Arg Cys
          20           25           30
Gly Gly Ser His Pro Gly Glu Leu Arg Leu Val Cys Asp Asp Pro Val
          35           40           45
Asp Arg Gly Ser Pro His Leu Gly Ser Gly
          50           55

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

```

Asp Ser Arg Gly Leu Arg Ser Tyr Phe Gln Val Ala Arg Trp Leu Leu
 1           5           10           15
His Gly Asp Ala Gly Arg Pro His Cys Ile Asn Cys
          20           25

```

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

557

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

```

Gln Ala Leu Arg Arg Gly Leu Gly Arg Arg Gly Gly Ser Leu Ser Gln
 1           5           10           15
Arg His Cys Cys Gly Gly Gly Cys Leu Trp Ser Phe Ser Lys Ser Ser
      20           25           30
Thr Gly Arg Gly Gly Val Leu Pro His Gly Val Gly Arg Arg Arg Gln
      35           40           45
Arg Thr Gly Ala Leu Gly Phe Ser Ser Ser Thr Gly Gly Cys Trp Tyr
      50           55           60
Gly Ser Gly Asp Pro Cys Arg Gly Thr His His Gly Gly Gly Leu His
      65           70           75           80
Gly Arg Cys Gln Arg Val Pro Leu Pro Arg His Cys Pro Thr Trp Gly
      85           90           95
Cys Gly Arg Leu Gly Gly Arg Cys Gln Arg Cys Gln Ser Arg Leu Arg
      100           105           110
Leu His Gly Trp Glu Thr Phe Asn Arg Arg Pro Leu Val Cys His Pro
      115           120           125
Gly Thr His
      130

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

```

Ser Trp Xaa Gly Pro Arg Gly Asp Cys Pro Trp Ser Gly Phe Val Leu
 1           5           10           15
Ser Lys Gln Leu Trp His Tyr His Met Ala Glu Pro Ser Ala Asp Asp
      20           25           30
Val Ala Thr Val Ile Leu His Thr Arg Gln Leu Leu Pro Thr Gly
      35           40           45

```

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

```

Leu Leu Arg Gln Gly Leu Gly Asn Arg Ala Pro Pro Glu Pro Tyr Ser
 1           5           10           15
His Arg Gly Gly Pro Gly Gln Gln Gly Ala
      20           25

```

558

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

```

Gly Pro Gly Gly Val Arg Leu Gly Ser Val Gly Val Gly Asp Ala Pro
 1             5             10             15
Gly Ala His Gly Asp Val
                20

```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

```

Thr Pro Gly Pro Leu Pro Cys Gly Val Thr Pro Leu Val Ala Leu Arg
 1             5             10             15
Gly Gly Val Val Arg
                20

```

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

```

Met Ala Ser Arg Trp Ala Arg Gly Glu Ser Leu Ser Val Arg Val Cys
 1             5             10             15
Asn His Arg Arg Arg Pro Gln Trp Ala Thr Gln Arg Ser Ser Leu Leu
                20             25             30
Tyr Gln Ala Val Gln Ala Leu Leu Asp Gly Asn Cys Ala Gly Gln His
                35             40             45
Ala Gly Leu Arg Gly Asn Leu Thr Ser Ser Arg Leu
                50             55             60

```

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

559

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

His Pro Glu Gly Gly Thr Leu Arg Asp Val Gly Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

Gly Gly Gly Asp Pro Tyr Pro Arg Gly Asp Gln Ala His Val Leu Leu
1 5 10 15
Gln Thr Ala Ser Pro Ala Asn Ser Phe Ser Ser Cys Ser
20 25

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Ala Leu Leu Arg
1

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Trp His Ser Gly Leu Leu Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:570:

560

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Arg Glu Ser Ala Gly His Gly Leu Arg Ser Gly Pro Lys Cys Tyr His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Trp Gly Ala Leu His Pro Ser Ala Pro Val Ala Asp Ala Glu Cys Gly
 1 5 10 15
Ala Leu

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Gly Gln His Arg Asp Arg Asp Gly Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Arg Leu Arg Thr Asp
 1 5

561

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Gly	Arg	Phe	Ala	Thr	Ser	Gly	Cys	Cys	Pro	Pro	Ser	Asp	Arg	Glu	Cys
1				5					10					15	
Cys	Glu	Asn	Ser	Arg	Thr	Ala	His	Arg	Cys	Xaa	His	Gly	Gly	Leu	Gln
		20						25						30	
Tyr	Thr	Leu	Ser	Leu	Trp										
		35													

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Pro	Arg	Asp	Ala	Cys	Val	Gly	Arg	Arg	His	Thr	Pro	His	Ser	Ile	Ala
1				5					10					15	
Cys	Thr	Tyr	Leu	Gly	Tyr	Gly	Glu	Gln	Leu	Arg					
		20						25							

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Glu	Asp	Pro	Val	Gly	Asp	Leu	Leu	Ala	Gly	Gly	His	Pro	Val	Leu	Arg
1				5					10					15	
Leu	Ile														

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

562

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Ser His Pro Arg Val
1 5

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Ile Arg Gly Lys Arg Leu Gln Arg Gly Ser Phe Arg Thr Lys Ser Leu
1 5 10 15
Ile Ser Thr Glu Arg Cys His Thr Lys Ala Asn Gly
20 25

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Asp Val Leu Leu Cys
1 5

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

Glu Glu Arg Asn Thr Leu Leu Phe Phe Arg Val Asp Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

563

(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Asp Gly Asp Pro Glu Pro Tyr Ser Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Gln Gly Ala His Ser Ala Arg Ile Ala Ser Trp Val Leu Gly Gly Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Gly Thr Pro Arg Asp Pro Cys Leu Leu Leu Leu His Met Val Arg Gly
 1 5 10 15
 Pro Thr Tyr Ser Gly His Ser Gly Gln Thr Thr Ser Gly Glu Ala Gly
 20 25 30
 Gly Val Leu Val Gly Gly Arg His His Gln Gly Leu Arg Asp Gln Ser
 35 40 45
 Gly Gln Cys Trp Glu Glu Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

(2) INFORMATION FOR SEO ID NO:585:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:585:

(2) INFORMATION FOR SEQ ID NO:586:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

(2) INFORMATION FOR SEQ ID NO:587:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

BNSDOCID: <WO___9521922A2 | >

565

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

Pro Ala Ser Gly Asp Thr
1 5

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Arg Asp Ser Gly Pro Phe Tyr Pro Asp Cys Gln Lys Gly Gly Val Leu
1 5 10 15
Gln Arg Ser

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Gly Gly Glu Gly Pro Pro Pro His Cys Val Pro Pro Pro Gly Leu Pro
1 5 10 15
Asp Ser

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

566

Lys Ala His Ser Gly Arg Pro Gly Ala Gly Cys Lys Gly Arg Cys Trp
 1 5 10 15
 Gly Gly Leu Arg Leu Pro Val His Pro Gln Pro Ala Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

Gly Asp Ala Lys Ala Val Gly Ile Lys Glu Asp Pro Val Arg His Leu
 1 5 10 15
 Cys Gly Cys His Leu Leu Arg Gln
 20

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Xaa Gly Arg Gly Thr Arg Asp Arg Ala Leu Arg Pro Gly Leu Gly Pro
 1 5 10 15
 Ser Arg Met Gly Ala Arg Pro Gly Glu Ile Xaa Cys Leu Trp His Asn
 20 25 30
 Gly Asp Pro Gly Arg Gly Ala Ser Gly Arg Glu Val Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Val Leu Gly Cys Val Asp His Lys Cys

567

1

5

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

Gln Leu Phe Asp Leu Leu His Gln Ser Glu Ser Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

Glu Asp Arg Thr Glu Lys Cys Leu Ala Ser His Arg Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Leu Leu Asn Cys Val Arg Glu Ala Cys Met Arg Pro Leu Arg Gly Pro
1 5 10 15
Gly Pro Asn Pro Gly Phe Val Arg Val Arg Val
20 25

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

568

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Ala Leu Val Ser Arg Phe Thr Gly His Ser Pro Leu Leu Leu His Leu
1 5 10 15
Ala Arg

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

Val Gln Cys Gly Trp Xaa Lys Ala Phe Leu Pro Asp His Gly Leu Ser
1 5 10 15
Glu Thr Thr Arg Ser His Val Glu Arg Val Gln
20 25

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Pro Tyr Gly Phe Gly His Trp Leu His Ser Pro Leu Pro Leu Xaa Ser
1 5 10 15
His His Thr Val Gly His His Pro Ala Cys Ala Asn Met Arg Phe Phe
20 25 30
Pro Gly Trp Trp His Xaa Val
35

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Ser Gly Leu Val Ser Gly Ser Trp
1 5

569

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Leu Leu Gln Val Ser Pro Gly Gln Thr Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

His His Arg Gly Pro Pro Arg Thr Ser Ser Val Glu Gly Tyr Arg Arg
 1 5 10 15
 His Asn Gln Asn Lys Asp Gly Gly Trp Glu Gly Ser Glu Arg Pro Gln
 20 25 30
 Ala Pro Trp Ser Ser Arg Pro Pro Gln Glu Gly Arg Gly Ile Ala Asn
 35 40 45
 Thr His Ala Pro Val Ala Arg Leu Gly Gly Val Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Gly Pro Val Val Ala Ser Arg Thr Pro Ala Ser Ser Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

570

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

```

Asp Cys Trp Tyr Pro Arg Gly Phe Pro Ser Val Pro Pro Leu His Gly
 1           5           10           15
Gly Gly Ser Ser Ile Gly Phe His Ser Xaa Ala Glu Ser Leu Ala Val
          20           25           30
Val Gly Val Leu Ser Pro Ala His Arg Ser Ala Leu Trp Val Asn
      35           40           45

```

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```

Ile His Leu Leu Arg Pro Glu Ser Asp Leu Ser Pro Val Gln Lys Gly
 1           5           10           15
Ile Glu

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GCCGCTGAAT TCATGCCTTG TTATTCTAC TCAAAC

36

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

571

GCCGCAGGAT CCTCGAACGA CCGCTCCTGC CAC

33

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GCCGCAGGAA TTCATGGCTT GGCTGTGGTT GCTG

34

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Tyr Ser Thr Tyr Gly Met Tyr Leu Thr Gly Arg Cys Ser Arg Asn Tyr
 1 5 10 15

Asp Val Ile Ile Cys Asp Glu Cys His Ala Thr Asp Arg Thr Thr Val
 20 25 30

Leu Gly Ile Gly Lys Val Leu Thr Glu Ala Pro Ser Lys Asn Val Arg
 35 40 45

Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly Val Ile Pro Thr Pro
 50 55 60

His Ala Asn Ile Thr Glu Ile Gln Leu Thr Asp Glu Gly Thr Ile Pro
 65 70 75 80

Phe His Gly Lys Lys Ile Lys Glu Glu Asn Leu Lys Lys Gly Arg His
 85 90 95

Leu Ile Phe Glu Ala Thr Lys Lys His Cys Asp Glu Leu Ala Asn Glu
 100 105 110

Leu Ala Arg Lys Gly Ile Thr Ala Val Ser Tyr Tyr Arg Gly Cys Asp

572

115	120	125
Ile Ser Lys Met Pro Glu Gly Asp Cys Val Val Val Ala Thr Asp Ala		
130	135	140
Leu Cys Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Tyr Asp Cys Ser		
145	150	155 160
Leu Met Val Glu Gly Thr Cys His Val Asp Leu Asp Pro Thr Phe Thr		
	165	170 175
Met Gly Val Arg Val Cys Gly Val Ser Ala Ile Val Lys Gly Gln Arg		
	180	185 190
Arg Gly Arg Thr Gly Arg Gly Arg Ala Gly Ile Tyr Tyr Tyr Val Asp		
	195	200 205
Gly Ser Cys Thr Pro Ser Gly Met Val Pro Glu Cys Asn Ile Val Glu		
	210	215 220
Ala Phe Asp Ala Ala Lys Ala Trp Tyr Gly Leu Ser Ser Thr Glu Ala		
	225	230 235 240
Gln Thr Ile Leu Asp Thr Tyr Arg Thr Gln Pro Gly Leu Pro Ala Ile		
	245	250 255
Gly Ala Asn Leu Asp Glu Trp Ala Asp Leu Phe Ser Met Val Asn Pro		
	260	265 270
Glu Pro Ser Phe Val Asn Thr Ala Lys Arg Thr Ala Asp Asn Tyr Val		
	275	280 285
Leu Leu Thr Ala Ala Gln Leu Gln Leu Cys His Gln Tyr Gly Tyr Ala		
	290	295 300
Ala Pro Asn Asp Ala Pro Arg Trp Gln Gly Ala Arg Leu Gly Lys Lys		
	305	310 315 320
Pro Cys Gly Val Leu Trp Arg Leu Asp Gly Cys Asp Ala Cys Pro Gly		
	325	330 335
Pro Glu Pro Ser Glu Val Thr Arg Tyr Gln Met Cys Phe Thr Glu Val		
	340	345 350
Asn Thr Ser Gly Thr Ala Ala Leu Ala Val Gly Val Gly Val Ala Met		
	355	360 365
Ala Tyr Leu Ala Ile Asp Thr Phe Gly Ala Thr Cys Val Arg Arg Cys		
	370	375 380
Trp Ser Ile Thr Ser Val Pro Thr Gly Ala Thr Val Ala Pro Val Val		
	385	390 395 400
Asp Glu Glu Glu Ile Val Glu Glu Cys Ala Ser Phe Ile Pro Leu Glu		
	405	410 415
Ala Met Val Ala Ala Ile Asp Lys Leu Lys Ser Thr Ile Thr Thr Thr		

573

420	425	430
Ser Pro Phe Thr Leu Glu Thr Ala Leu Glu Lys Leu Asn Thr Phe Leu		
435	440	445
Gly Pro His Ala Ala Thr Ile Leu Ala Ile Ile Glu Tyr Cys Cys Gly		
450	455	460
Leu Val Thr Leu Pro Asp Asn Pro Phe Ala Ser Cys Val Phe Ala Phe		
465	470	475
Ile Ala Gly Ile Thr Thr Pro Leu Pro His Lys Ile Lys Met Phe Leu		
485	490	495
Ser Leu Phe Gly Gly Ala Ile Ala Ser Lys Leu		
500	505	

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Cys Gln Lys Gly Tyr Lys Gly Pro Trp Ile Gly Ser Gly Met Leu Gln		
1	5	10
Ala Arg Cys Pro Cys Gly Ala Glu Leu Ile Phe Ser Val Glu Asn Gly		
20	25	30
Phe Ala Lys Leu Tyr Lys Gly Pro Arg Thr Cys Ser Asn Tyr Trp Arg		
35	40	45
Gly Ala Val Pro Val Asn Ala Arg Leu Cys Gly Ser Ala Arg Pro Asp		
50	55	60
Pro Thr Asp Trp Thr Ser Leu Val Val Asn Tyr Gly Val Arg Asp Tyr		
65	70	75
Cys Lys Tyr Glu Lys Leu Gly Asp His Ile Phe Val Thr Ala Val Ser		
85	90	95
Ser Pro Asn Val Cys Phe Thr Gln Val Pro Pro Thr Leu Arg Ala Ala		
100	105	110
Val Ala Val Asp Arg Val Gln Val Gln Xaa Tyr Leu Gly Glu Pro Lys		
115	120	125
Thr Pro Trp Thr Thr Ser Ala Cys Cys Tyr Gly Pro Asp Gly Lys Gly		
130	135	140

574

Lys Thr Val Lys Leu Pro Phe Arg Val Asp Gly His Thr Pro Gly Gly
 145 150 155 160
 Arg Met Gln Leu Asn Leu Arg Asp Arg Leu Glu Ala Asn Asp Cys Asn
 165 170 175
 Ser Ile Asn Asn Thr Pro Ser Asp Glu Ala Ala Val Ser Ala Leu Val
 180 185 190
 Phe Lys Gln Glu Leu Arg Arg Thr Asn Gln Leu Leu Glu Ala Ile Ser
 195 200 205
 Ala Gly Val Asp Thr Thr Lys Leu Pro Ala Pro Ser Gln Ile Glu Glu
 210 215 220
 Val Val Val Arg Lys Arg Gln Phe Arg Ala Arg Thr Gly Ser Leu Thr
 225 230 235 240
 Leu Pro Pro Pro Pro Arg Ser Val Pro Gly Val Ser Cys Pro Glu Ser
 245 250 255
 Leu Gln Arg Ser Asp Pro Leu Glu Gly Pro Ser Xaa Leu Pro Ser Ser
 260 265 270
 Pro Pro Val Leu Gln Leu Ala Met Pro Met Pro Leu Leu Gly Ala Gly
 275 280 285
 Glu Cys Asn Pro Phe Thr Ala Ile Gly Cys Ala Met Thr Glu Thr Xaa
 290 295 300
 Gly Xaa Pro Xaa Xaa Leu Pro Ser Tyr Pro Pro Lys Lys Glu Val Ser
 305 310 315 320
 Glu Trp Ser Asp Glu Ser Trp Ser Thr Thr Thr Thr Ala Ser Ser Tyr
 325 330 335
 Val Thr Gly Pro Pro Tyr Pro Lys Ile Arg Gly Lys Asp Ser Thr Gln
 340 345 350
 Ser Ala Thr Ala Lys Arg Pro Thr Lys Lys Lys Leu Gly Lys Ser Glu
 355 360 365
 Phe Ser Cys Ser Met Ser Tyr Thr Trp Thr Asp Val Ile Ser Phe Lys
 370 375 380
 Thr Ala Ser Lys Val Leu Ser Ala Thr Arg Ala Ile Thr Ser Gly Phe
 385 390 395 400
 Leu Lys Gln Arg Ser Leu Val Tyr Val Thr Glu Pro Arg Asp Ala Glu
 405 410 415
 Leu Arg Lys Gln Lys Val Thr Ile Asn Arg Gln Pro Leu Phe Pro Pro
 420 425 430
 Ser Tyr His Lys Gln Val Arg Leu Ala Lys Glu Lys Ala Ser Lys Val
 435 440 445

575

Val Gly Val Met Trp Asp Tyr Asp Glu Val Ala Ala His Thr Pro Ser
 450 455 460

Lys Ser Ala Lys Ser His Ile Thr Gly Leu Arg Gly Thr Asp Val Leu
 465 470 475 480

Asp Leu Gln Lys Cys Val Glu Ala Gly Glu Ile Pro Ser His Tyr Arg
 485 490 495

Gln Thr Val Ile Val Pro Lys Glu Glu Val Phe Val Lys Thr Pro Gln
 500 505 510

Lys Pro Thr Lys Lys Pro Pro Arg Leu Ile
 515 520

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Pro Val Ile Ser Thr Gln Thr Ser Pro Val Pro Ala Pro Arg Thr
 1 5 10 15

Arg Lys Asn Lys Gln Thr Gln Ala Ser Tyr Pro Val Ser Ile Lys Thr
 20 25 30

Ser Val Glu Arg Gly Gln Arg Ala Xaa Arg Lys Val Gln Arg Asp Ala
 35 40 45

Arg Pro Arg Asn Tyr Lys Ile Ala Gly Ile His Asp Gly Leu Gln Thr
 50 55 60

Leu Ala Gln Ala Ala Leu Pro Ala His Gly Trp Gly Arg Gln Asp Pro
 65 70 75 80

Arg His Lys Ser Arg Asn Leu Gly Ile Leu Leu Asp Tyr Pro Leu Gly
 85 90 95

Trp Ile Gly Asp Val Thr Thr His Thr Pro Leu Val Gly Pro Leu Val
 100 105 110

Ala Gly Ala Val Val Arg
 115

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids

576

(B) TYPE: amino acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

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Gly Ser Gly Trp Thr Asp Glu Asp Glu Arg Asp Leu Val Glu
1           5           10           15

Thr Lys Ala Ala Ala Ile Glu Ala Ile Gly Ala Ala Leu His Leu Pro
20           25           30

Ser Pro Glu Ala Ala Gln Ala Ala Leu Glu Ala Leu Glu Glu Ala Ala
35           40           45           50

Val Ser Leu Leu Pro His Val Pro Val Ile Met Gly Asp Asp Cys Ser
55           60           65           70

Cys Arg Asp Glu Ala Phe Gln Gly His Phe Ile Pro Glu Pro Asn Val
75           80           85

Thr Glu Val Pro Ile Glu Pro Thr Val Gly Asp Val Glu Ala Leu Lys
90           95           100

Leu Arg Ala Ala Asp Leu Thr Ala Arg Leu Gln Asp Leu Glu Ala Met
105          110          115

Ala Leu Ala Arg Ala Glu Ser Ile Glu Asp Ala Arg Ala Ala Ser Met
120          125          130

Pro Ser Leu Thr Glu Val Asp Ser Met Pro Ser Leu Glu Ser Ser Pro
135          140          145          150

Cys Ser Ser Phe Glu Gln Ile Ser Leu Thr Glu Ser Asp Pro Glu Thr
155          160          165

Val Val Glu Ala Gly Xaa Pro Leu Glu Phe Val Asn Ser Asn Thr Gly
170          175          180

Xaa Ser Pro Ala Arg Arg Ile Val Arg Ile Arg Gln Ala Cys Cys Cys
185          190          195

Asp Arg Ser Thr Met Lys Ala Met Pro Leu Ser Phe Thr Val Gly Glu
200          205          210          215

Cys Leu Phe Val Thr Arg Tyr Asp Pro Asp Gly His Gln Leu Phe Asp
220          225          230

Glu Arg Gly Pro Ile Glu Val Ser Thr Pro Ile Cys Glu Val Ile Gly
235          240          245

Asp Ile Arg Leu Gln Cys Asp Gln Ile Glu Glu Thr Pro Thr Ser Tyr
250          255          260

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577

Ser Tyr Ile Trp Ser Gly Ala Pro Leu Gly Thr Gly Arg Ser Val Pro
 265 270 275
 Gln Pro Met Thr Arg Pro Ile Gly Thr His Leu Thr Cys Asp Thr Thr
 280 285 290 295
 Lys Val Tyr Val Thr Asp Pro Asp Arg Ala Ala Glu Arg Ala Glu Lys
 300 305 310
 Val Thr Ile Trp Arg Gly Asp Arg Lys Tyr Asp Lys His Tyr Glu Ala
 315 320 325
 Val Val Glu Ala Val Leu Lys Lys Ala Ala Ala Thr Lys Ser His Gly
 330 335 340
 Trp Thr Tyr Ser Gln Ala Ile Ala Lys
 345 350

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Tyr Ser Gln Ala Ile Ala Lys Val Arg Arg Arg Ala Ala Ala Gly Tyr
 1 5 10 15
 Gly Ser Lys Val Thr Ala Ser Thr Leu Ala Thr Gly Trp Pro His Val
 20 25 30
 Glu Glu Met Leu Asp Lys Ile Ala Arg Gly Gln Glu Val Pro Phe Thr
 35 40 45
 Phe Val Thr Lys Arg Glu Val Phe Phe Ser Lys Thr Thr Arg Lys Pro
 50 55 60
 Pro Arg Phe Ile Val Phe Pro Pro Leu Asp Phe Arg Ile Ala Glu Lys
 65 70 75 80
 Met Ile Leu Gly Asp Pro Gly Ile Val Ala Lys Ser Ile Leu Gly Asp
 85 90 95
 Ala Tyr Leu Phe Gln Tyr Thr Pro Asn Gln Arg Val Lys Ala Leu Val
 100 105 110
 Lys Ala Trp Glu Gly Lys Leu His Pro Ala Ala Ile Thr Val Xaa Ala
 115 120 125
 Thr Cys Phe Asp Ser Ser Ile Asp Glu His Asp Met Gln Val Glu Ala

578

130	135	140
Ser Val Phe Ala Ala Ala Ser Asp Asn Pro Ser Met Val His Ala Leu		
145	150	155 160
Cys Lys Tyr Tyr Ser Gly Gly Pro Met Val Ser Pro Asp Gly Val Pro		
	165	170 175
Leu Gly Tyr Arg Gln Cys Arg Ser Ser Gly Val Leu Thr Thr Ser Ser		
	180	185 190
Ala Asn Ser Ile Thr Cys Tyr Ile Lys Val Ser Ala Ala Cys Arg Arg		
	195	200 205
Val Gly Ile Lys Ala Pro Ser Phe Phe Ile Ala Gly Asp Asp		
	210	215 220

(2) INFORMATION FOR SEQ ID NO:615:

- (I) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GGGGCCGAAT TCTACAGCAC ATATGGCATG TAC

33

(2) INFORMATION FOR SEQ ID NO:616:

- (I) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGGGAAAAGC TTATTAGTGT TTTTGGTAG CCTCAAAG

38

(2) INFORMATION FOR SEQ ID NO:617:

- (I) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid

579

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GGGGCCGAAT TCATCTTTGA GGCTACCAA AAAC

34

(2) INFORMATION FOR SEQ ID NO:618:

(I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GGGGAAAAGC TTATTAATAG TAGTATATGC CAGCTCTC

38

(2) INFORMATION FOR SEQ ID NO:619:

(I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GGGGCCGAAT TCGGGAGAGC TGGCATATAC TAC

33

(2) INFORMATION FOR SEQ ID NO:620:

(I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GGGGAAAAGC TTATTAGTCAT TGGGAGCAGCA TAGCC

35

(2) INFORMATION FOR SEQ ID NO:621:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GGGGCCGAAT TCTATGGCTA TGCTGCTCCC AATG

34

(2) INFORMATION FOR SEQ ID NO:622:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GGGGAAAAGC TTATTATGCAC ACTCCTCCAC GATTTC

36

(2) INFORMATION FOR SEQ ID NO:623:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GGGGCCGAAT TCGAGGAAAT CGTGGAGGAG TGT

33

(2) INFORMATION FOR SEQ ID NO:624:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid

581

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGGGAAAAGC TTATTACTTG GACGCAATTG CGCCTCC

37

(2) INFORMATION FOR SEQ ID NO:625:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGGGCCGAAT TCTCAGCAAT AGTTAAAGGC CAG

33

(2) INFORMATION FOR SEQ ID NO:626:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GGGGAAAAGC TTATTAATTT GCTCCTATCG CAGGTAAC

38

(2) INFORMATION FOR SEQ ID NO:627:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

582

GGGGCCGAAT TCCCTGGGTTA CCTGCGATAG GA

32

(2) INFORMATION FOR SEQ ID NO:628:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GGGGAAAAGC TTATTACAGA ACCCCACAAG GTTTTTTC

38

(2) INFORMATION FOR SEQ ID NO:629:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GGGGAAGAAT TCTGCCAGAA GGGGTACAAG GGC

33

(2) INFORMATION FOR SEQ ID NO:630:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GGAAAAGGAT CCTTAACAGC AAGCAGATGT CGTCCA

36

(2) INFORMATION FOR SEQ ID NO:631:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

583

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GGGGAAGAAT TCACTCCTTG GACGACATCTG CT

32

(2) INFORMATION FOR SEQ ID NO:632:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GGAAAAGGAT CCTTAACCTT CTAACGGGTC ACTTCG

36

(2) INFORMATION FOR SEQ ID NO:633:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GGGGAAGAAT TCCTGCAACG AAGTGACCCG TTA

33

(2) INFORMATION FOR SEQ ID NO:634:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GGGGAAGGAT CCTTAAGTTG CAGACAGAAC TTTAGA

36

(2) INFORMATION FOR SEQ ID NO:635:

584

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GGGGCCGAAT TCACTGCTTC TAAAGTTCTG TCT

33

(2) INFORMATION FOR SEQ ID NO:636:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GGAAAAGGAT CCTTAGATAA GCCTTGGGGG TTTCTT

36

(2) INFORMATION FOR SEQ ID NO:637:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GGGGAAGAAT TCTACGGTCC TGACGTAAGG GT

32

(2) INFORMATION FOR SEQ ID NO:638:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GGAAAAGGAT CCTTAGTCAA CGCCAGCTGAA ATTGC

35

(2) INFORMATION FOR SEQ ID NO:639:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GGGGAAGAATT CCTTGAGGCA ATTTTCAGCTG GC

32

(2) INFORMATION FOR SEQ ID NO:640:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GGAAAAGGAT CCTTACAACT GCAGAACAGG TGGTGA

36

(2) INFORMATION FOR SEQ ID NO:641:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GGAAAAGGAT CCAGTGACGC TTGGTGCCTG GTC

33

(2) INFORMATION FOR SEQ ID NO:642:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid

586

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GGGGAAAAGC TTAAAGTTTA TTGTACAGGA ACCG

34

(2) INFORMATION FOR SEQ ID NO:643:

- (I) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GGGGAAGAAT TCCGGCTAGG TCGGTTCTG TAC

33

(2) INFORMATION FOR SEQ ID NO:644:

- (I) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GGAAAAGGAT CCTTATGTCC CATGCACGAC CACAGC

36

(2) INFORMATION FOR SEQ ID NO:645:

- (I) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

587

GGGGAAGAAT TCTGGTTTGA GGCTGTGGTC GTG

33

(2) INFORMATION FOR SEQ ID NO:646:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GGAAAAGGAT CCTTACAAGGC CGCCCCAATG GCCTC

35

(2) INFORMATION FOR SEQ ID NO:647:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GGGGAAGAAT TCGCCGCCAT CGAGGCCATTG GG

32

(2) INFORMATION FOR SEQ ID NO:648:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GGAAAAGGAT CCTTACACCT CGGTGAGCGA AGGCATC

37

(2) INFORMATION FOR SEQ ID NO:649:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

588

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GGGGAAGAAT TCGCAGCTTC GATGCCTTCG CTC

33

(2) INFORMATION FOR SEQ ID NO:650:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGAAAAGGAT CCTTAAATCA CTTACATAT AGGAGTAG

38

(2) INFORMATION FOR SEQ ID NO:651:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GGGGAAGAAT TCGAGGTATC TACTCCTATAT GTG

33

(2) INFORMATION FOR SEQ ID NO:652:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GGAAAAGGAT CCTTATTTAGC TATAGCCTGG GAATAG

36

589

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

CATCAGCTCT GAACACCGCC GCAC

24

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GCCGAGAAGC ATGCAGTTGT TAAGG

25

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GCCAGCTGTT CAGTCCATCT CC

22

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

CTCTACTGCA CACGTCAGGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

CCAGAGCCAC CAGGCATCCG C

21

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

CAGGCAGAAG CCTATGTCCT CCAGG

25

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GTGGTAGTAG CCGAGAGATG CCTG

24

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

591

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CACTCCATCG CCTGCACTTA TCTCG

25

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

CTCGAATTGC AAGTTGGGTG CTTGG

25

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATGTGACA AGTGTGAGGC ACG

23

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

592

GGAGATGCTA AAGCTGTGGG AATC

24

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAGGACGTGG CACTAGAGAC AGAG

24

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNG CGCA

34

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GCTTCGGCCA TTGGTTACAT TCTCC

666

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

593

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GGTCATCATC CCGCATGTGC TAAC

24

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GGGATTTAGG ACCAAGACCT C

21

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

CCAAAAGTCG AAAGGCACCT TCC

23

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

CAACCGTGCC TCTGCCAGCT TC

22

(2) INFORMATION FOR SEQ ID NO:671:

594

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

TYGCTYACKGC KACCCCHCCK G

21

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

TGCCMGCTYT CCCMCKGCC

19

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5091 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

TACGTTTGGG TTCTTCCCAG GAGTCCCCC CCTTAACAAC TGCATGCTTC TCGGCACTGA	60
GGTGTCAGAG GTATTGGGTG GGGCGGGCCT CACTGGGGGG TTTTACGAAC CTCTGGTGCG	120
GCGGTGTTCA GAGCTGATGG GTCGGCGGAA TCCGGTCTGC CCGGGGTTTG CATGGCTCTC	180
TTCCGGGACGG CCTGATGGGT TCATACATGT TCAGGGCCAC TTGCAGGAGG TGGATGCGGG	240
CAACTTCATT CCGCCCCAC GCTGGTTGCT CTTGGACTTT GTATTTGTCC TGTTATACCT	300
GATGAAGCTG GCAGAGGCAC GGTGGTCCC GCTGATCCTC CTCTGCTAT GGTGGTGGGT	360

595

GAACCAGTTG	GCGGTCCTTG	KTGTGSCGGC	TGCKCRCGCC	GCCGTGGCTG	GAGAGGTGTT	420
TGCGGGCCCT	GCCTTGTCCT	GGTGTCTGGG	CCTACCCTTC	GTGAGTATGA	TCCTGGGGCT	480
AGCAAACCTG	GTGTTGTACT	TCCGCTGGAT	GGGTCTCTCA	CGCCTGATGT	TCCTCGTGTT	540
GTGGAAGCTC	GCTCGGGGGG	CTTTCCCGCT	GGCATTACTG	ATGGGGATTT	CCGCCACTCG	600
CGGCCGCACC	TCTGTGCTTG	GCGCCGAATT	CTGCTTTGAT	GTCACCTTTG	AAGTGGACAC	660
GTCAGTCTTG	GGTTGGGTGG	TTGCTAGTGT	GGTGGCTTGG	GCCATAGCGC	TCCTGAGCTC	720
TATGAGCGCG	GGGGGGTGGA	AGCACAAAGC	CATAATCTAT	AGGACGTGGT	GTAAAGGGTA	780
CCAGGCYCTT	CGCCAGCGCG	TGGTGCGTAG	CCCCCTCGGG	AGGGGCGGCC	CACCAAGCCG	840
CTGACGATAR	GCCTGGTGTC	TGGCCTCTTA	CATCTGGCCG	GACGCTGTGA	TGTTGGTGTT	900
TGTGGCCATG	GTCCTCCTCT	TCGGCCTTTT	CGACGCGCTC	GATTGGGCCT	TGGAGGAGCT	960
CCTTGTTGTCG	CGGCCTTCGT	TGCGTCGTTT	GGCAAGGGTG	GTGGAGTGTT	GTGTGATGGC	1020
GGGCGAGAAG	GCCACTACCG	TCCGGCTTGT	GTCCAAGATG	TGCGCGAGAG	GGGCCTACCT	1080
GTTTGACCAC	ATGGGGTCGT	TCTCGCGCGC	GGTCAAGGAG	CGCTTGCTGG	AGTGGGACGC	1140
GGCTTTGGAG	MCCCTGTCAT	TCACTAGGAC	GGACTGTGCG	ATCATACGAG	ACGCCGCCAG	1200
ACCCTGAGCT	GCGGCCAATG	CGTCATGGGC	TTGCGTGGTG	GCTAGGCGCG	GCGATGAGGT	1260
CCTGATTGGG	GTCTTTTCAGG	ATGTGAACCA	CTTGCCTCCG	GGGTTTGYYC	CTACAGCGCC	1320
TGTTGTGATC	CGTCGGTGCG	GAAAGGGCTT	CCTCGGGGTC	ACTAAGGCTG	CCTTGACTGG	1380
TCGGGATCCT	GACTTACACC	CAGGAAACGT	CATGTTTTTG	GGGACGGCTA	CCTCGCGCAG	1440
CATGGGAACG	TGCTTAAACG	GGTTGCTGTT	CACGACATTC	CATGGGGCTT	CTTCCCGAAC	1500
CATTGCGACA	CCTGTGGGGG	CCCTTAACCC	AAGGTGGTGG	TCGGCCAGTG	ATGACGTCAC	1560
GGTCTATCCC	CTCCCCGATG	GAGCTAACTC	GTTGGTTCCC	TGCTCGTGTC	AGGCTGAGTC	1620
CTGTTGGGTC	ATYCGATCCG	ATGGGGCTCT	TTGCCATGGC	TTGAGCAAGG	GGGACAAGGT	1680
AGAACTGGAC	GTGGCCATGG	AGGTTGCTGA	CTTTCGTGGG	TCGTCTGGGT	CTCCTGTCCT	1740
ATGCGACGAG	GGGCACGCTG	TAGGAATGCT	CGTGTCCGTC	CTTCATTCGG	GGGGGAGGGT	1800
GACCGCGGCT	CGATTCACTC	GGCCGTGGAC	CCAAGTCCCA	ACAGACGCCA	AGACTACCAC	1860
TGAGCCACCC	CCGGTGCCAG	CTAAAGGGGT	TTTCAAAGAG	GCTCCTCTTT	TCATGCCAAC	1920
AGGGGCGGGG	AAAAGCACAC	GCGTCCCTTT	GGAGTATGGA	AACATGGGGC	ACAAGGTCCT	1980
GATTCTCAAC	CCGTCGGTTG	CCACTGTGAG	GGCCATGGGC	CCTTACATGG	AGAGGCTGGC	2040
GGGGAAACAT	CCTAGCATTT	TCTGTGGACA	CGACACAACA	GCTTTCACAC	GGATCACGGA	2100

CTCTCCATTG ACGTACTCTA CCTATGGGAG GTTTCCTGGCC AACCCGAGGC AGATGCTGAG	2160
GGGAGTTTCC GTGGTCATCT GTGATGAGTG CCACAGTCAT GACTCAACTG TGTGCTGGG	2220
TATAGGCAGG GTCAGGGACG TGGCGCGGGG GTGTGGAGTG CAATTAGTGC TCTAGCCTAC	2280
TGCGACTCCC CCGGGCTCGC CTATGACTCA GCATCCATCC ATAATTGAGA CAAAGCTGGA	2340
CGTTGGTGAG ATCCCCTTTT ATGGGCATGG TATCCCCCTC GAGCGTATGA GGA CTGGTTCG	2400
CCACCTTGTA TTCTGCCATT CCAAGGCGGA GTGCGAGAGA TTGGCCGGCC AGTTCTCCGC	2460
GCGGGGGGTT AATGCCATCG CCTATTATAG GGGTAAGGAC AGTTCCATCA TCAAAGACGG	2520
AGACCTGGTG GTTTGTGCGA CAGACGCGCT CTCTACCGGG TACACAGGAA ACTTCGATTC	2580
TGTCACCGAC TGTGGGTTGG TGGTGGAGGA GGTCGTTGAG GTGACCCTTG ATCCCACCAT	2640
TACCATTTC TGTGCGACTG TCCCTGCTTC GGCTGAATTG TCGATGCAGC GGCGCGGACG	2700
CACGGGGAGA GGTCGGTCGG GCCGCTACTA CTACGCTGGG GTCGGTAAGG CTCCCGCGGG	2760
GGTGGTGCGG TCTGGTCCGG TCTGGTCGGC AGTGGAAAGCT GGAGTGACCT GGTATGGAAT	2820
GGAACTGAC TTGACAGCAA ACCTTCTGAG ACTTTACGAC GACTGCCCTT ACACCGCAGC	2880
CGTCGCAGCT GACATTGGTG AAGCCGCGGT GTTCTTTGCG GGCCTCGCGC CCCTCAGGAT	2940
GCATCCCGAT GTTAGCTGGG CAAAAGTTCG CGGCGTCAAT TGGCCCCCTCC TGGTGGGTGT	3000
TCAGCGGACG ATGTGTCGGG AAACACTGTC TCCCGGCCCG TCGGACGACC CTCAGTGGGC	3060
AGGTCTGAAA GGCCCGAATC CTGTCCCACT ACTGCTGAGG TGGGGCAATG ATTTGCCATC	3120
AAAAGTGGCC GGCCACCACA TAGTTGACGA TCTGGTCCGT CGGCTCGGTG TGGCGGAGGG	3180
ATACGTGCGC TGTGATGCTG GRCCCATCCT CATGGTGGGC TTGGCCATAG CGGGCGGCAT	3240
GATCTACGCC TCTTACACTG GGTGCTAGT GGTGGTAACA GACTGGGATG TGAAGGGAGG	3300
TGGCAATCCC CTTTATAGGA GTGGTGACCA GGCCACCCCT CAACCCGTGG TGCAGGTCCC	3360
CCCGGTAGAC CATCGGCCGG GGGGGGAGTC TGCGCCACGG GATGCCAAGA CAGTGACAGA	3420
TGCGGTGGCA GCCATCCAGG TGAAGTGGCA TTGGTCTGTG ATGACCCTGT CGATCGGGGA	3480
AGTCCTCACC TTGGCTCAGG CTAAGACAGC CGAGGCCTAC GCAGCTACTT CCAGGTGGCT	3540
CGCTGGCTGC TACACGGGGA CGCGGGCCGT CCCCCTGTA TCAATTGTTG ACAAGCTCTT	3600
CGCCGGGGGT TGGGCCGCGG TGGTGGGTCA CTGTACAGC GTCATTGCTG CGGCGGTGGC	3660
TGCCTATGGA GCTTCTCGAA GTCCTCCACT GGCCGCGGCG GCGTCCTACC TCATGGGGTT	3720
GGGCGTCGGA GGCAACGCAC AGGCGCGCTT GGCTTCAGCT CTTCTACTGG GGGCTGCTGG	3780
GTACGGCTCT GGGGGACCCC TGTCAGTGGG ACTCACCATG GCGGGGGCCT TCATGGGACA	3840

597

GGTGCCAGCG TGTCCCTCC CTCGTCACTG TCCTACTTGG GGCTGTGGGA GGTGGGAGG	3900
GCGTTGTCAA CGCTGCCAGT CTCGTCTTCG ACTTCATGGC TGGGAAACTT TCAACAGAAG	3960
ACCTTTGGTA TGCCATCCCG GTACTCACTA GTCCTGGRGC GGGCCTCGCG GGGATTGCCC	4020
TTGGTCTGGT TTTGTACTCA GCAAACAACT CTGGCACTAC CACATGGCTG AACCGTCTGC	4080
TGACGACGTT GCCACGGTCA TCTTGACATC CCGACAGCTA CTTCCAACAG GCTGACTACT	4140
GCGACAAGGT CTCGGCAATC GTGCGCCGCC TGAGCCTTAC TCGCACCGTG GTGGCCCTGG	4200
TCAACAGGGA GCCTAAGGTG GATGAGGTCC AGGTGGGGTA CGTCTGGGAT CTGTGGGAGT	4260
GGGTGATGCG CCAGGTGCGC ATGGTGATGT CTAGACTCCG GGCCCTCTGC CCTGTGGTGT	4320
CACCTCCCTT GTGGCACTGC GGGGAGGGGT GGTCCGGTGA ATGGCTTCTC GATGGGCACG	4380
TGGAGAGTCG TTGTCTGTGC GGGTGTGTAA TCACCGGCGA CGTCCTCAAT GGGCAACTCA	4440
AAGATCCAGT TTA CTCTACC AAGCTGTGCA GGCACACTG GATGGGAACT GTGCCGGTCA	4500
ACATGCTGGG CTACGGGGAA ACCTCACCTC TTCTCGCCTC TGACACCCCG AAGGTGGTAC	4560
CCTTCGGGAC GTCGGGGTGG GCTGAGGTGG TGGTGACCCC TACCCACGTG GTGATCAGGC	4620
GCACGTCCTG TTACAACTG CTTGCGCAGC AAATTCCTTC AGCAGCTGTA GCTGAGCCCT	4680
ACTACGTTGA TGGCATTCCG GTCTCTTGGG AGGCTGACGC GAGAGCGCCG GCCATGGTCT	4740
ACGGTCCGGG CCAAAGTGTT ACCATTGATG GGGAGCGCTA CACCCTCCG CACCAGTTGC	4800
GGATGCGGAA TGTGGCGCCC TCTGAGGTTT CATCTGAGGT CAGCATCGAG ATCGGGACGG	4860
AGACTGAAGA CTCAGAACTG ACTGAGGCCG ATTTGCCACC AGCGGCTGCT GCCCTCCAAG	4920
CGATAGAGAA TGCTGCGAGA ATTCTCGAAC CGCACATCGA TGTCAYCATG GAGGATTGCA	4980
GTACACCCTC TCTCTGTGGT AGTAGCCGAG AGATGCCTGT GTGGGGAGAA GACATACCCC	5040
GCACTCCATC GCCTGCACTT ATCTCGGTTA CGGAGAGCAG CTCAGATGAG A	5091

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

TCGCCACTGC TACCCCTCCG GGCTCCGTCA CTGTGTCCCA TCCTAACATC GAGGAGGTTG	60
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598

CTCTGTCCAC CACCGGAGAG ATCCCCTTTT ACGGCAAGGC TATCCCCCTC GAGGTGATCA	120
AGGGGGGAAG ACATCTCATC TTCTGCCACT CAAAGAAGAA GTGCGACGAG CTCGCCGCGA	180
AGCTGGTCGC ATTGGGCATC AATGCCGTGG CCTACTACCG CGGTCTTGAC GTGTCTGTCA	240
TCCCCACCAG CGGCGATGTT GTCGTCGTGT CGACCGATGC TCTCATGACT GGCTTTACCG	300
GCGACTTCGA CTCTGTGATA GACTGCAACA CGTGTGTCAC TCAGACAGTC GATTTTAGCC	360
TTGACCCTAC CTT	373

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GACGTTGCTG AGATCCCCTT	20
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(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

CGAAGTTTCC TGTGTACCC	19
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(2) INFORMATION FOR SEQ ID NO:677:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

ATCCCCTTTT ATGGGCATGG CATACCCCTG GAGAGGATGC GGACCGGCAG GCACCTCGTA 60
ATCCCCTTTT ATGGGCATGG CATACCCCTG GAGAGGATGC GGACCGGCAG GCACCTCGTA 120
AATGCCATTG CCTATTATAG GGGGAAAGAC AGTTCT 156

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

ATCCCCTTTT ATGGGCATGG AATCCCCCTC GAGCGGATGC GGACCGGGCG CCACCTCGTG 60
TTCTGCCATT CAAAGGCGGA GTGCGAGCGG TTGGCTGGCC AGTTCTCTTC GCGGGGGGTG 120
AATGCCATTG CCTATTACAG GGGGAAAGAC AGTTCC 156

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CCAATCTCTC GCACTCCGCC TTG 23

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

CTCACCAACG TCCAGCTTTG TCTC

24

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

CTCGTATGAT GCGACAGTCC GTCC

24

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GTAGTGGCCT TCTCGCCCGC CATC

24

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

CACTCCACCA CCCTTGCCAA ACG

23

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid

601

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

CCTGGTACCC TTTACACCAC GTCC

24

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GATTATGGCC TTTGTGCTTC CACCC

25

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CTCCAAAGCC GCGTCCCACT CCAGC

25

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

602

CATCATCAAA GACGGAGACC TGGTGG

26

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GCATGATCTA CGCCTCTTAC ACTGG

25

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GTCGCTAGTG GTGGTAACAG ACTGG

25

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGTGCGCATG GTGATGTCTA GACTC

25

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

603

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GGTCCGGTGA ATGGCTTCTC GATGG

25

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

ACCAGTTGCG GATGCGGAAT GTG

23

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GCATCGAGAT CGGGACGGAG ACTG

24

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNG GCCA

34

(2) INFORMATION FOR SEQ ID NO:695:

604

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

CAGTTCAAGC TTGTCCAGGA ATTCNNNNNC CGGA

34

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

CATCAGCTCT GAACACCGCC GCAC

24

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GCCGAGAAGC ATGCAGTTGT TAAGG

25

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

605

GCCAGCTGTT CAGTCCATCT CC

22

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

CTCTACTGCA CACGTCAGGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

CCAGAGCCAC CAGGCATCCG C

21

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

CAGGCAGAAG CCTATGTCCT CCAGG

25

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

606

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GTGGTAGTAG CCGAGAGATG CCTG

24

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

CACTCCATCG CCTGCACTTA TCTCG

25

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

CTCGAATTGC AAGTTGGGTG CTTGG

25

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATGTGACA AGTGTGAGGC ACG

23

607

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GGAGATGCTA AAGCTGTGGG AATC

24

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAGGACGTGG CACTAGAGAC AGAG

24

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GCCGCTGAAT TCATGCCTTG TTATTTCTAC TCAAAC

36

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

608

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCCGCAGGAT CCTCGAACGA CCGCTCCTGC CAC

33

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GCCGCAGGAA TTCATGGCTT GGCTGTGGTT GCTG

34

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GCIACIGCIA CNCCNCCNGG

20

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

ATGGTIAIIG TNGGRTCHAR R

21

609

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

ATGGGCATGG CATCCCCCTG GA

22

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

TCCTTGATGA TTGAACTGTC

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GGCACCTCGT GTTCTGCCA

19

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGCACCTCGTG TTCTGCCA

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

AGGTCTCCGT CCTTGATGAT

20

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

TTATGGGCAT GGCATCCCC TGGAGCGGAT GAGGACCGGT AGGCACCTGG TATTCTGCCA	60
CTCAAAGGCG GAGTGTGAGA GGCTGGCCGG CCAATTCTCC TCACGGGGGG TTAATGCTGT	120
TGCCTATTAT AGGGGTAAGG ACAGTTCAAT CATCAAGGAT GGTGACCTGG TGGTGTGCGC	180
TACTGACGCG CTATCTACC	199

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

TTATGGGCAT GGCATACCTC TCGAACGGAT GCGGACCGGA AGGCACCTCG TGTTCTGCCA	60
TTCAAAGGCG GAGTGCAGC GGCTCGCTGG TCAGTTTTCT GCGAGGGGGG TAAACGCCAT	120
TGCITATTAT AGGGGCAAAG ACAGTTCCAT CATCAAGGAC GGAGACCTAG TGGTGTGCGC	180
CACAGACGCG CTATCCACG	199

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

TTATGGGCAT GGCATTCTC TGGAGCGGAT GCAGACCGGT AGACATCTTG TGTTCCGCCA	60
CTCGAAGGCG GAGTGCAGC GGCTTGCCGG CCAGTTCTCC TCTAGGGGGG TCAACGCCAT	120
TGCCTATTAC AGGGGTAAGG ACAGCTCCAT CATCAAGGAC GGAGACCTCG TTGTGTGCGC	180
CACTGATGCG CTCTCTACG	199

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

TTATGGGCAT GGCATACCCC TCGAACGGAT GCGAACCGGA GGGCACCTCG TGTTCTGTCA	60
TTCCAAGGCG GAGTGCAGC GGCTTGCTGG CCAGTTCTCT GCGAGGGGGG TGAATGCCAT	120
TGCCTATTAT AGGGGCAAAG ACAGTTCCAT CATCAAGGAT GGCGACCTGG TGGTGTGCGC	180

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612

TACGCACGCG CTATCCACC

199

WHAT IS CLAIMED IS:

1. A purified polynucleotide or fragment thereof derived from hepatitis GB virus (HGBV) capable of selectively hybridizing to the genome of HGBV or the complement thereof.

2. The purified polynucleotide or fragment thereof of claim 1 wherein said polynucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

3. The purified polynucleotide or fragment thereof of claim 1 wherein said polynucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 40% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

4. The purified polynucleotide or fragment thereof of claim 1 wherein said polynucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

5. A recombinant polynucleotide or fragment thereof derived from hepatitis GB virus (HGBV) capable of selectively hybridizing to the genome of HGBV or the complement thereof.

6. The recombinant polynucleotide of claim 5 wherein said nucleotide comprises a sequence that encodes at least one epitope of HGBV.

7. The recombinant polynucleotide of claim 6 wherein said recombinant nucleotide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at

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least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

8. The recombinant polynucleotide of claim 5 wherein said polynucleotide is contained within a recombinant vector.

9. The polynucleotide of claim 8 further comprising a host cell transformed with said vector.

10. A hepatitis GB virus (HGBV) recombinant polynucleotide or fragment thereof comprising a nucleotide sequence derived from an HGBV genome.

11. The HGBV recombinant polynucleotide of claim 10 wherein said polynucleotide is contained within a recombinant vector.

12. The HGBV recombinant polynucleotide of claim 10 further comprising a host cell transformed with said vector.

13. The HGBV recombinant polynucleotide of claim 10, wherein said sequence encodes an epitope of HGBV.

14. The HGBV recombinant polynucleotide of claim 13, wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

15. The HGBV recombinant polynucleotide of claim 13 wherein said polynucleotide is contained within a recombinant vector.

16. The HGBV recombinant polynucleotide of claim 15 further comprising a host cell transformed with said vector.

17. A recombinant expression system comprising an open reading frame of DNA or RNA derived from hepatitis GB virus (HGBV) wherein said

open reading frame comprises a sequence of HGBV genome or cDNA and wherein said open reading frame is operably linked to a control sequence compatible with a desired host.

18. The expression system of claim 17 further comprising a cell transformed with said recombinant expression system.

19. The expression system of claim 18 further comprising a polypeptide of at least about eight amino acids in length produced by said cell.

20. Purified hepatitis GB virus (HGBV).

21. The purified virus of claim 20 further comprising a preparation of HGBV polypeptide or fragment thereof.

22. A purified polypeptide derived from hepatitis GB virus (HGBV) comprising an amino acid sequence or fragment thereof wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

23. A recombinant polypeptide comprising an amino acid sequence or fragment thereof wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

24. A recombinant polypeptide comprising an amino acid sequence or fragment thereof characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

25. An antibody directed against at least one hepatitis GB virus (HGBV) epitope.
26. The antibody of claim 25 wherein said antibody is polyclonal.
27. The antibody of claim 25 wherein said antibody is monoclonal.
28. A fusion polypeptide comprising at least one hepatitis GB virus (HGBV) polypeptide or fragment thereof .
29. A particle that is immunogenic against hepatitis GB virus (HGBV) infection, comprising a non-HGBV polypeptide having an amino acid sequence capable of forming a particle when said sequence is produced in a eukaryotic or prokaryotic host, and at least one HGBV epitope.
30. A polynucleotide probe for hepatitis GB virus (HGBV) wherein said polynucleotide probe is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.
31. An assay kit for determining the presence of hepatitis GB virus (HGBV) antigen or antibody in a test sample comprising a container containing a polypeptide possessing at least one HGBV epitope present in an HGBV antigen.
32. The assay kit of claim 31, wherein said polypeptide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.
33. The assay kit of claim 32 wherein said polypeptide is attached to a solid phase.
34. A kit for determining the presence of hepatitis GB virus (HGBV) antigen or antibody in a test sample comprising a container containing an antibody

which specifically binds to an HGBV antigen, wherein said antigen comprises an HGBV epitope encoded by a sequence having at least about 60% sequence similarity to a sequence of HGBV.

35. The kit of claim 34 wherein said antibody is attached to a solid phase.

36. A kit for determining the presence of hepatitis GB virus (HGBV) polynucleotides in a test sample suspected of containing said polynucleotides, comprising a container containing a polynucleotide probe wherein said polynucleotide probe comprises a nucleotide sequence characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

37. A method for producing a polypeptide containing at least one hepatitis GB virus (HGBV) epitope comprising incubating host cells transformed with an expression vector comprising a sequence encoding a polypeptide characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

38. A method for detecting hepatitis GB virus (HGBV) nucleic acid in a test sample suspected of containing HGBV comprising:

- a. reacting the test sample with a probe for an HGBV polynucleotide encoded by a sequence of HGBV or fragment thereof wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C, under conditions and for a time which allows the formation of a complex between the probe and the HGBV nucleic acid in the test sample;
- b. detecting the complex which contains the probe.

39. The method of claim 38 further comprising the step of amplifying the probe of step (a) by the polymerase chain reaction (PCR) technique.

40. The method of claim 38 further comprising the step of amplifying the probe of step (a) by the ligase chain reaction (LCR) technique.

41. A method for detecting hepatitis GB virus (HGBV) antigen in a test sample suspected of containing HGBV comprising:

- a. contacting the test sample with an antibody or fragment thereof which specifically binds to at least one HGBV antigen, for a time and under conditions sufficient to allow the formation of antibody/antigen complexes;
- b. detecting said complex containing the antibody.

42. The method of claim 41 wherein said antibody is attached to a solid phase.

43. The method of claim 41 wherein said antibody is a monoclonal or polyclonal antibody.

44. A method for detecting hepatitis GB virus (HGBV) antibodies in a test sample suspected of containing said antibodies, comprising:

- a. contacting the test sample with a probe polypeptide wherein said polypeptide contains at least one HGBV epitope comprising an amino acid sequence or fragment thereof is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C, for a time and under conditions sufficient to allow antigen/antibody complexes to form;
- b. detecting said complexes which contain the probe polypeptide.

45. The method of claim 42 wherein said probe polypeptide is attached to a solid phase.

46. The method of claim 42 wherein said solid phase is selected from the group consisting of beads, microtiter wells, walls of test tube, nitrocellulose strips, magnetic beads and non-magnetic beads.

47. The method of claim 44 wherein said polypeptide is a recombinant protein or a synthetic peptide which encodes at least one epitope of HGBV is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

48. The method of claim 44 wherein said sequence is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

49. A vaccine for treatment of hepatitis GB virus (HGBV) infection comprising a pharmacologically effective dose of an immunogenic HGBV polypeptide or fragment thereof which polypeptide is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C, in a pharmaceutically acceptable excipient.

50. A vaccine for treatment of hepatitis GB virus (HGBV) infection comprising an inactivated or attenuated HGBV in a pharmacologically effective dose in a pharmaceutically acceptable excipient.

51. A tissue culture grown cell infected with hepatitis GB virus (HGBV).

52. The tissue culture grown cell of claim 51 wherein said HGBV is transfected into a cell.

53. The tissue culture grown cell of claim 51 wherein said HGBV comprises a subgenomic fragment of the HGBV gene.

54. A method for producing antibodies to hepatitis GB virus (HGBV) comprising administering to an individual an isolated immunogenic polypeptide or fragment thereof comprising at least one HGBV epitope in an amount sufficient to produce an immune response.

55. A synthetic peptide encoding an epitope of hepatitis GB virus (HGBV) comprising a sequence of HGBV or fragment thereof is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

56. The synthetic polypeptide of claim 55 attached to a solid support.

57. A diagnostic reagent comprising a polynucleotide derived from hepatitis GB virus (HGBV), wherein said polynucleotide or fragment thereof encodes at least one epitope of HGBV and is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

58. A diagnostic reagent comprising a polypeptide or fragment thereof derived from hepatitis GB virus (HGBV), wherein said polypeptide or fragment thereof encodes at least one epitope of HGBV and is characterized by a positive stranded RNA genome wherein said genome comprises an open reading frame (ORF) encoding a polyprotein wherein said polyprotein comprises an amino acid sequence having at least 35% identity to an amino acid sequence selected from the group consisting of HGBV-A, HGBV-B and HGBV-C.

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FIGURE 1

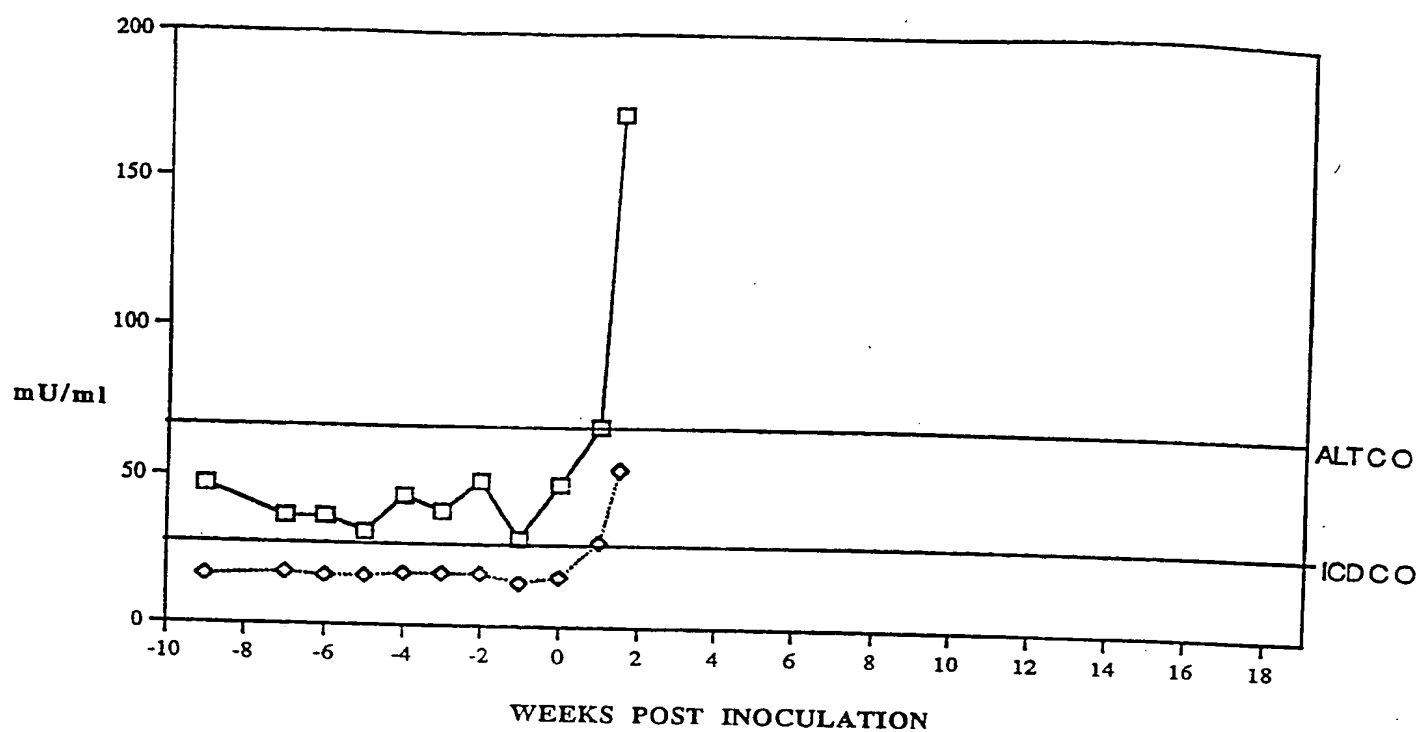
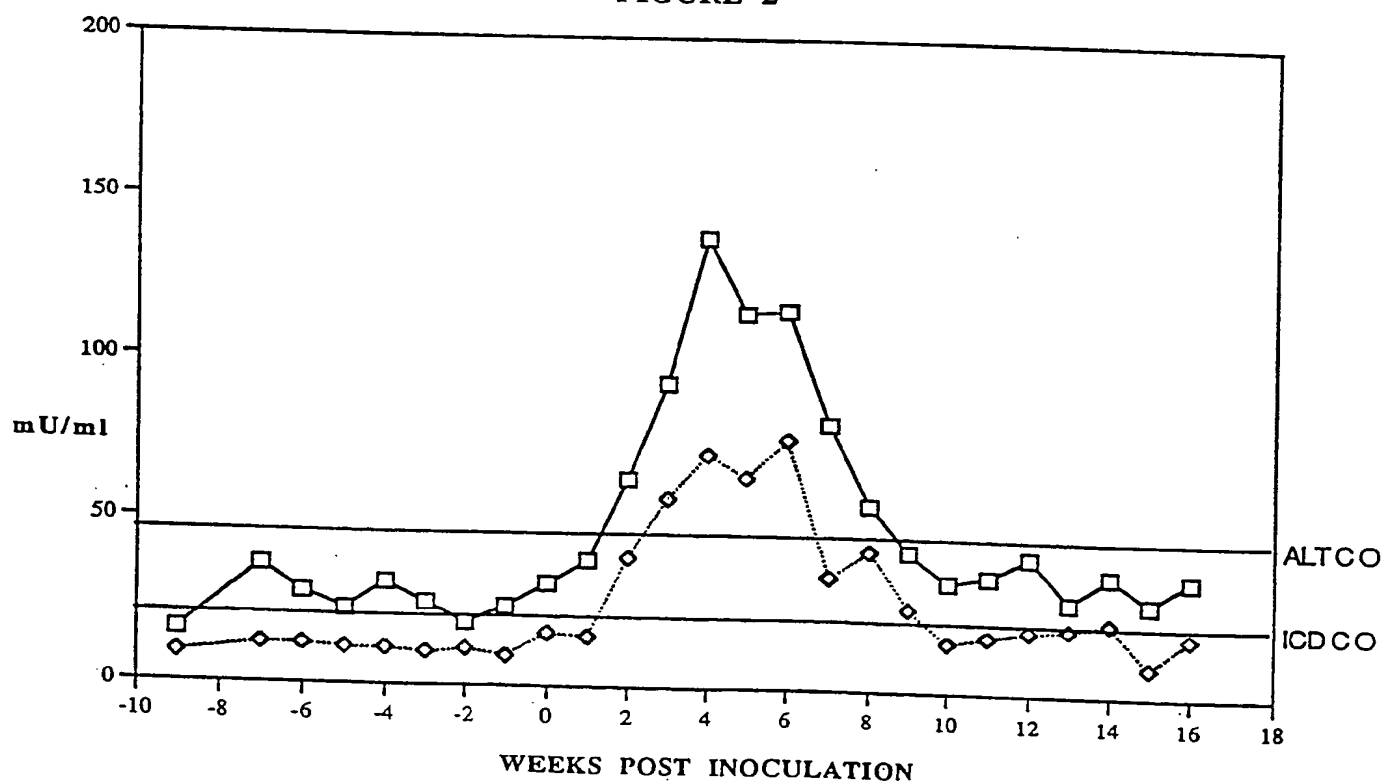


FIGURE 2



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FIGURE 3

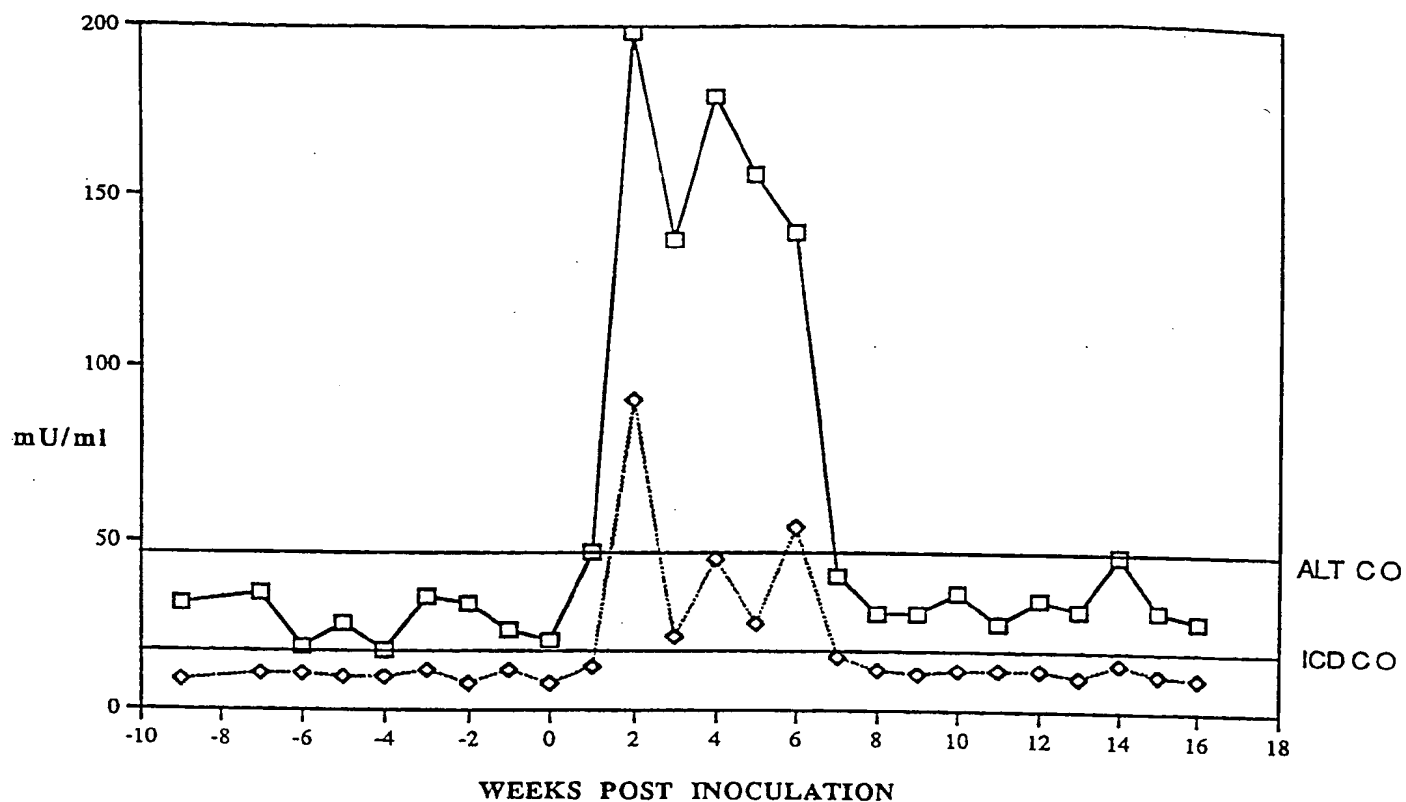
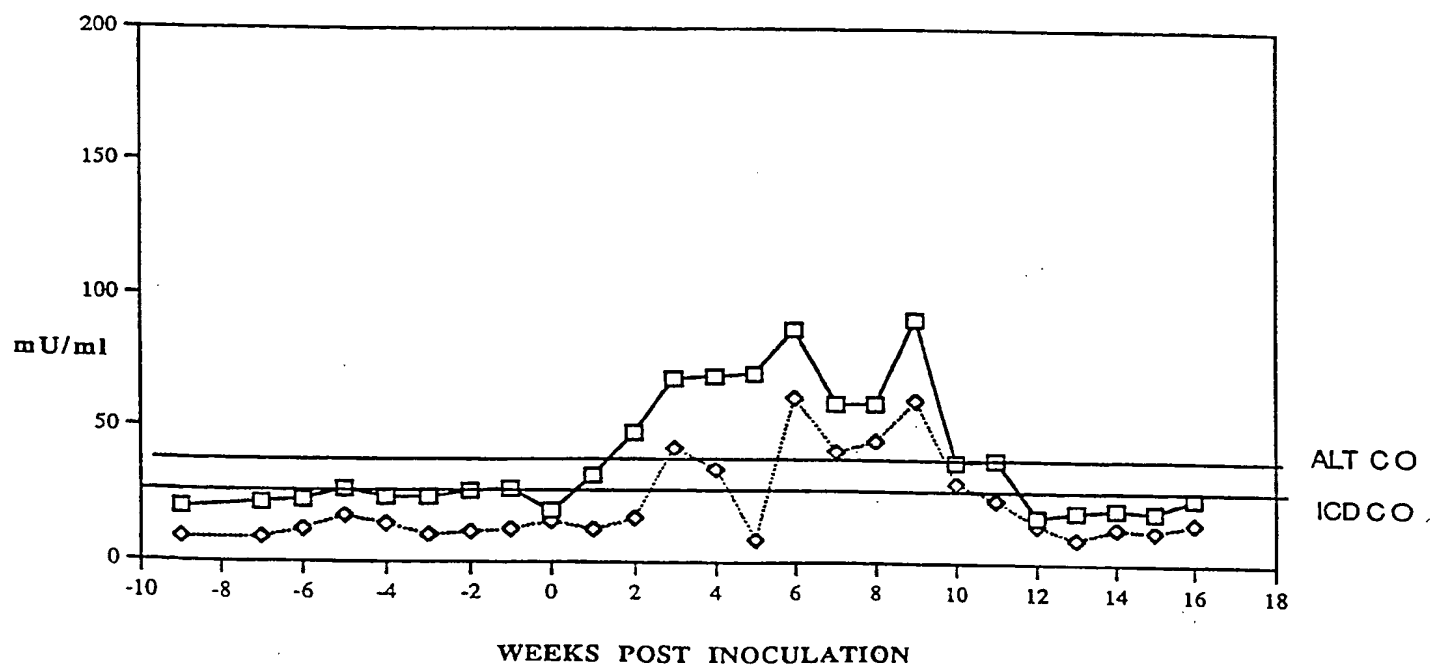


FIGURE 4



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FIGURE 5

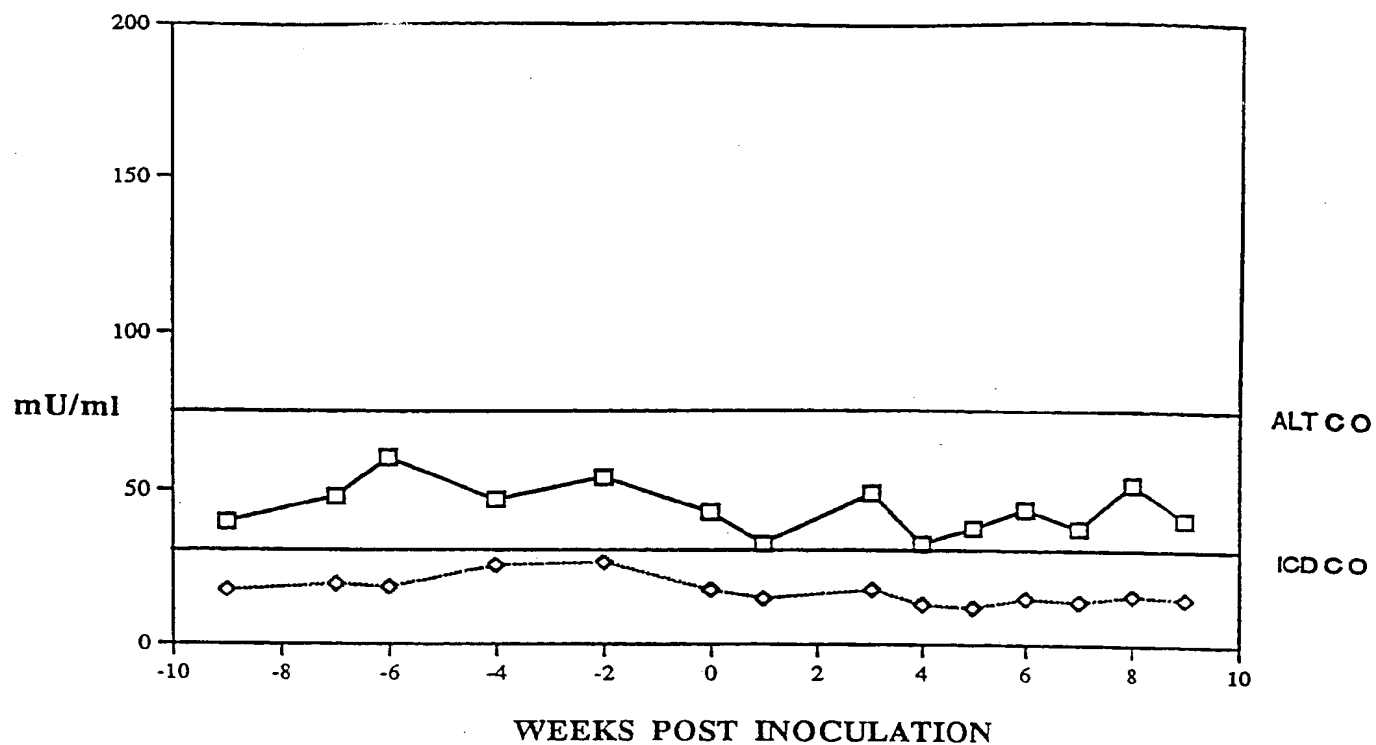
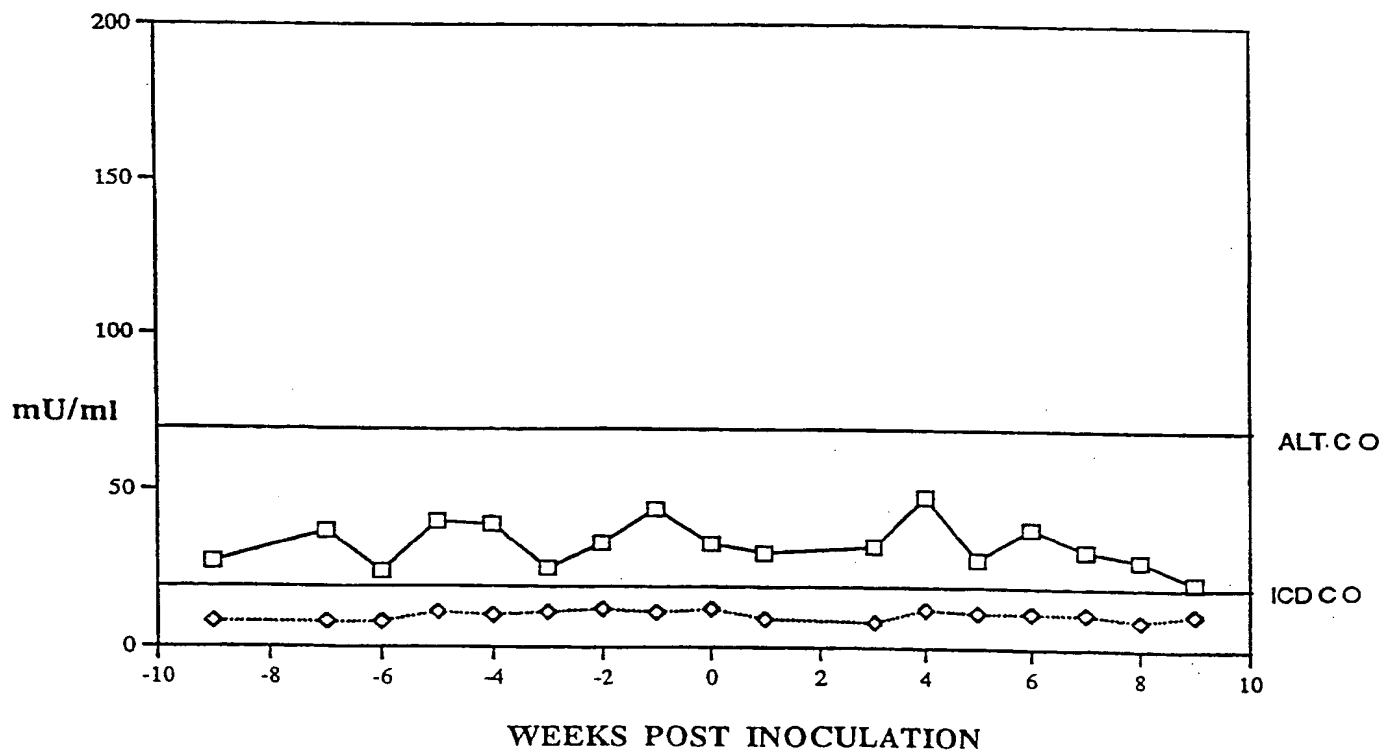


FIGURE 6



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FIGURE 7

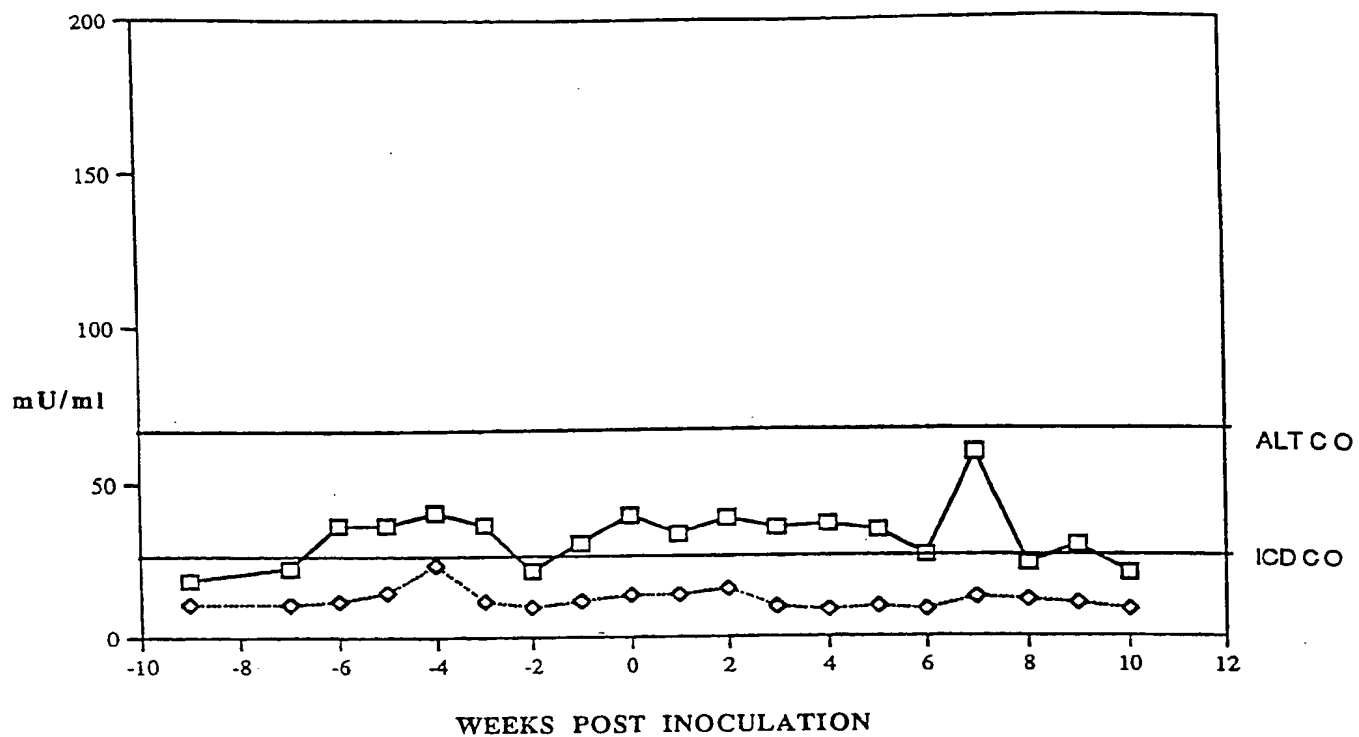
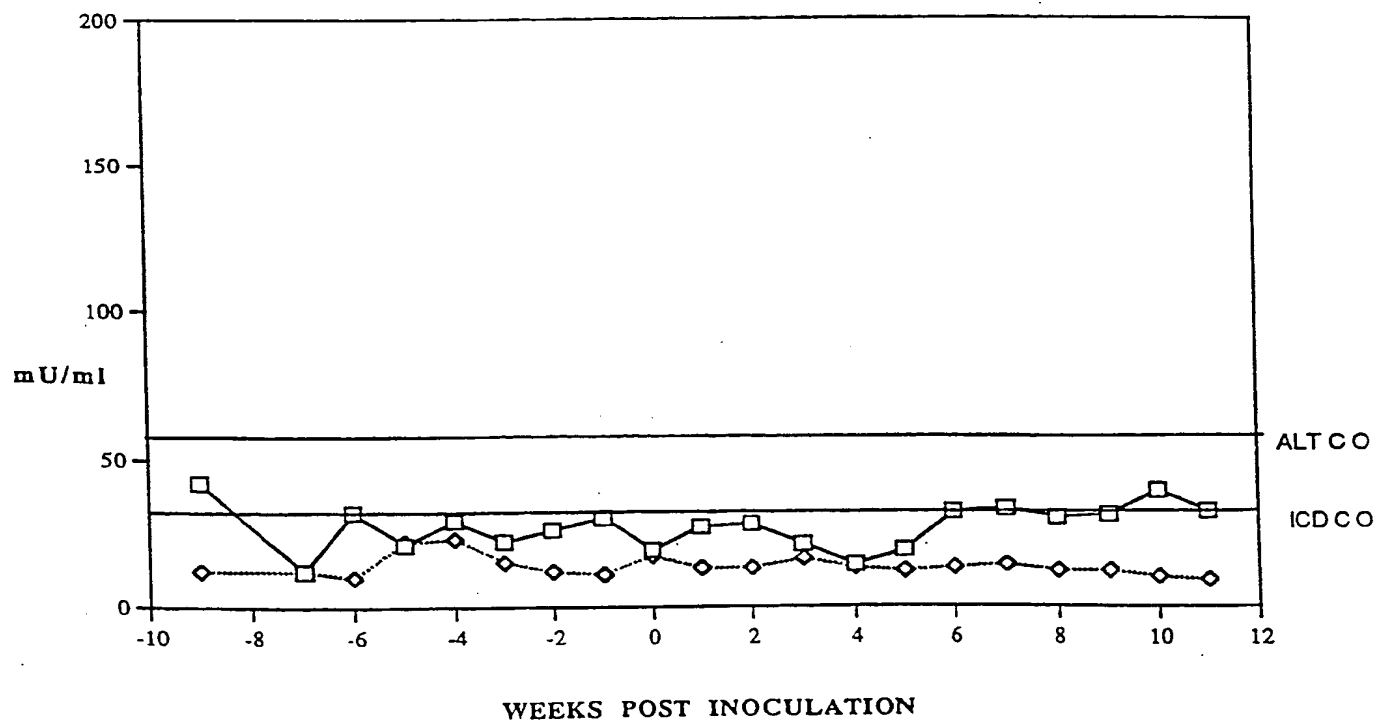


FIGURE 8



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FIGURE 9

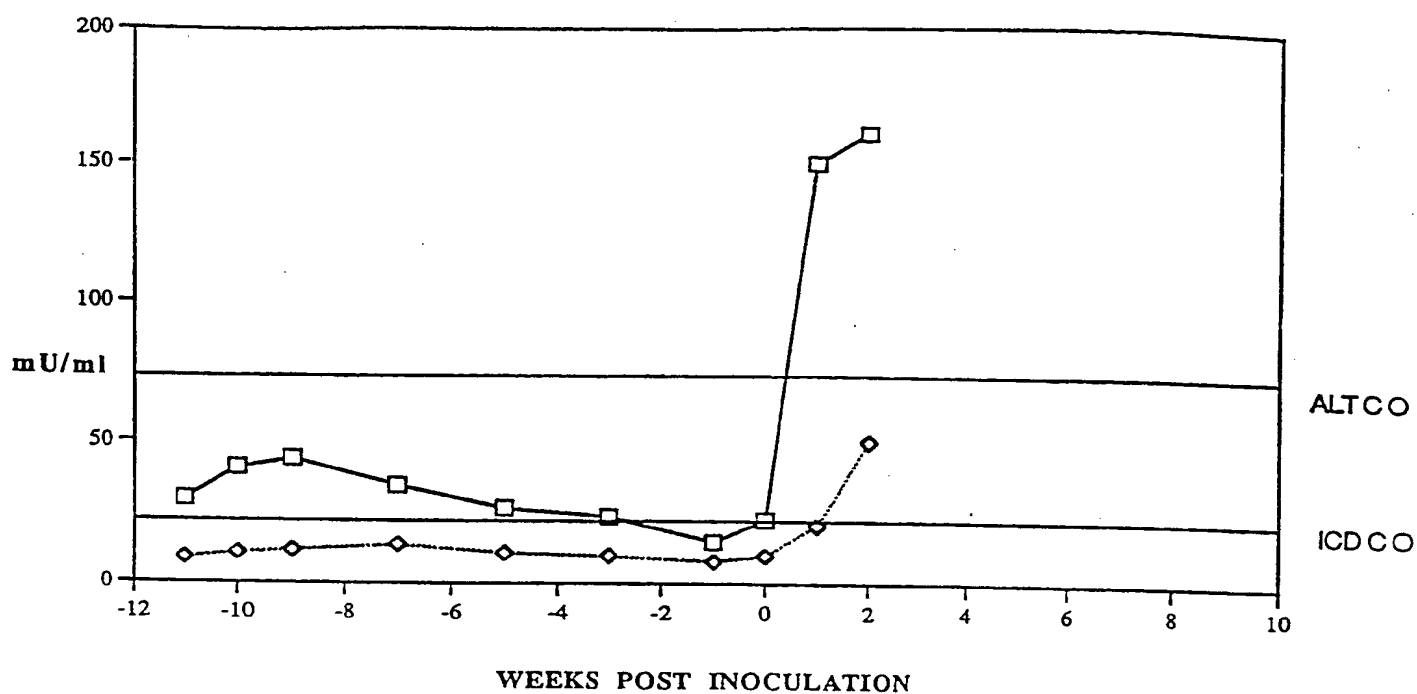
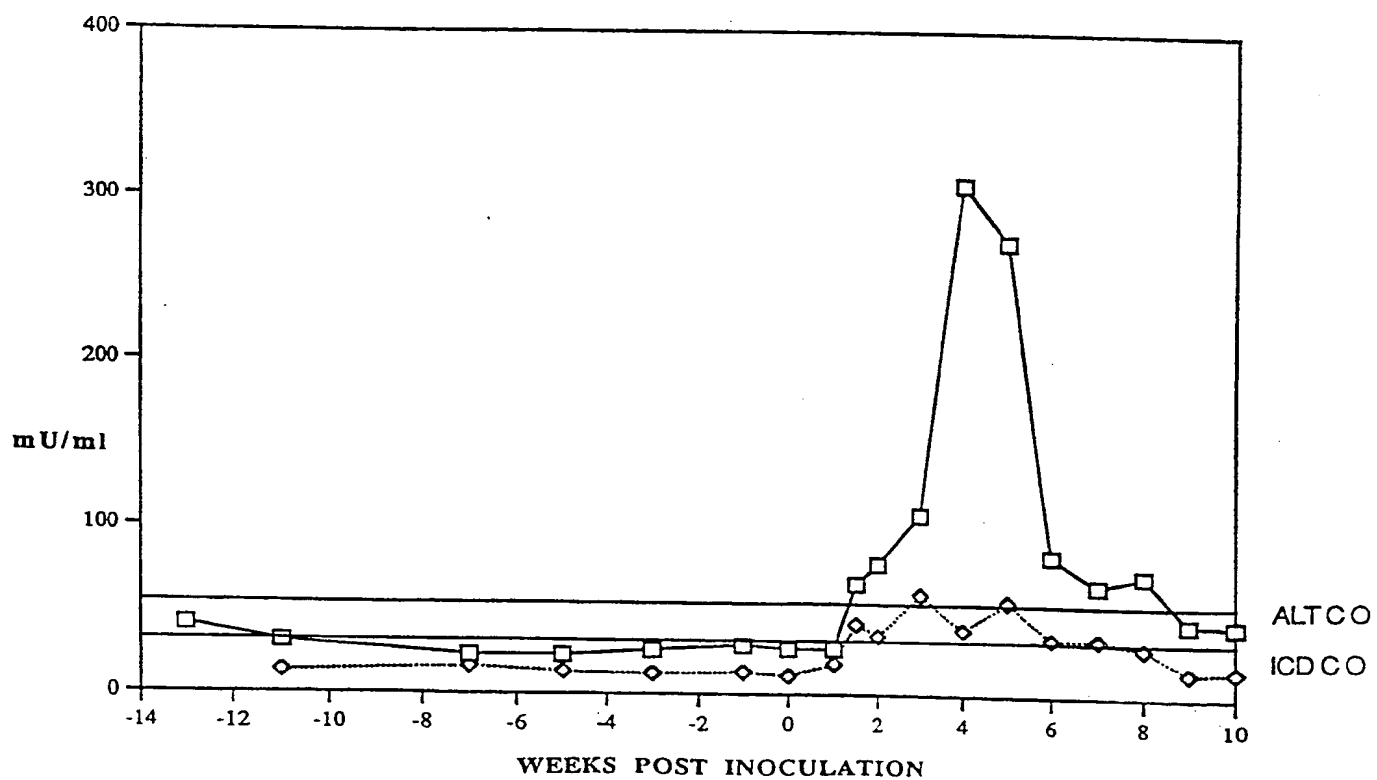


FIGURE 10



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FIGURE 11

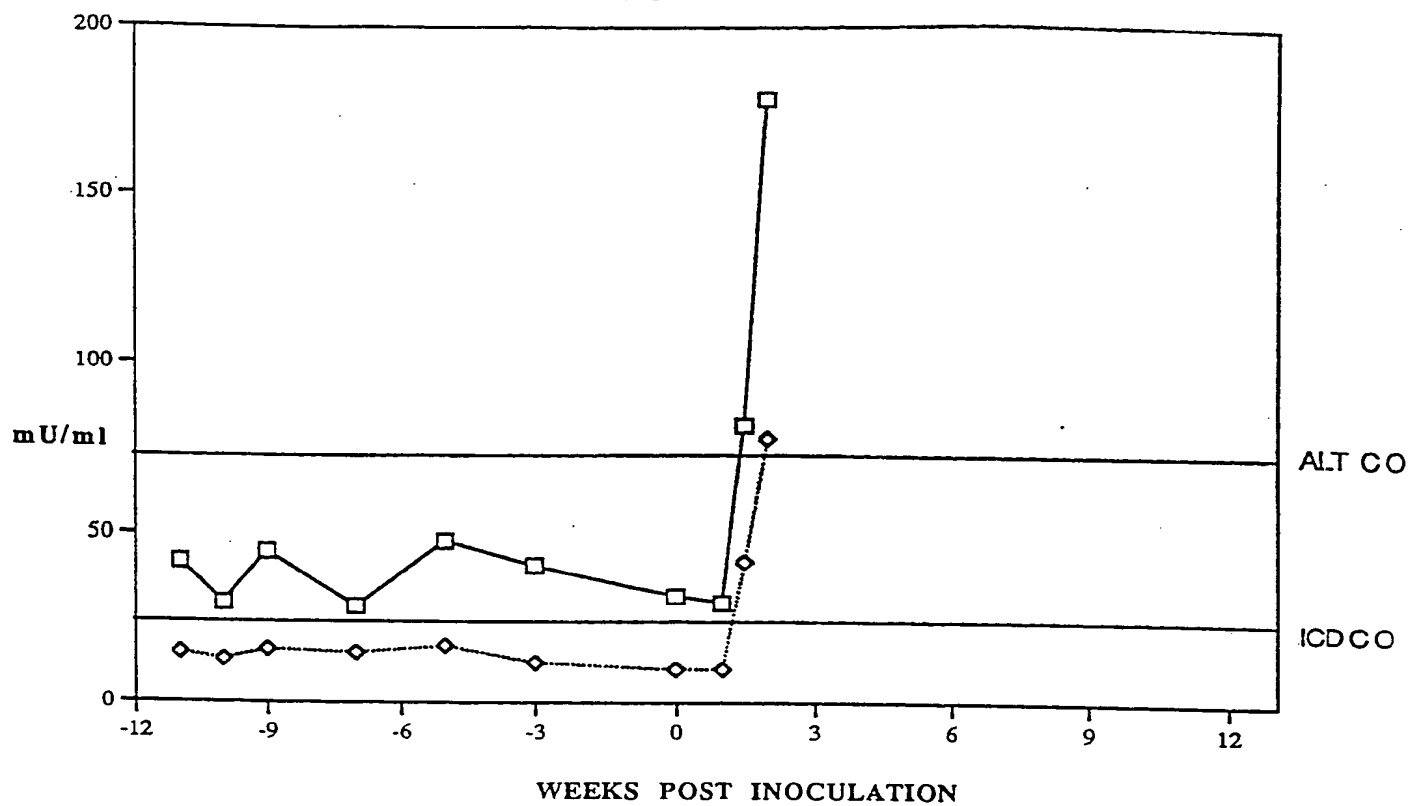
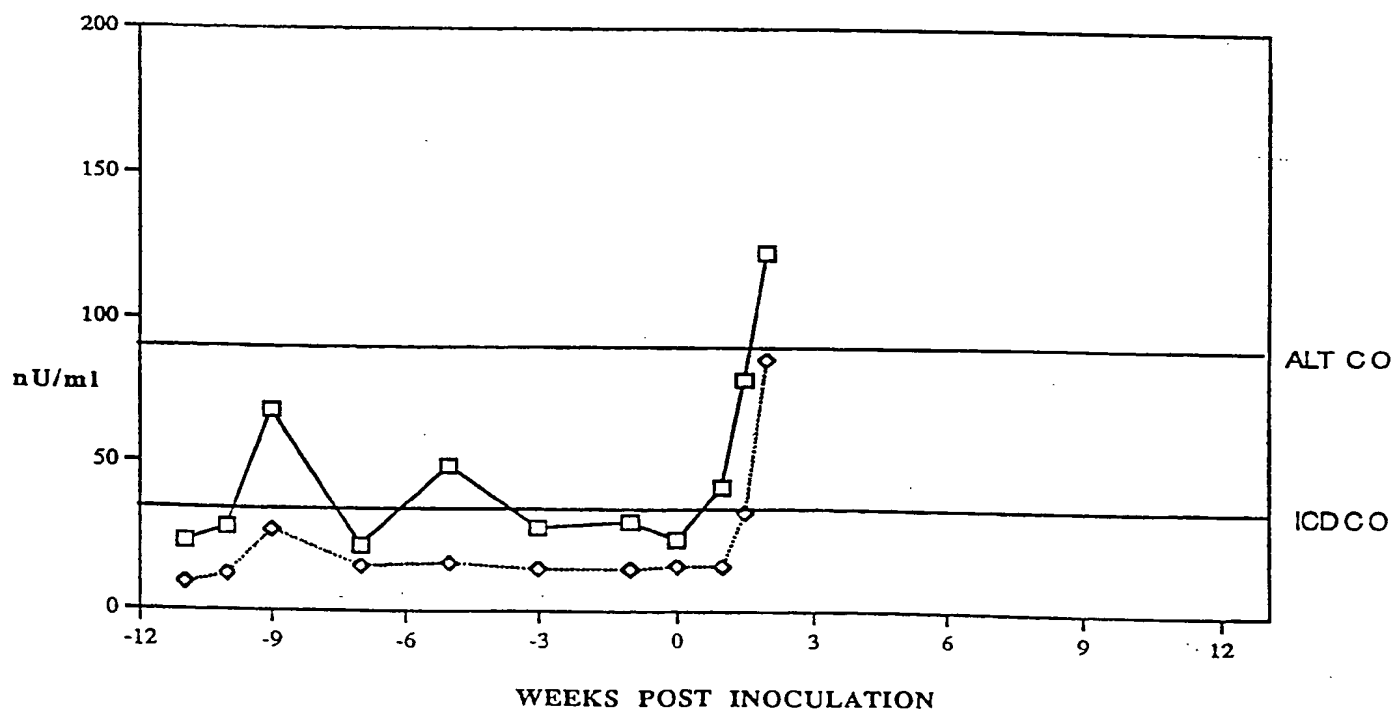
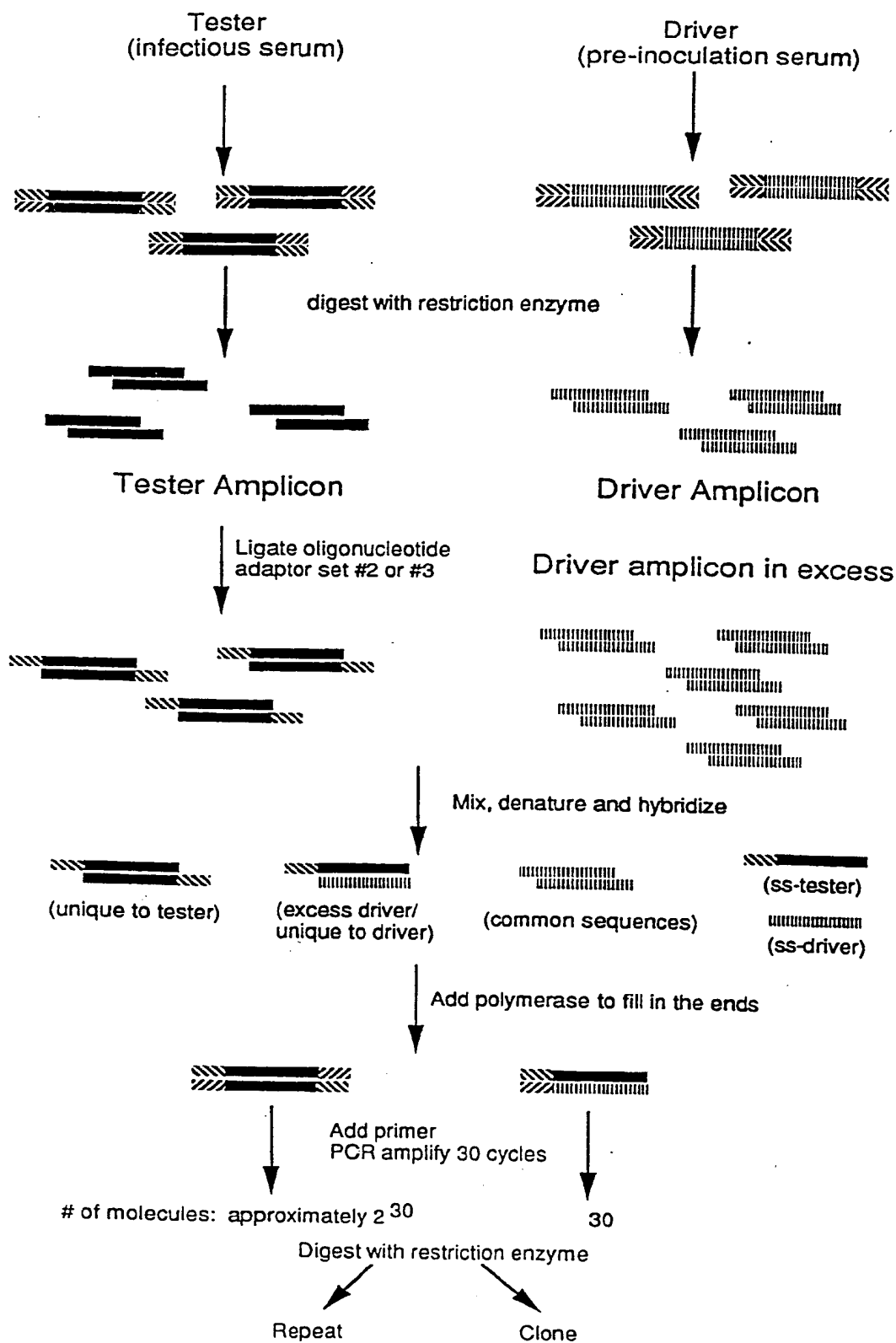
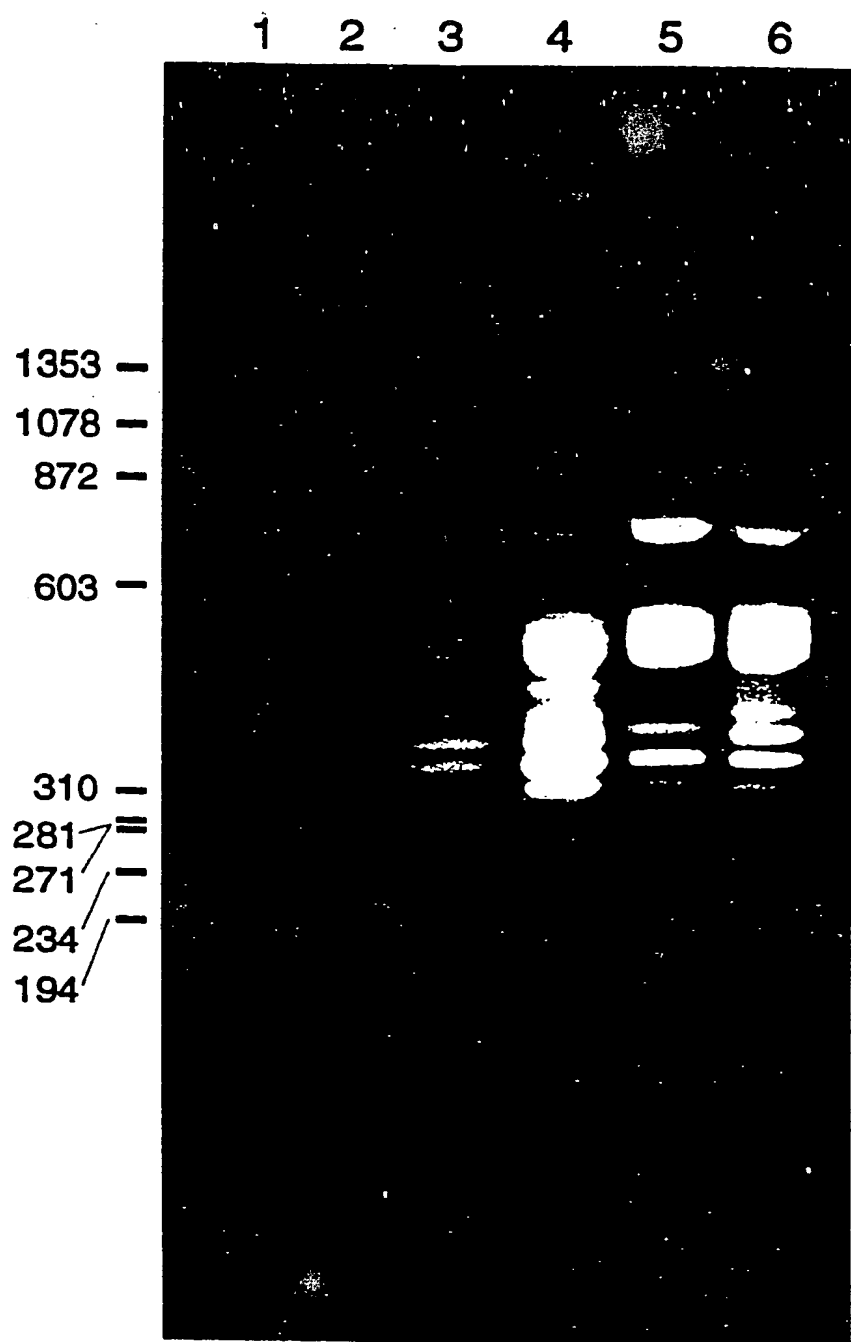


FIGURE 12



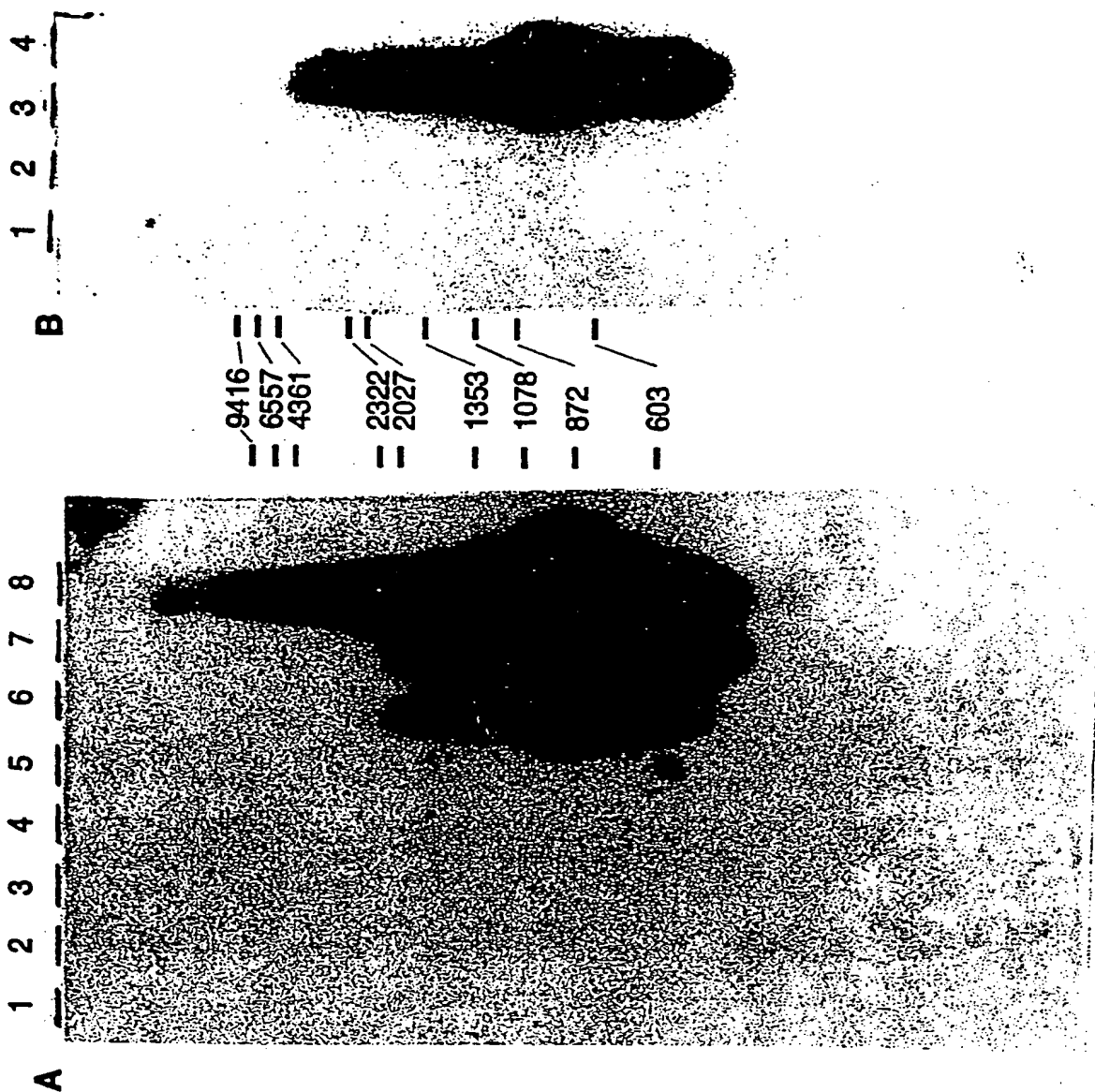
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FIGURE 13

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FIGURE 14



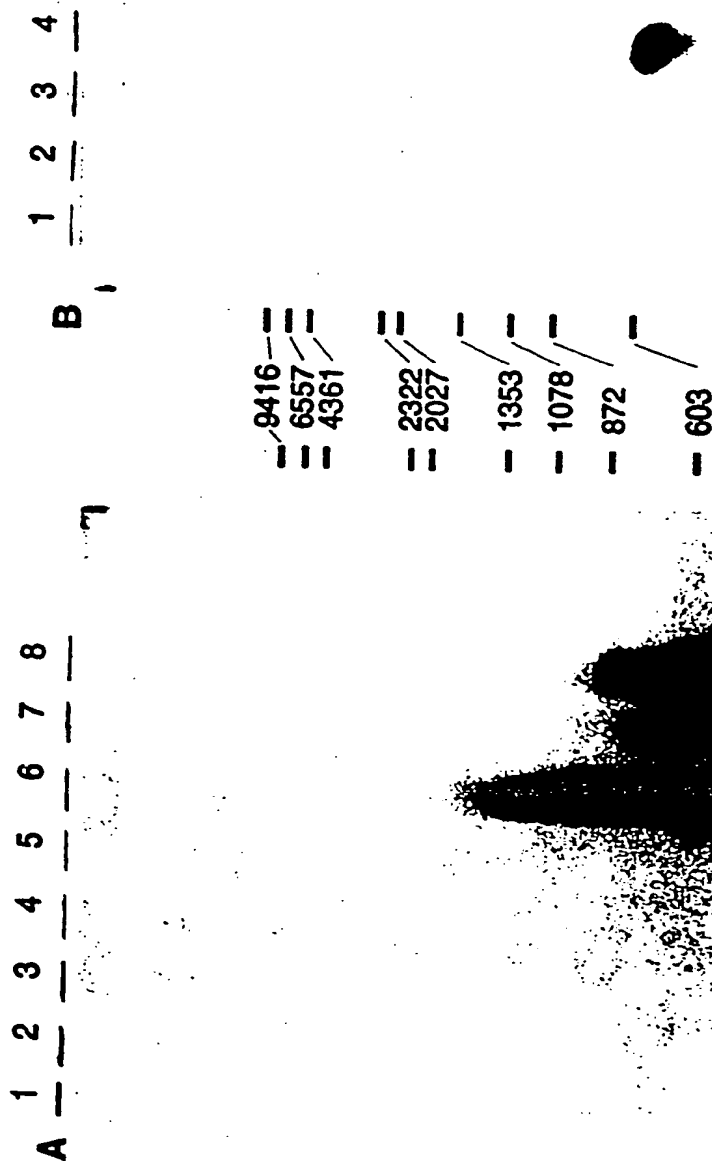
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FIGURE 15



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FIGURE 16



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FIGURE 18

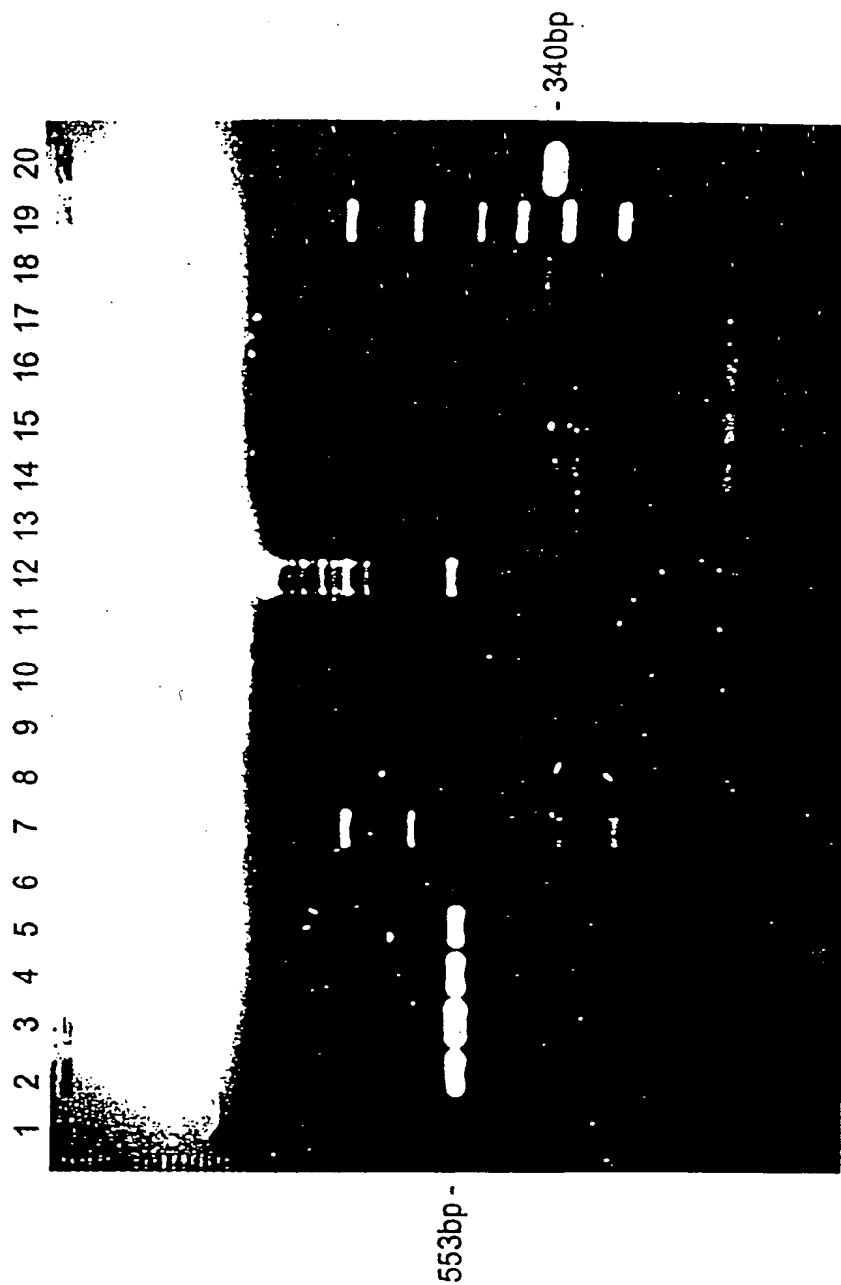
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20



553bp -

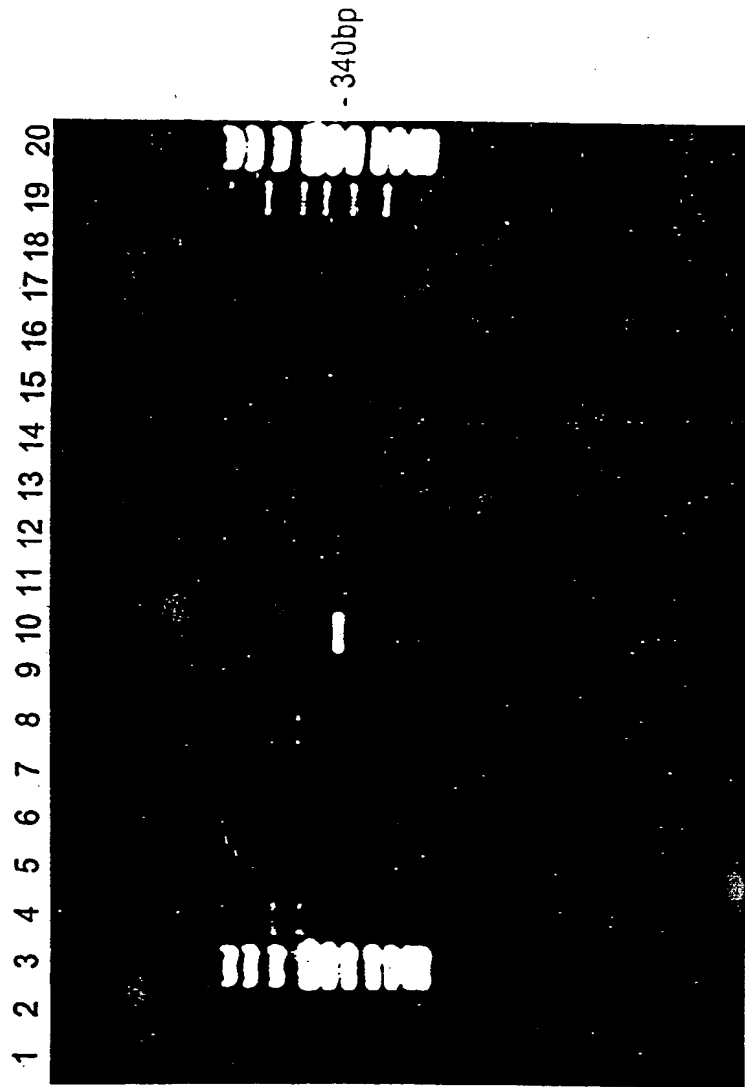
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FIGURE 17



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FIGURE 19



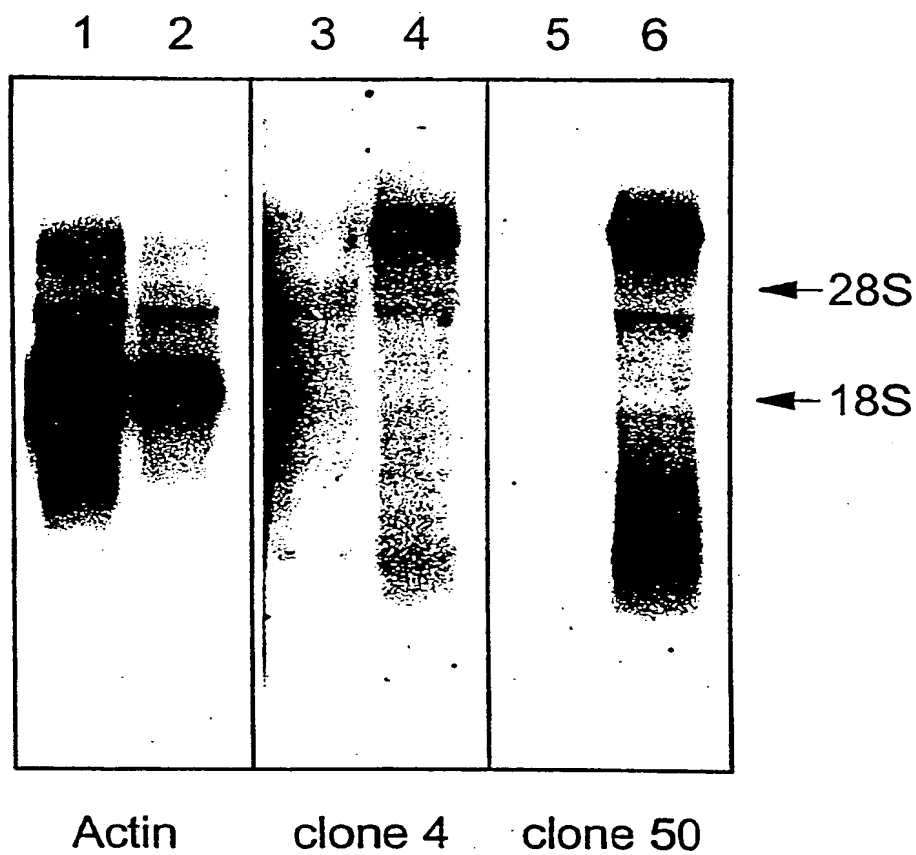
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FIGURE 20



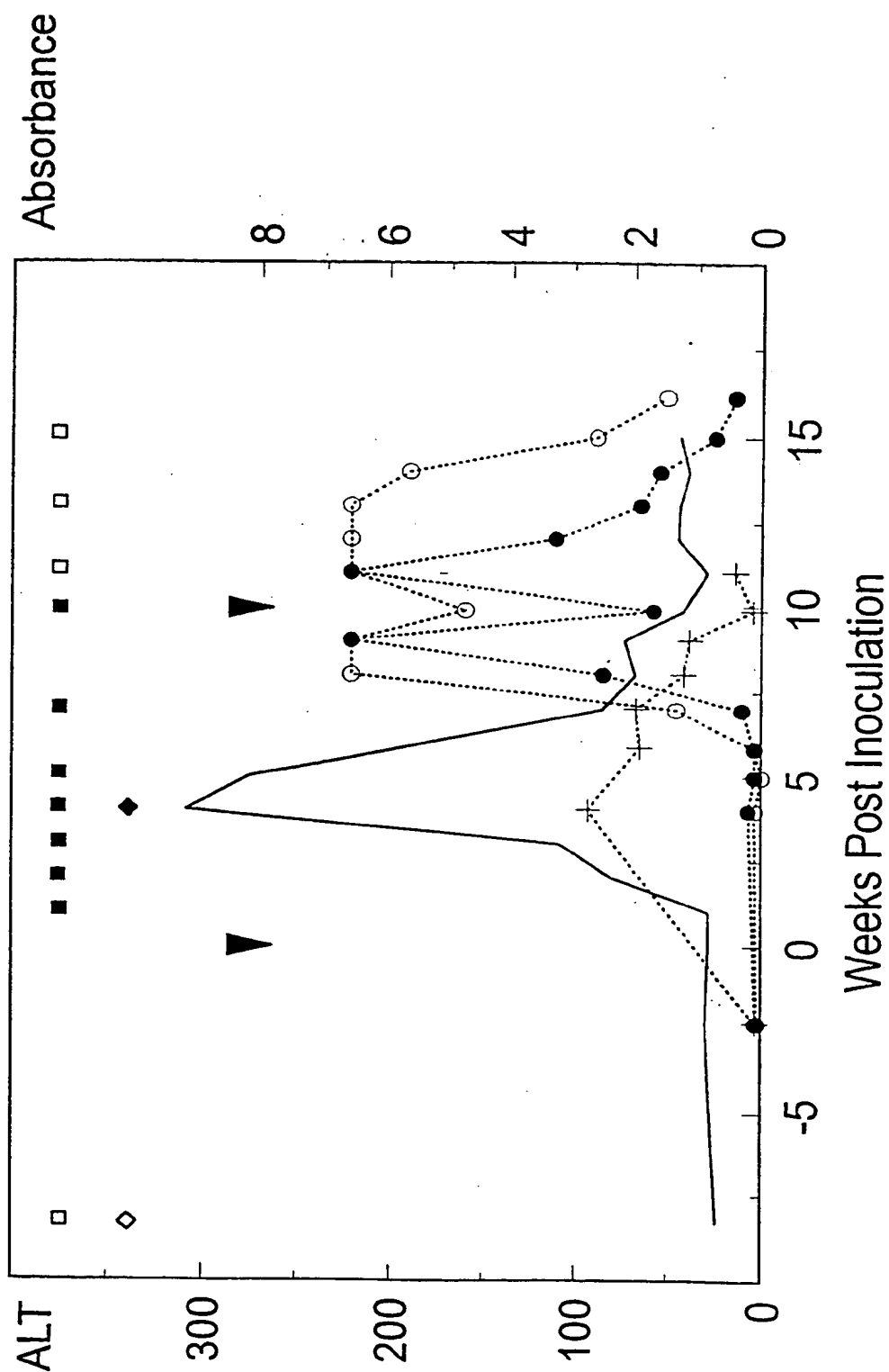
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FIGURE 21A



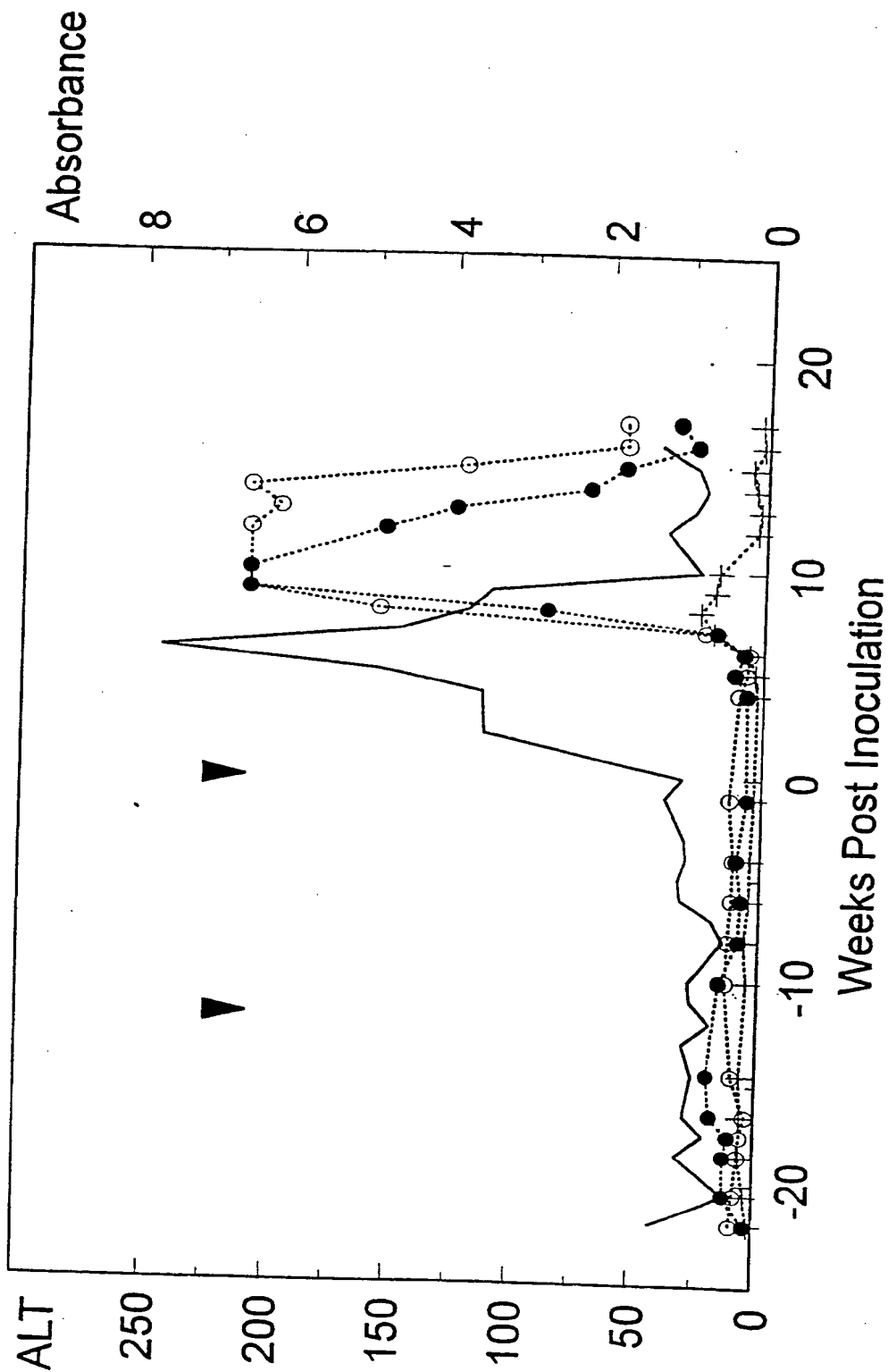
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FIGURE 29



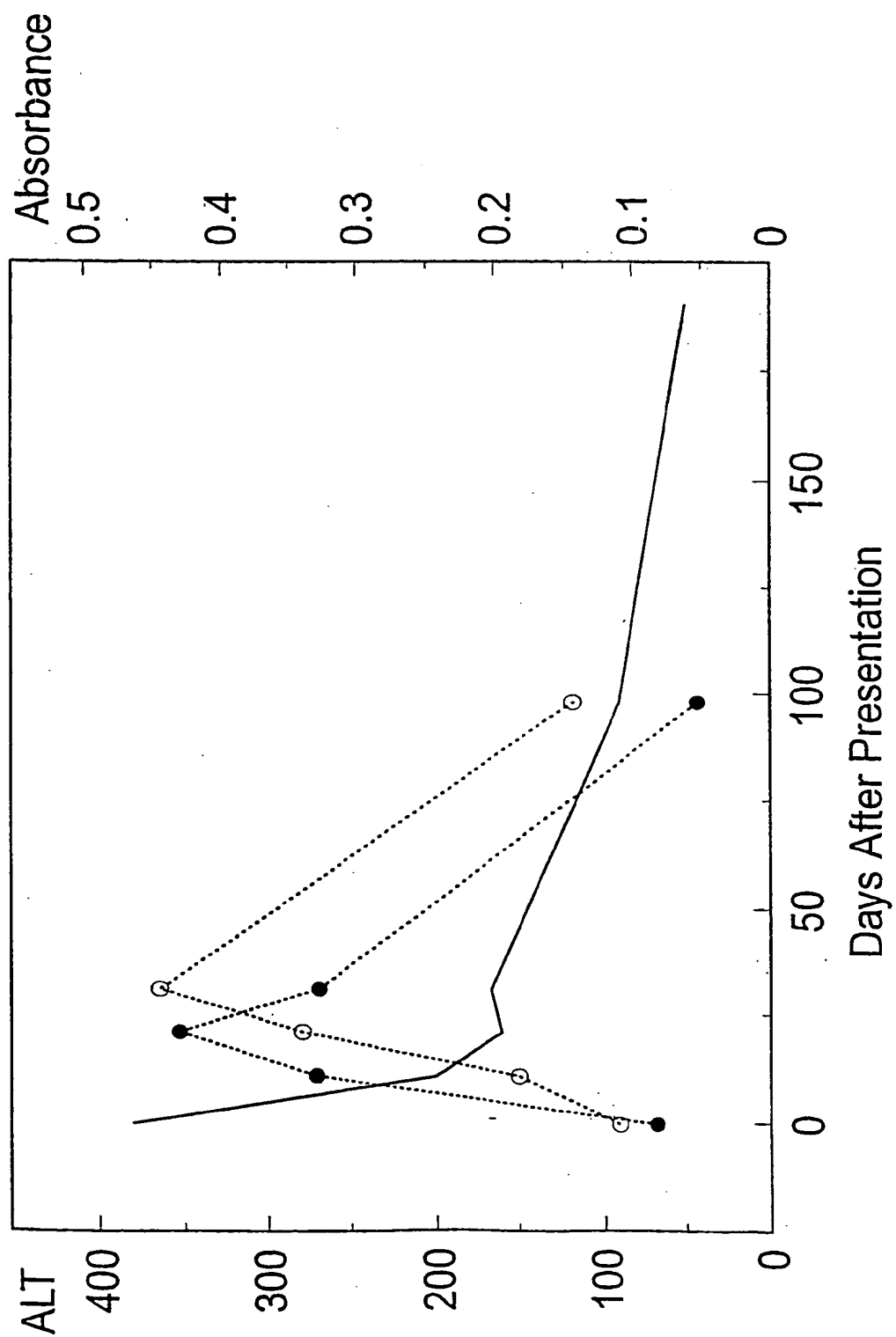
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FIGURE 30



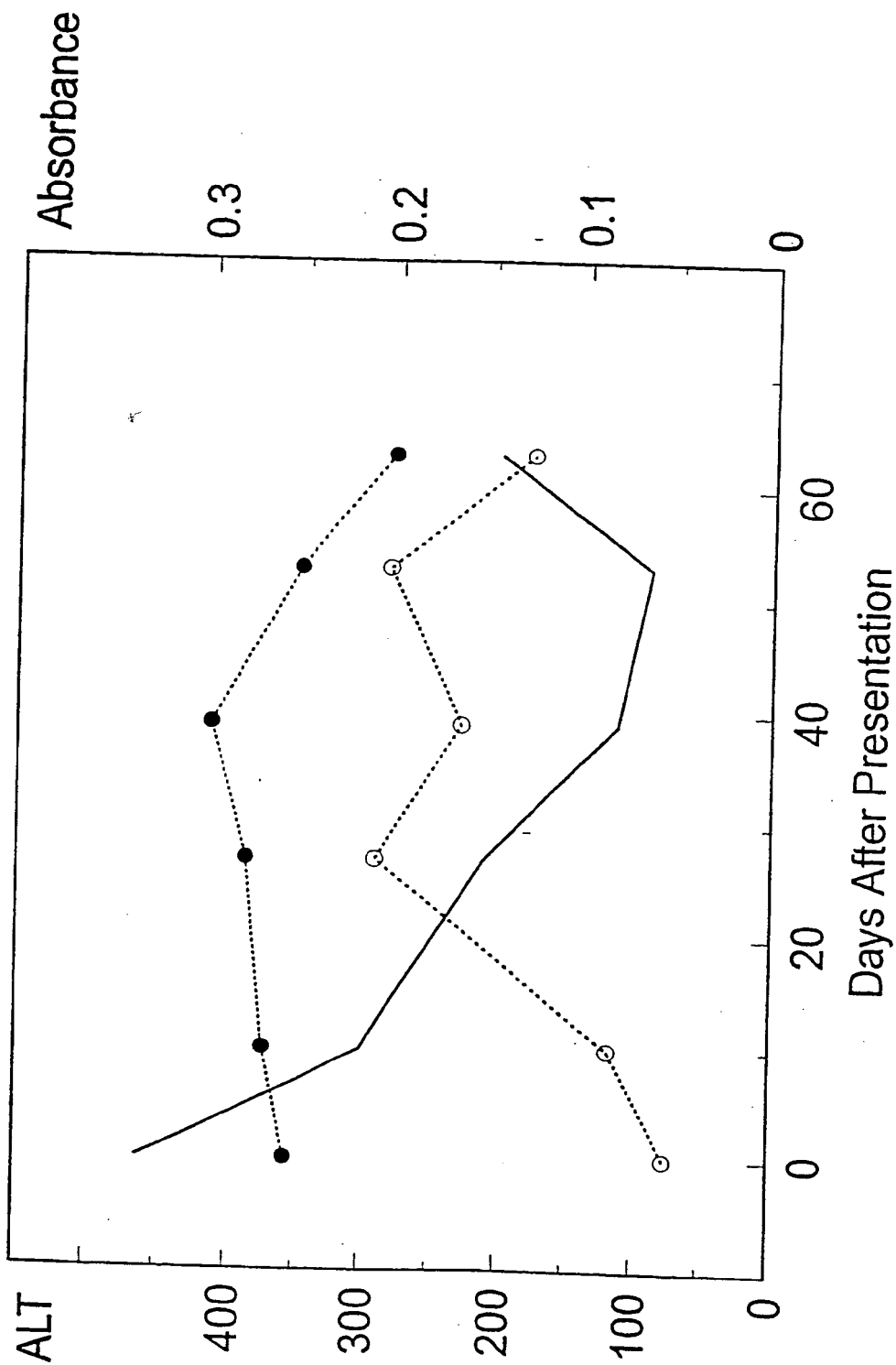
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FIGURE 31



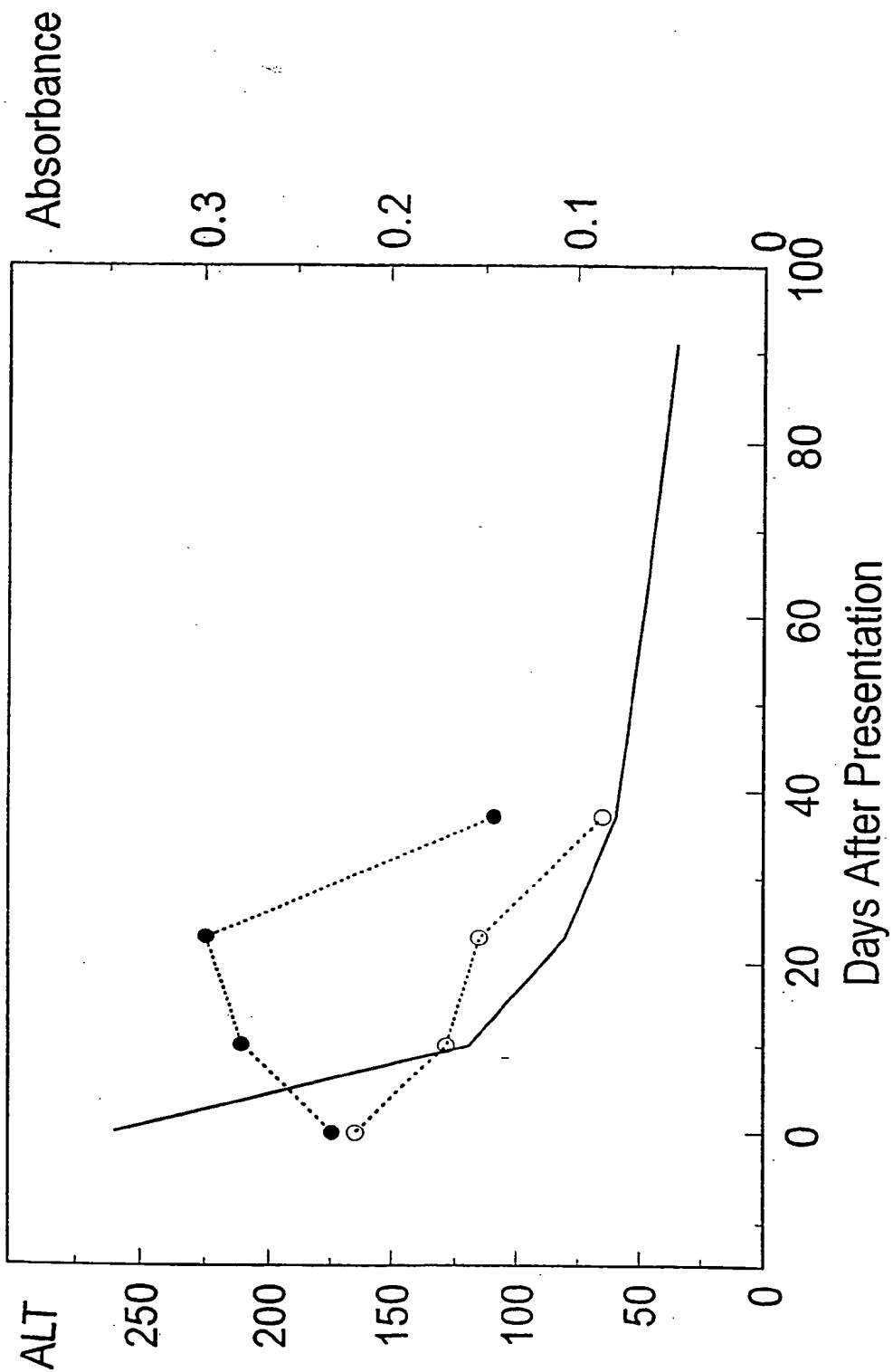
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FIGURE 32



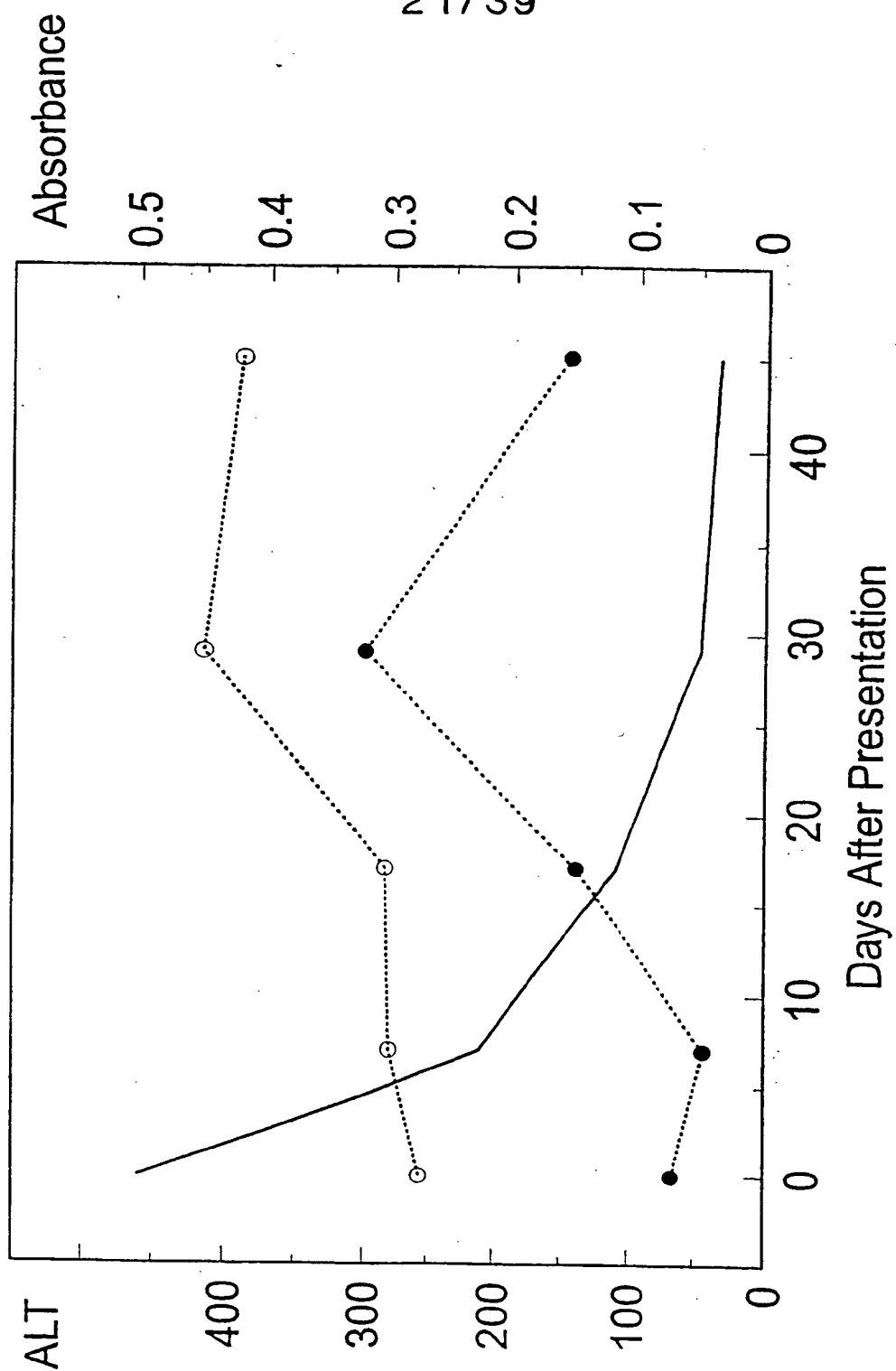
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FIGURE 33



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FIGURE 34



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FIGURE 35

A.

Contig B SEQ ID# 166(1297)	MYL..TGRCS	RIFYDVIICDE	CHATDRTTVL	GICKVLTEAP	SKNVRLVVLA
HCV-1 SEQ ID# 179(1298)	KFLADGGCSG	GAYDIIICDE	CHSTDATSIL	GIGTVLDQAE	TAGARLVVLA
Contig A SEQ ID# 157(1407)	RFMANPRKYL	RGNDVVICDE	LHVTDPSTIL	GMGRARLLAR	ECGVRLLLFA
Consensus	-----	---D--ICDE	-H-TD-T--L	G-G-----A-	----RL---A
			**	*	
Contig B SEQ ID# 166(1345)	TATPPGVIPT	PHANITEIQL	TDEGTIPFHG	KKIKEENLKK	GRHLIFEATK
HCV-1 SEQ ID# 179(1348)	TATPPGSVTV	PHPNIEEVAL	STTGEIPFYG	KAIPLEVIKG	GRHLIFCHSK
Contig A SEQ ID# 157(1457)	TATPPVSPMA	KHESIHEEML	GSEGEVPPYC	QFLPLSRYAT	GRHLLFCHSK
Consensus	TATPP-----	-H--I-E--L	---G--PF--	-----	GRHL-F---K
	***	*			
Contig B SEQ ID# 166(1395)	KHCDELANEL	ARKGITAVSY	YRGCDISKMP	.EGDCVVVAT	DALCTGYTGD
HCV-1 SEQ ID# 179(1398)	KKCDELAACL	VALGINAVAY	YRGLDVSVIP	TSGDVVVVAT	DALMTGYTGD
Contig A SEQ ID# 157(1507)	VECTRLSSAL	ASFGVNTVVY	FRGKETDI..	PTGDVVCVAT	DALSTGYTGN
Consensus	--C--L---L	---G---V-Y	-RG-----	--GD--V-AT	DAL-TGYTG-
	*			*	
Contig B SEQ ID# 166(1444)	FDSVYDCSLM	VEGTCHVDLD	PTFTMGVRVC	GVSAIVKGQR	RGRTGRGRAG
HCV-1 SEQ ID# 179(1448)	FDSVIDCNTC	VTQTVDFSLD	PTFTIETITL	PQDAVSRTQR	RGRTGRGKPG
Contig A SEQ ID# 157(1555)	FDTVTDCGLM	VEEVVEVTLD	PTITIGVKTV	PAPAEALRAQ	RGRGCRGKAG
Consensus	FD-V-DC---	V-----LD	PT-T-----	---A---QR	RGR-GRG--G
	*			*	** **

B.

Contig B SEQ ID# 166(2599)	AAKLSDQHRA	GIHTIARQYH	AGGPMAIYDG	REIGYRRCRS	SGVYTTSSSN
HCV-1 SEQ ID# 180(2662)	CCDLDPQARV	AIKSLTERLY	VGGPLTNSRG	ENCGYRRCRA	SGVLTSSCGN
Contig A SEQ ID# 157(2798)	AA...SDNPS	MVHALC.KYY	SGGPMVSPDG	VPLGYRQCRS	SGVLTSSAN
Consensus	-----	-----	-GGP-----G	---GYR-CR-	SGV-TTS--N
				*	* * *
Contig B SEQ ID# 166(2649)	SLTCWLKVNA	AAEQAGMKNP	RFLICGDDCT	VIWKSAGADA	DKQAMRVFAS
HCV-1 SEQ ID# 180(2712)	TLTCYIKARA	ACRAAGLQDC	TMLVCGDDL	VICESAGVQE	DAASLRAFTE
Contig A SEQ ID# 157(2844)	SITCYIKVSA	ACRRVGIRAP	SFFIAGDDCL	IIYENDGTDP	CPALKAALAN
Consensus	--TC--K--A	A-----G--	-----GDD--	-I-----G--	-----

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FIGURE 36

```

SEQ ID 76  agcTactAGC GactCCCCcg GGTcgcCCTA TGACTAGCA tCCATCCATA aTTGAGACAA AGctGGac.. .gTTGGTGAG ATCCCCCTTTT ATGGGcaTGG
SEQ ID 37  TCCTACGGC GACCCACCG GTCTCTCCGA TGCCGAGCA TGAATCTATT CATGAGGAGA TGTTGGGCAG TGAGGGGAG GTCCCCCTTCT ATTGCCAATT
SEQ ID 44  TTGCCACGGC TACCCCCCTT GGAGTATCC CTACACACA TGCCACACATA actGAGATc AATTAACCGA TGAAGGCACT ATCCCCCTTC ATGGAATAAA
SEQ ID 100 TCCCCACTGC TACCCCTCG GGTCCGTCA CTGTGTCCCA TCCTACATC GAGAGGTTG CTCTGTCCAC CACCGGAGAG ATCCCCCTTTT ACGCCAAGGC

SEQ ID 76  TATCCCCCTC GAGGg.TATg agGACTGGT. CCCCACCTTG TATtCTGccA TtccAAGCG GAGTGCAGAG GattGGCCGg CCAGTTCTCC GgCGGgGGG
SEQ ID 37  CCTCCCACTG AGTAGGTATG CTACTGGg.. AGACACCTGC TGTtTTGTCA TTCCAAGTGA GATGCACATA GGTATCCTC AGCTTTGGCC AGCTTTGGTG
SEQ ID 44  GATTaaggAG GAAATCTGA aGAAGGg.. AGACACCTTA TCTTTGAGGC TACCATAAAA CACTGTGAtg AGCTtGCTAA CGAGTTAGCT CGAAAGGGA
SEQ ID 100 TATCCCCCTC GAGGTGATCA AGGGGGA... AGACATCTCA TCTTCTGCCA CTCAAGAAG AAGTGGGAG AGCTCGCCGC GAAGCTGGTC GCATTGGCA

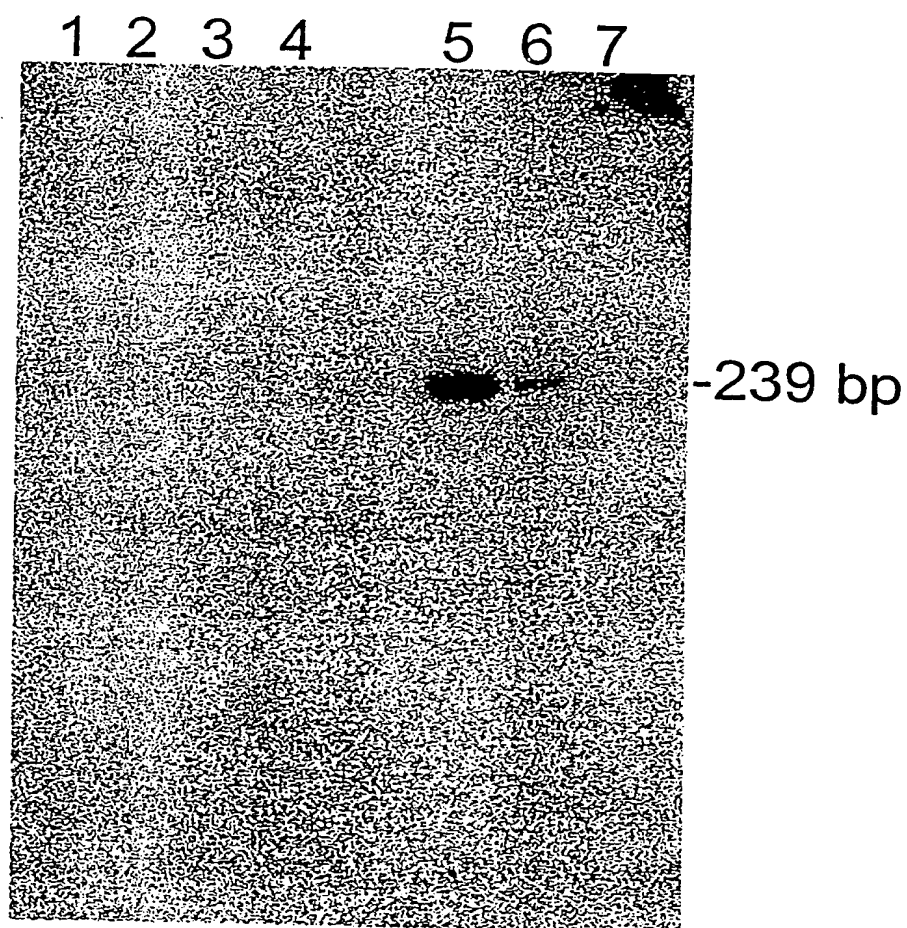
SEQ ID 76  TtAATgCgAT CgCc.TATTA TAGGGTAAG GACAGTTCCA TcATCAAAga CGAgacCTg GTGGLTTGTG .CGACAGAG .Cg.CTCTCT ACCGGGTACA
SEQ ID 37  TCACACCGT TGTGTACTTC AGAGCMAAG AA....ACTG ACATTCCAAC TGTGACGTG TGCGTTG... .CGCCACAGA CGCACTTTCC ACTGGTTACA
SEQ ID 44  TAACAGCTGT CcCTTAC.TA TAGGGATGT GACATCTCAa AAATCC...C TGAGGGCGAC tGtStaGTAg tTGccactGa TGcCTTgtGT aCagGtTaCa
SEQ ID 100 TCAATGCCGT GGCCTAC.TA CCGGGTCTT GACGTGTCTG TcATCCCGAC CAGCGCGAT GTTCTCSTCG TGTCGACCGA TGCTCTCATG ACTGGCTTTA

SEQ ID 76  CAGGAaACTT CGATTCTGTC ACCACTGTG GGTGGTGGT GGAGGAGGTC GTTGAGGTGA CCCTtGAtCC cACCaT
SEQ ID 37  CTGGCAATTT TGACACCGTA ACAGACTGTG GTTTAATGGT TGAGAGGTA GTGGAAGTGA CCTTGACCC GACCAAT
SEQ ID 44  CTGGTgACTT TgATTCCGTG TAtGactGCa GcCTCaTgGT AGAAGGCaCa TGCCaTGTtG aCCTTGaCCC TaCTTT
SEQ ID 100 CCGGCGACTT CGACTCTGTG ATAGACTGCA ACAGTGTGT CACTCAGACA GTCGATTtTA GCCTTGACCC TACCTT

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FIGURE 37



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FIGURE 38

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SEQ ID 98      ATC CCC TTT TAT GGG CAT GGC ATA CCC CTG GAG AGG ATG CGG ACC GGC AGG CAC CTC GTA
SEQ ID 97      ATC CCC TTT TAT GGG CAT GGA ATC CCC CTC GAG CGG ATG CGG ACC GGC CGC CAC CTC GTG
SEQ ID 76      ATC CCC TTT TAT GGG CAT GGT ATC CCC CTC GAG CGT ATG AGG ACT GGT CGC CAC CTT GTA
Consensus      ATC CCC TTT TAT GGG CAT GG- AT- CCC CT- GAG -G- ATG -GG AC- GG- -G- CAC CT- GT-
translat.      I P F Y G G H G I P L E R M R T G R H L V

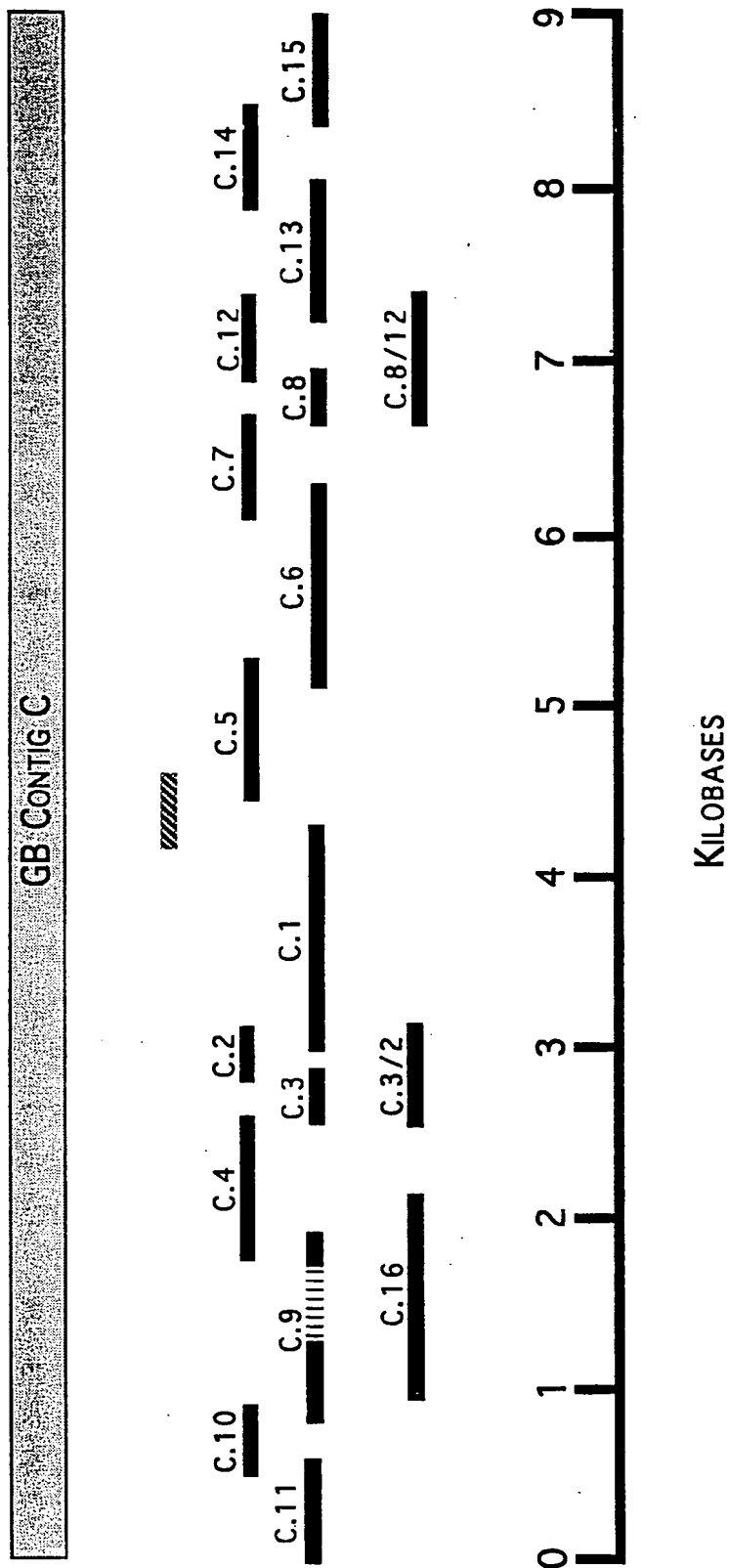
SEQ ID 98      TTC TGC CAT TCA AAG GCG GAG TGC GAG CGG CTT GCT GGC CAG TTC TCA GCC CGG GGG GTA
SEQ ID 97      TTC TGC CAT TCA AAG GCG GAG TGC GAG CGG TTG GCT GGC CAG TTC TCT TCG CGG GGG GTG
SEQ ID 76      TTC TGC CAT TCC AAG GCG GAG TGC GAG AGA TTG GCC GGC CAG TTC TCC GCr CGG GGG GTY
Consensus      TTC TGC CAT TC- AAG GCG GAG TGC GAG -G- -T- GC- GGC CAG TTC TC- -C- CGG GGG GT-
translat.      F C H S K A E C E R L A G Q F S A/S R G V

SEQ ID 98      AAT GCC ATT GCC TAT TAT AGG GGG AAA GAC AGT TCT
SEQ ID 97      AAT GCC ATT GCC TAT TAT TAC AGG GGG AAA GAC AGT TCC
EQ ID 76      AAT GCC ATC GCC TAT TAT AGG GGT AAG GAC AGT TCC
Consensus      AAT GCC AT- GCC TAT TA- AGG GG- AA- GAC AGT TC-
translat.      N A N A Y Y R G K D S S

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FIGURE 39



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FIGURE 40

```

GB-C  T TAT GGG CAT GGT ATC CCC CTC GAG CGT ATG AGG ACT GGT CGC CAC
CTT GTA TTC TGC CAT TCC AAG GCG GAG TGC GAG AGA
GB-C.4  - - - - -C - - - -G - - -C - - -A-G - - -
--G - - - -C -A - - - -T - - -G
GB-C.5  - - - - -C -A -T - - -A -G - - -C - -C -A A-G - - -
--C -G - - - -A - - - -C-G
GB-C.6  - - - - -C -T -T -G - - -G - - -CA - -C - -A-A -T
--G - -C - -G - - - -C-G
GB-C.7  - - - - -C -A - - -A -G - - -C-A - -C -A G-G - - -
--C -G - -T - - - -C-G

```

```

GB-C  TTG GCC GGC CAG TTC TCC GCG CGG GGG GTT AAT GCC ATC GCC TAT
TAT AGG GGT AAG GAC AGT TCC ATC ATC AAA GAC GGA GAC
GB-C.4  C - - - -A - - -T-A - - - - -T G-T - - -
-- - - - -A - - -G -T -T - -
GB-C.5  C-C -T -T - - -T -T - -A - - -A -C - - -T -T - - -
--C -A - - - -G - - -
GB-C.6  C-T - - - - -T-T A - - -C -C - - -T - - -
--C - - - -C - - -G - - -
GB-C.7  C-T -T - - - - -T - -A - - -G - - -T - - -
--C -A - - - - -G -T -C - -

```

```

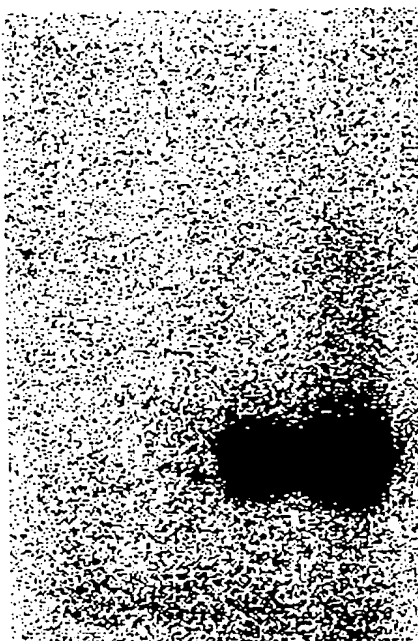
GB-C  CTG GTG GTT TGT GCG ACA GAC GCG CTC TCT ACC
GB-C.4  - - - -G -C -T -T - - -A - - -
GB-C.5  -A - - -G -C -C - - -A -C -G
GB-C.6  -C -T -G -C -C -T - - - -G
GB-C.7  - - - -G -C -T -G C - - -A -C - -

```

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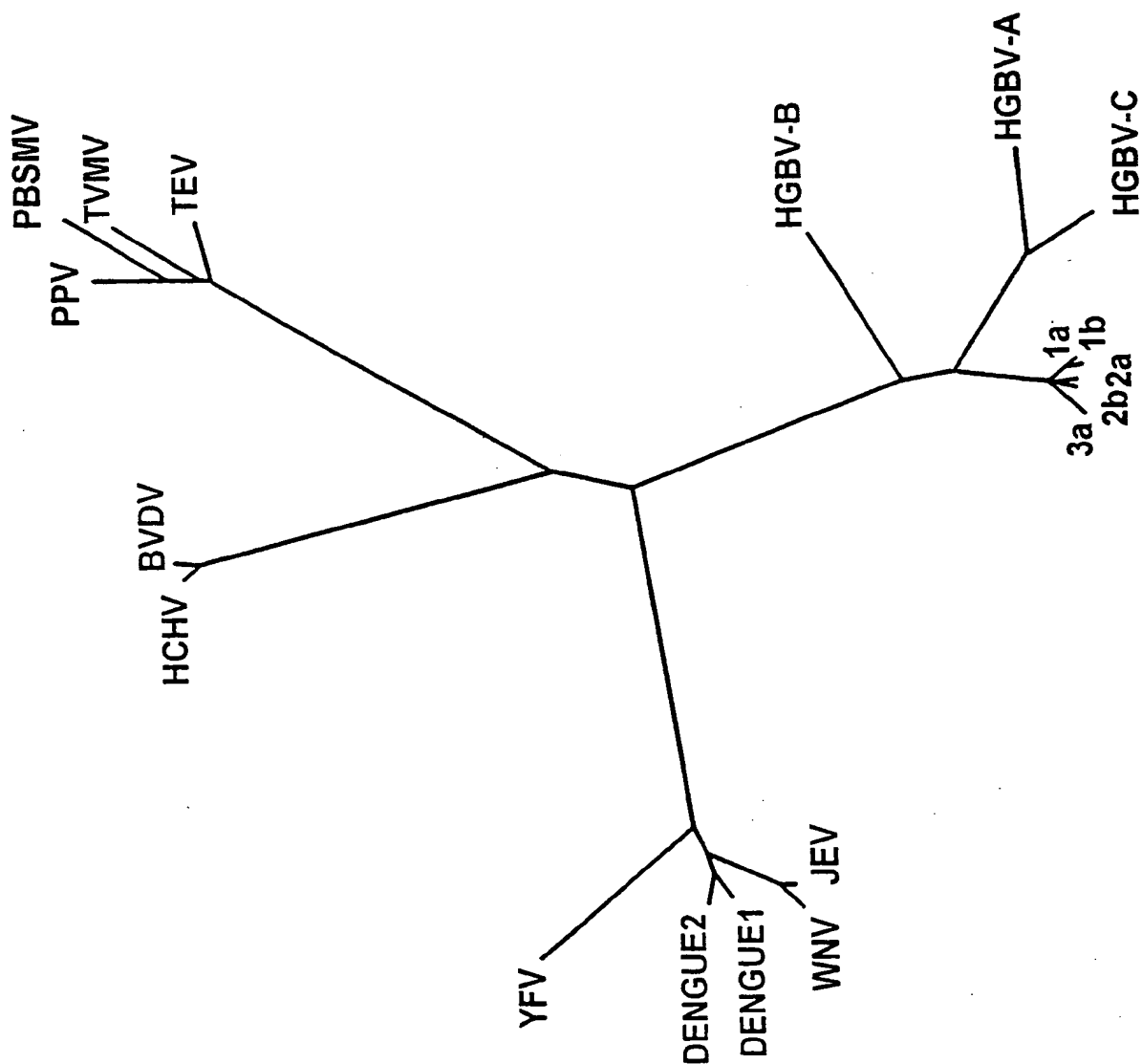
FIGURE 41

1 2 3 4



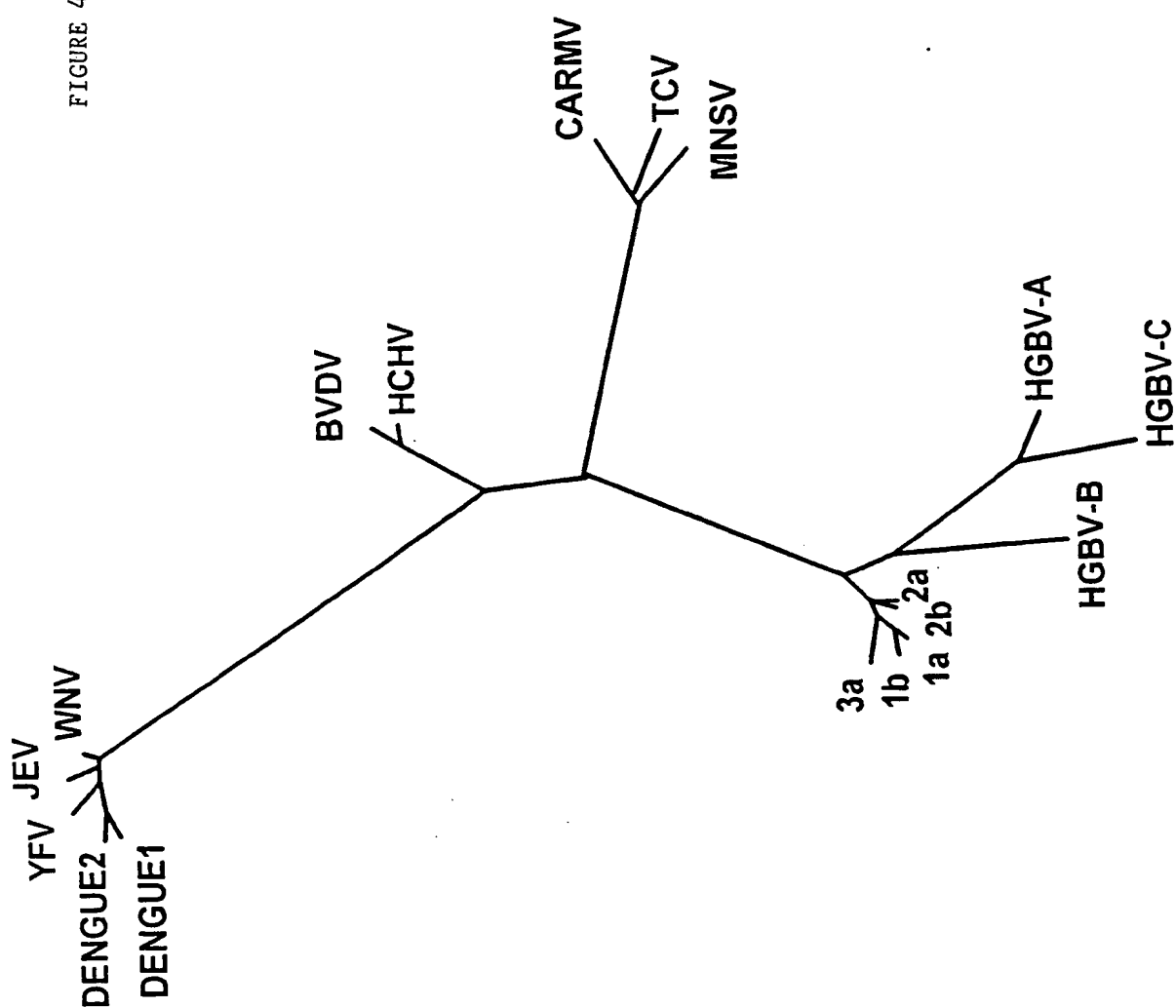
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FIGURE 42



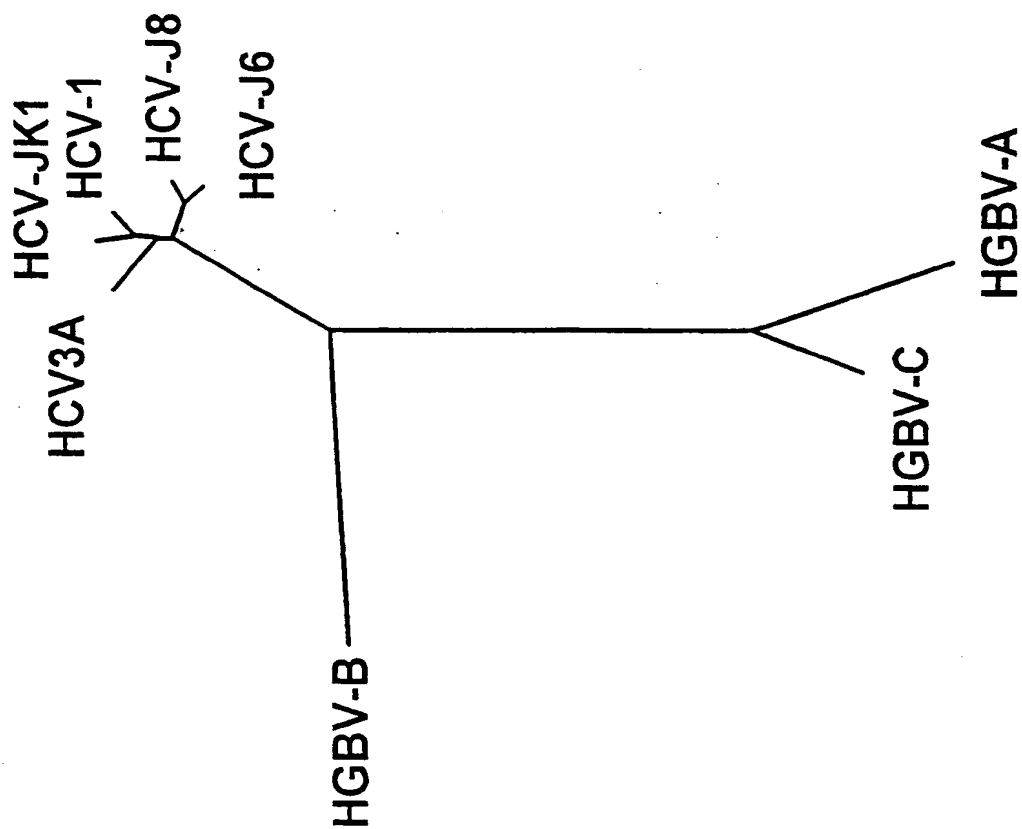
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FIGURE 43



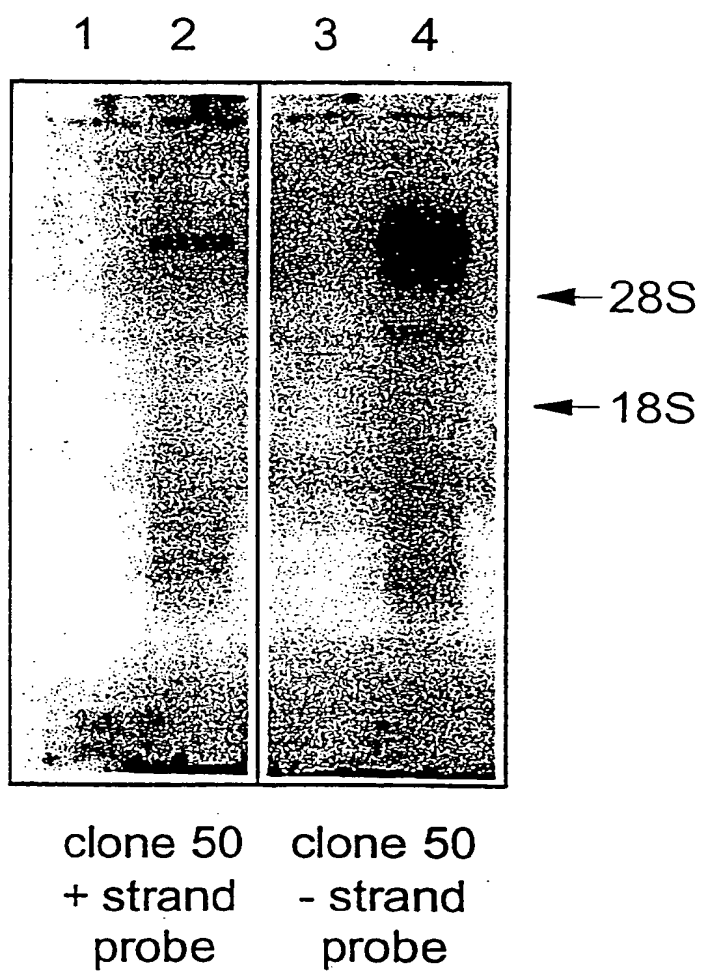
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FIGURE 44



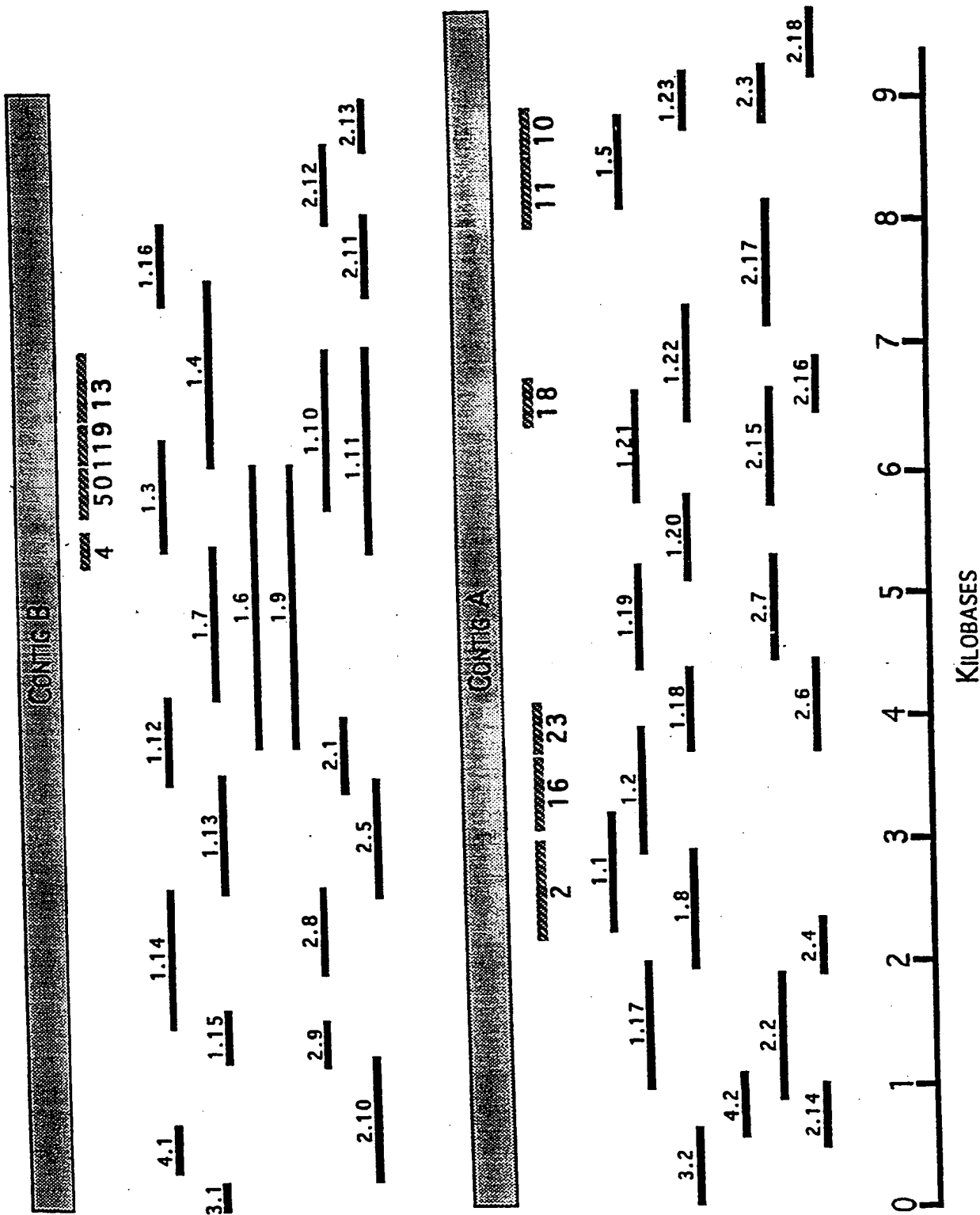
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FIGURE 21B



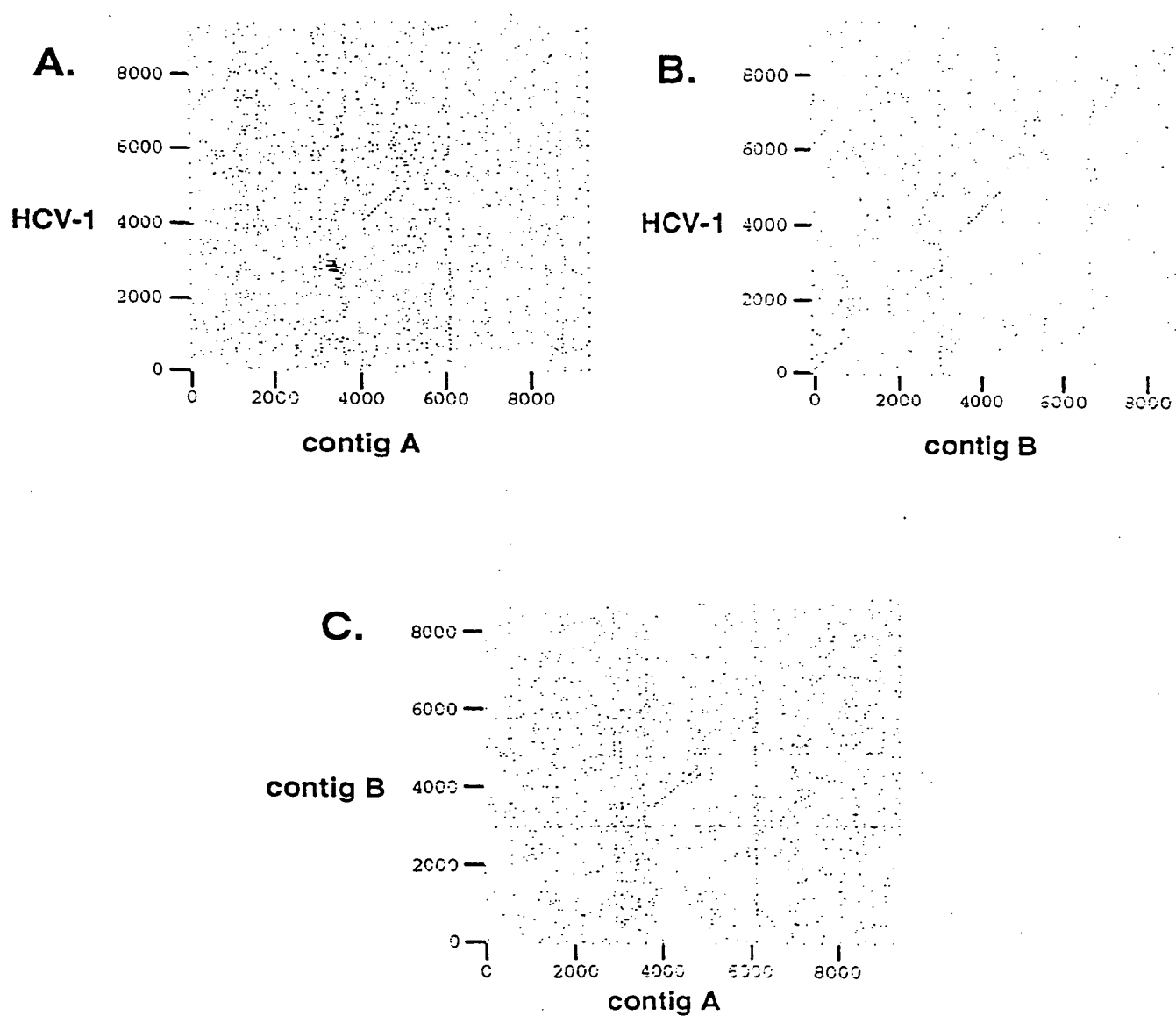
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FIGURE 22



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FIGURE 23



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FIGURE 24

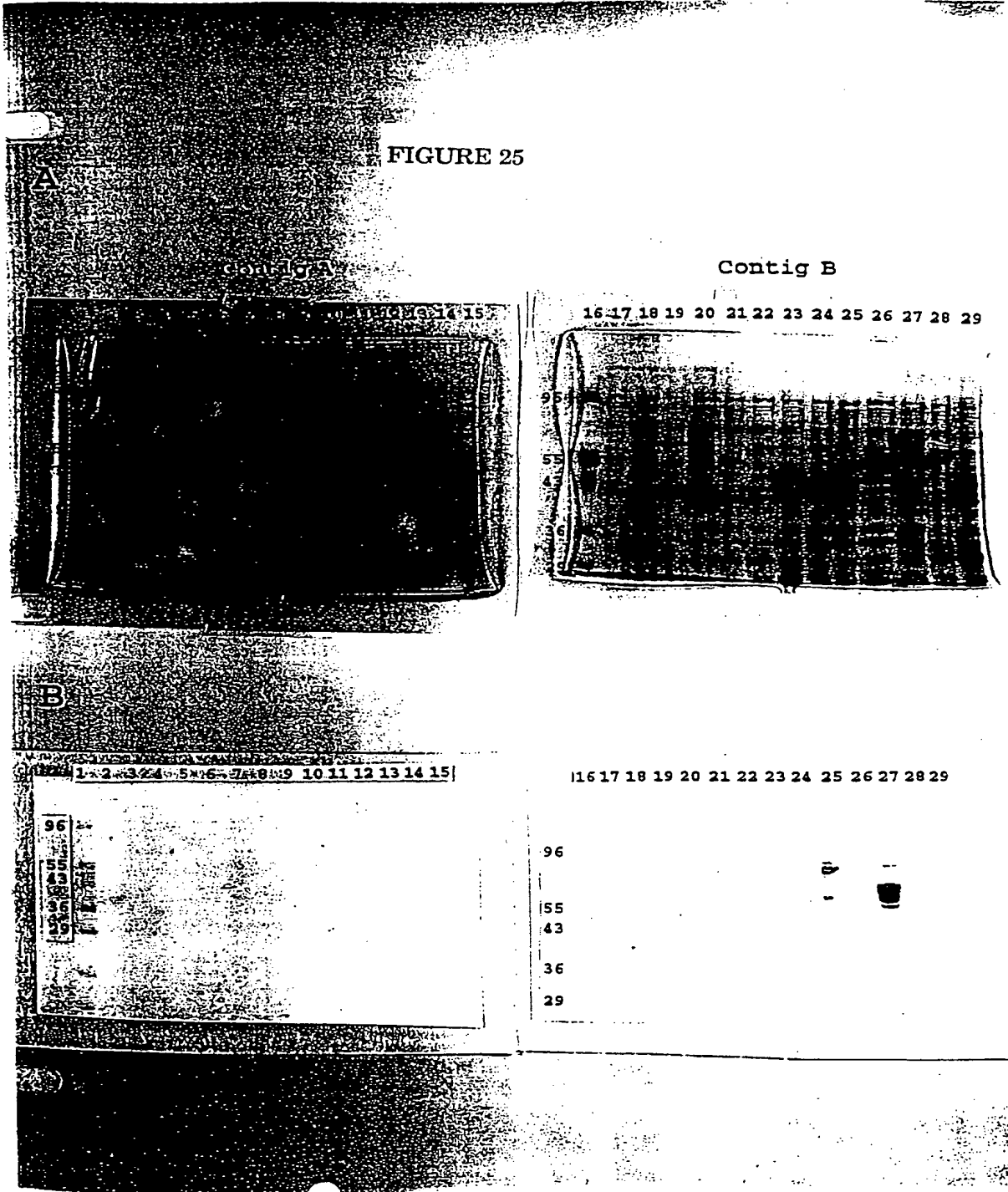
A.

Contig B SEQ ID# 166(1297)	MYL..TGRCS	RNYDVIICDE	CHATDRTTVL	GIGKVLTEAP	SKNVRLVVLA
HCV-1 SEQ ID# 179(1298)	KFLADGGCSG	GAYDIIICDE	CHSTDATSIL	GIGTVLDQAE	TAGARLVVLA
Contig A SEQ ID# 157(1407)	RFMANPRKYL	RGNDVVICDE	LHVTDPTSIL	GMGRARLLAR	ECGVRLLLFA
Consensus	-----	---D---ICDE	-H-TD-T--L	G-G-----A-	----RL---A
			** *		
Contig B SEQ ID# 166(1345)	TATPPGVIPT	PHANITEIQL	TDEGTIPFHG	KKIKEENLKK	GRHLIFEATK
HCV-1 SEQ ID# 179(1348)	TATPPGSVTV	PHPNIEEVAL	STTGEIPFYG	KAIPLEVIKG	GRHLIFCHSK
Contig A SEQ ID# 157(1457)	TATPPVSPMA	KHESIHEEML	GSEGEVPFYC	QFLPLSRYAT	GRHLIFCHSK
Consensus	TATPP-----	-H--I-E--L	---G--PF--	-----	GRHL-F---K
	***	*			
Contig B SEQ ID# 166(1395)	KHCDELANEL	ARKGITAVSY	YRGCDISKMP	.EGDCVVVAT	DALCTGYTGD
HCV-1 SEQ ID# 179(1398)	KKCDELAACL	VALGINAVAY	YRGLDVSVIP	TSGDVVVVAT	DALMTGYTGD
Contig A SEQ ID# 157(1507)	VECTRLSSAL	ASFGVNTVVY	FRGKETDI..	PTGDCVCVCAT	DALSTGYTGN
Consensus	--C--L---L	---G---V-Y	-RG-----	--GD--V-AT	DAL-TGYTG-
	*			*	*
Contig B SEQ ID# 166(1444)	FDSVYDCSLM	VEGTCHVDLD	PTFTMGVRVC	GVSAIVKGQR	RGRTGRGRAG
HCV-1 SEQ ID# 179(1448)	FDSVIDCNTC	VTQTVDVSLD	PTFTIETITL	PQDAVSRTQR	RGRTGRGKPG
Contig A SEQ ID# 157(1555)	FDTVTDCGLM	VEEVVEVTLD	PTITIGVKTV	PAPAEALRAQR	RGRCGRGKAG
Consensus	FD-V-DC---	V-----LD	PT-T-----	---A---QR	RGR-GRG--G
	*			*	***

B.

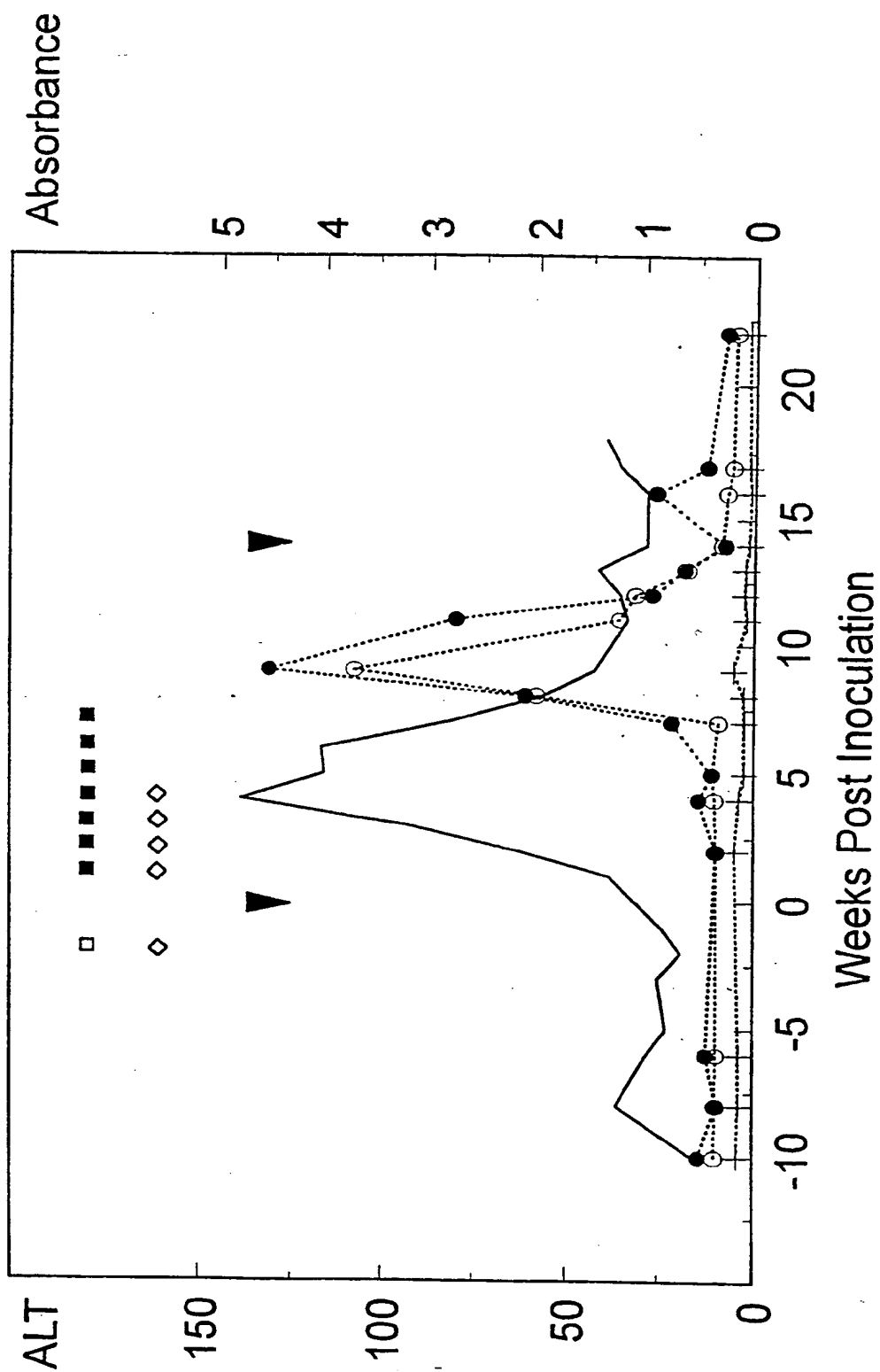
Contig B SEQ ID# 166(2599)	AAKLSQHR	GIHTIARQYH	AGGPMIAYDG	REIGYRRCRS	SGVYTTSSSN
HCV-1 SEQ ID# 180(2662)	CCDLDPQARV	AIKSLTERLY	VGGPLTNSRG	ENCGYRRCRA	SGVLTSSCGN
Contig A SEQ ID# 157(2798)	AA...SDNPS	MVHALC.KYY	SGGPMVSPDG	VPLGYRQCRS	SGVLTSSAN
Consensus	-----	-----	-GGP-----G	---GYR-CR-	SGV-TTS--N
				*	* *
Contig B SEQ ID# 166(2649)	SLTCWLKVNA	AAEQAGMKNP	RFLICGDDCT	VIWKSAGADA	DKQAMRVFAS
HCV-1 SEQ ID# 180(2712)	TLTCYIKARA	ACRAAGLQDC	TMLVCGDDL	VICESAGVQE	DAASLRAFTE
Contig A SEQ ID# 157(2844)	SITCYIKVSA	ACRFVGIKAP	SFFIAGDDCL	IYENDGTDP	CPALKAALAN
Consensus	--TC--K--A	A-----G----	-----GDD--	-I-----G----	-----

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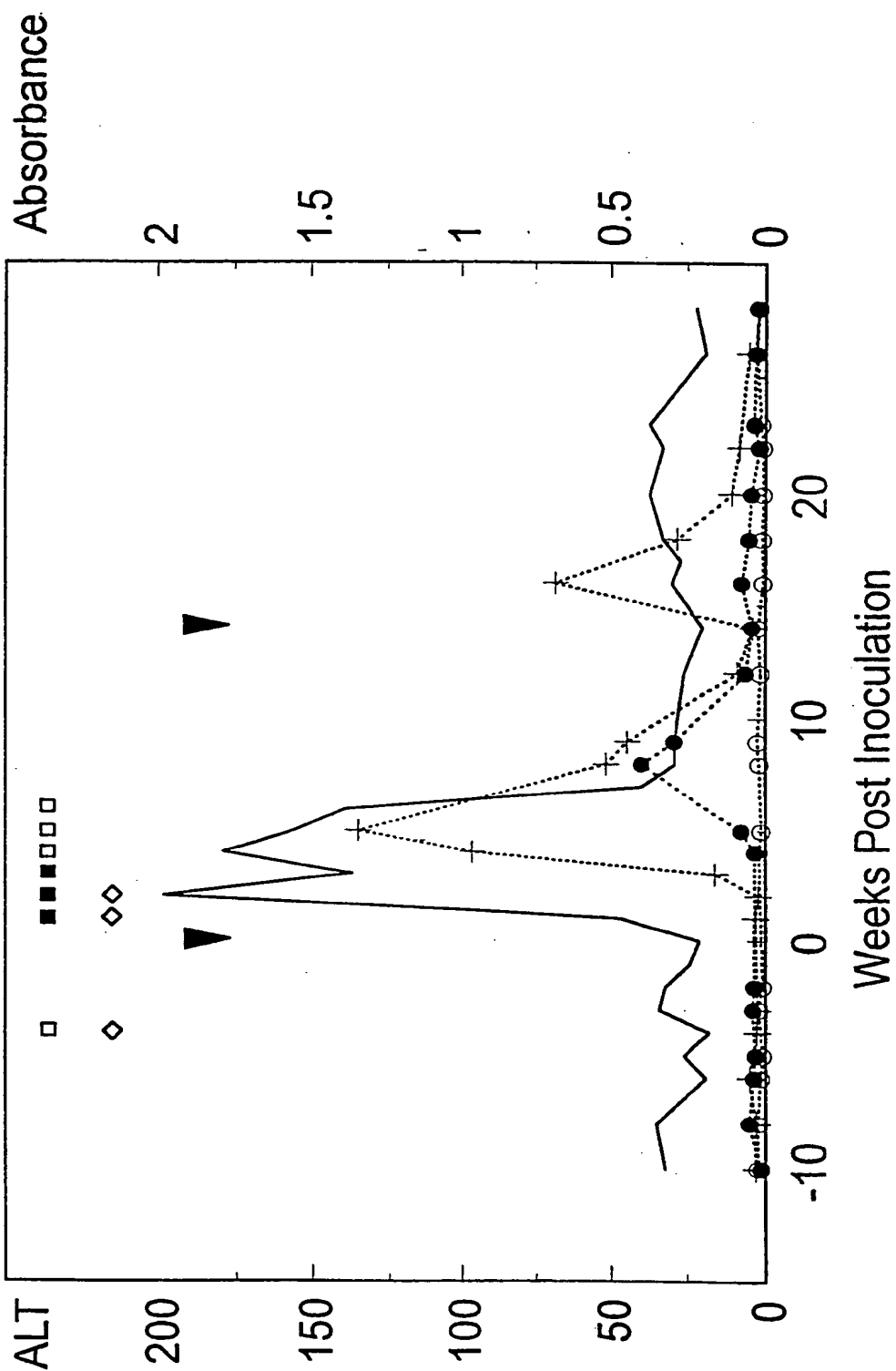
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FIGURE 26



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FIGURE 27



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FIGURE 28

